Midwest Geobiology Symposium 2025
Program Booklet

Purdue University
West Lafayette, IN
September 26-27th, 2025

PURDUE UNIVERSITY | Department of Earth, Atmospheric, and Planetary Sciences

Welcome to Purdue University!

We are thrilled to host the 13th annual Midwest Geobiology Symposium here in West Lafayette, Indiana, a campus known as the cradle of astronauts and a hub for Earth, planetary, and life sciences. This year's meeting continues the tradition of bringing together early career researchers and established scientists from across the Midwest to explore the vibrant, interdisciplinary world of geobiology.

Our goal is to provide a collegial and inclusive space to share cutting-edge science, exchange ideas, and foster community across departments, disciplines, and institutions. The Midwest Geobiology Symposium has grown steadily since its founding in 2012 at Washington University in St. Louis. What began as a small gathering of 50 participants has evolved into a diverse network of students, postdocs, and faculty united by curiosity about how life and planetary environments interact and co-evolve.

This year's program will bring together over 100 undergraduate and graduate students, postdocs, research scientists, and professors! MWGB 2025 will feature 64 abstracts from 22 institutions, covering a wide range of geobiological topics from field-based studies to experimental and theoretical work. We are proud to showcase the voices and visions of the next generation of geobiologists, and we thank you for being part of it.

We gratefully acknowledge the generous support of our sponsors:
The Agouron Institute
Purdue University Department of Earth, Atmospheric, and Planetary Sciences
Purdue College of Science
The Paleontological Society

We're so glad you're here and look forward to a weekend of scientific exchange and community building!

Sincerely,
The 2025 Midwest Geobiology Symposium Organizing Committee

Emily Apel, Roger Bryant, Ashika Capirala, Émilie Laflèche, Stephanie Olson, Isabelle Rein (lead organizer), and Mia Trodden

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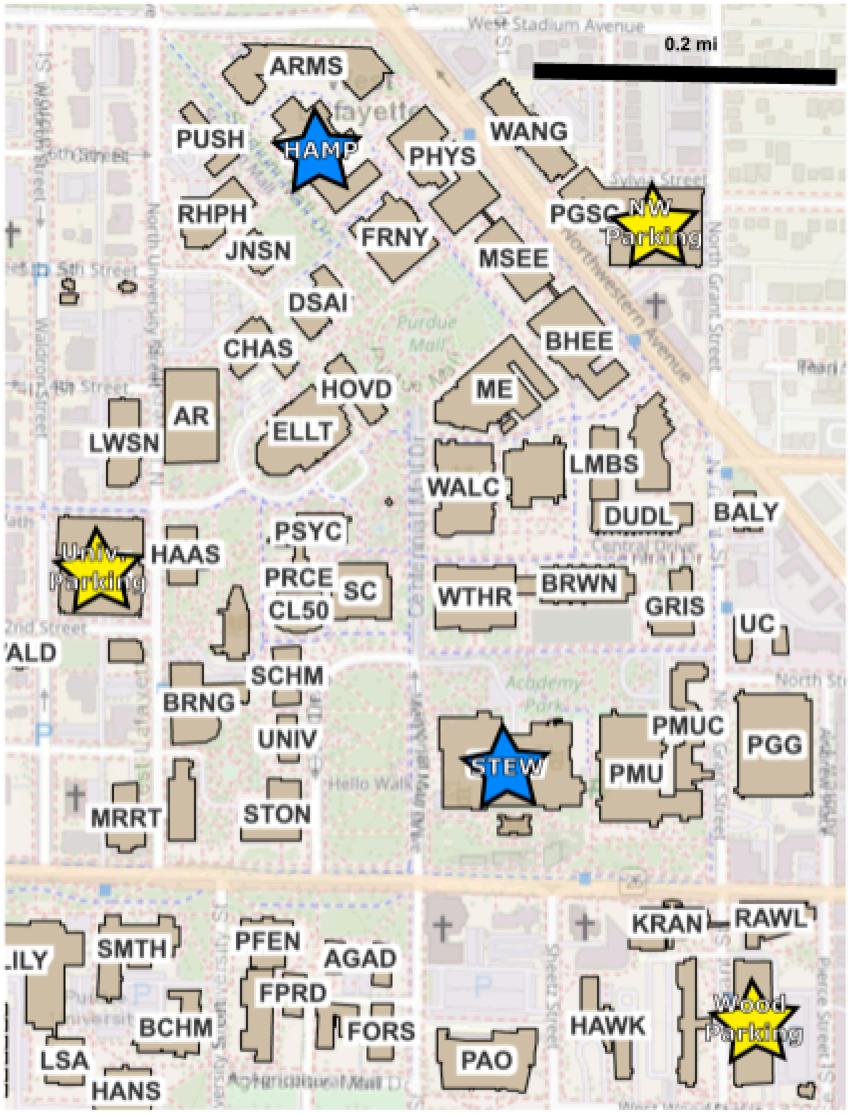
Campus Locations and Parking Maps

September 26th:
We will host this year's Social event at Ripple & Company in downtown Lafayette, IN. Food, drink, and good vibes will be provided! The restaurant is 2 miles from the Purdue campus. Street parking is available throughout downtown Lafayette in addition to a small free parking lot on the corner of Main and 11th Street.

September 27th:
The Symposium will take place in the Stewart Center on the Purdue University's Campus on September 27. Please join us starting at 8:30am in Room 214 for Opening Remarks and a light breakfast to kick off a day full of exciting science! Oral presentations will be given in the lecture hall Room 218. Poster presentations will be set up in Room 214.



Parking Information:
Three parking garages are nearest to the Stewart Center and offer **free weekend** parking:

Northwestern Avenue Parking Garage
504 Northwestern Avenue

University Street Parking Garage
201 North University Street

Wood Street Parking Garage
120 South Grant Street

Additional visitor parking is available at the Grant Street and Harrison Street parking garages at posted hourly rates. Day passes can be purchased online at www.purdue.edu/parking.

Schedule of Events

Friday September 26, 2025

6:00pm-10:00pm	Welcome Reception!	Ripple & Company: Upstairs

Saturday, September 27, 2025

8:30am-8:45am	**Continental Breakfast**	**Stewart Center Room 214**
8:45am-8:50am	**Opening Remarks** *Roger Bryant*	**Stewart Center**
8:50am-9:15am	**Keynote Presentation** *Stephanie Olson*	**Stewart Center**
9:15am-10:00am	Oral Session I	Stewart Center
10:00am-10:15am	Coffee Break	Stewart Center
10:20am-11:20am	Oral Session II	Stewart Center
11:25am-11:40am	Break	Stewart Center
11:40am-12:40pm	Poster Session I	Stewart Center
12:40pm-1:45pm	**Lunch**	**Stewart Center**
1:45pm-2:50pm	Oral Session III	Stewart Center
2:50pm-3:05pm	Coffee Break	Stewart Center
3:05pm-4:05pm	Poster Session II	Stewart Center
4:05pm-4:20pm	Break	Steward Center
4:20pm-5:20pm	Oral Session IV	Stewart Center
5:20pm-5:30pm	**Concluding Remarks**	**Stewart Center**

Order of Speakers
Sequence of Oral Presentations

Session 1 (9:15 AM - 10:00 AM):

- Dongyi Guo - Responses of Methanogens to Exogenous Metallophores with Dissolved and Mineral-Based Trace Metal Sources
- Pablo Almela - Pigment variations in snow algae and its impact on snowpack energy balance
- Christopher Hansen - Using Naled Ice to Access Winter Microbial and DOM Composition Beneath the Western Greenland Ice Sheet

Session 2 (10:20 AM - 11:20 AM):

- Afrid Abdaly Sheik - δD, $\delta'^{18}O$, and $\Delta'^{17}O$ Variations in Hydrothermal Minerals of the Miocene Geitafell Central Volcano, Iceland
- Haleigh Nyberg - Quantifying Planetary Origin of Life Potential: Connecting Global Climate to Local Wet Dry Cycling on Volcanic Islands
- Abigail Santis - Explorations of ~40 kyr biomarker records from Loktak Lake, India: Insights to Indian summer monsoon dynamics
- Katherine Quinlan - Spatial and Temporal Variability in Groundwater Oxidation-Reduction Chemistry and Microbiological Function

Session 3 (1:45 PM - 2:45 PM):

- Jordan Todes - Local and diagenetic restructuring of carbonate geochemistry shapes Early Triassic carbon cycle instability
- Emily Apel - Diagenetic or Not: Addressing the Effects of Diagenesis on Carbon Isotopes in PETM Planktic Foraminifera from Walvis Ridge with Secondary Ion Mass Spectrometry
- Kayla McCabe - Constraining the Temporal and Environmental Window for Waulsortian Mound Growth: Geochemical Signals from the Tournaisian Carbon Isotope Excursion
- John Herring - Exploring Marine Nitrogen Cycle Feedbacks in Phanerozoic Hothouse Climates

Session 4 (4:15 PM - 5:15 PM):

- Michelle Chamberlain - The Influence of Iron on Cyanobacteria Activity in a Precambrian Ocean Analog
- Diana Velazquez - Ancient Lakes as Archives of Earth's Oxygenation and Alkalinity Through Time
- Emilie Lafleche - Dissolved O2 Seasonality Impacted the Emergence and Diversification of Ediacaran Fauna
- Holly Rucker - Reconstructed Ancient Nitrogenases Preserve Canonical Isotopic Signatures Over 2 Billion Years

Sequence of Poster Presentations

Session 1: Tobi Hammond, Katherine Sluder, Sydney Williams, Dibya Chakraborty, Abigail Reed, Jennifer Melara-Valle, Adrián González, Chiza Mwinde, Yu Peng, Alessandro Mauceri, Bethany Egge, Mariana Aguilar, Maggie Hinkston, Mia Trodden, David Zakharov, Brianna Orrill, Hanna Konavaluk, Sarah Gonzalez Henao, Chris Greidanus, Meera Shah, Jennifer Houghton, Ishaan Madan, Jonathan Jernigan

Session 2: Mahalia Patrick, Paige Kohler, Therra Wilbrandt, Owen Madsen, Isabelle Rein, Paige Havener, Mercedez Hanlon, Kaydra Barbre, Samuel Fowler Hall, Naomy Aviles-Diaz, Henry Dawson, Kaitlin Koshurba, Ashika Capirala, Bavan Rajan, Elise Neal, Siruo Chen, Kayla Blair, Aya Klos, Farhan Bhuiyan, Abby Hartzer, Dominique Kelly, Raechel Hearth, Margo Crothers.

Oral Presentation Abstracts

Responses of Methanogens to Exogenous Metallophores with Dissolved and Mineral-Based Trace Metal Sources

Dongyi Guo,[1] Yizhi Sheng,[2] Jack Verbrugge,[1] and Hailiang Dong[1]

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Metallophores are biological exudates that enhance metal bioavailability by forming strong complexes with dissolved metals or promoting mineral dissolution. While many bacteria can utilize external metallophores ("xenometallophores") for trace metal acquisition, the response of methanogens, among Earth's earliest microbes, to exogenous metallophores remains unclear. In this study, we examined how the model methanogen *Methanosarcina acetivorans* responds to two metallophores, catecholate protochelin and hydroxamate desferrioxamine B (DFOB), under varying trace metal conditions. Our results demonstrated that *M. acetivorans* could not directly utilize metallophores or metal–metallophore complexes, as evidenced by reduced cell growth, methanogenesis, and nitrogen fixation efficiency when metallophores were introduced. This aligns with the absence of transport systems for metallophores or metal-metallophore complexes in *M. acetivorans*. However, although *M. acetivorans* was able to utilize metals from basalt and molybdenite for growth, different cellular responses were observed when metallophores were introduced in the presence of these solid mineral sources. In basalt treatments, both metallophores no longer inhibited growth, likely due to enhanced mineral dissolution by metallophores with the release of free trace metals. In contrast, with molybdenite as the sole Mo source, high concentrations of metallophores still inhibited growth, while lower concentrations had minimal effect, potentially due to Fe limitation caused by metal-metallophore complexation. Transcriptomic analysis revealed upregulation of genes related to nitrogen fixation and methanogenesis in the presence of basalt or molybdenite. The addition of protochelin or DFOB altered the expression of genes related to metal transport and energy metabolism, correlating with observed shifts in growth and metabolic activities. These findings provide new insights into methanogen metal acquisition in complex environments, enhancing understanding of early nitrogen fixation, microbial interactions, and microbe-mineral co-evolution.

Pigment variations in snow algae and its impact on snowpack energy balance

Pablo Almela,[1] James J. Elser,[2] and Trinity Hamilton[1]

[1] Department of Plant and Microbial Biology, University of Minnesota
[2] Flathead Lake Biological Station, University of Montana

In this study, we examined the reflectance, pigment composition, and community composition of three snow algae blooms showing distinct colors in the same snowfield in Glacier National Park (USA). Each color bloom was dominated by a different algae, each exhibiting a unique pigment signature but with astaxanthin as the predominant pigment across all three blooms. The spectral reflectance of red snow algae was consistently lower than that of green algae, while orange algae had intermediate reflectance values. Specifically, red algae reduced reflectance by approximately 55% across the PAR range, while green algae reduced reflectance by 25%. Red algae also demonstrated the highest radiative forcing, double that of green algae, leading to increased energy re-emission into the surrounding environment, which likely contributes to the localized melting of adjacent ice crystals. The high absorbance around 680 nm in cells with high astaxanthin content, such as the orange algae, suggests that semi-automatic detection methods could effectively identify these algae, as their spectral features remain distinct despite the presence of secondary carotenoids. Our data demonstrates the impact of snow algae taxonomic and pigment composition on the radiative balance of snowfields, underscoring taxonomy as a key determinant of bloom color under similar environmental conditions.

Using Naled Ice to Access Winter Microbial and DOM Composition Beneath the Western Greenland Ice Sheet

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Seasonal melting changes both the source and chemistry of water beneath glaciers descending from the Greenland Ice Sheet (GrIS). These shifts influence microbial communities and the predominant forms of dissolved organic matter (DOM) in subglacial meltwater. In summer, surface meltwater reaches the glacier bed, accelerates erosion, increases subglacial flow, and delivers labile DOM. During winter, flow decreases, and flowpaths become more isolated. While summer conditions are well-studied, subglacial environments remain difficult to access and characterize during the winter. Studying these systems can improve models of year-round biogeochemical cycling, better constrain subglacial DOM bioavailability, and explore how microorganisms could have persisted during global glaciation (e.g., Snowball Earth). To address this gap, we investigate whether naled ice, formed when subsurface water upwells and freezes in glacier forefields, contains a distinct microbial and DOM signal reflecting winter conditions beneath the GrIS. Specifically, we compared microbial and DOM composition in naled ice to spring and fall meltwater from Isunnguata Sermia, a land-terminating glacier in western Greenland, to (i) determine if there are seasonal shifts in microbial community composition and DOM signatures and (ii) test whether naled ice can serve as a record of winter ecosystems. Our analysis of 16S rRNA amplicon sequences and fluorescent DOM metrics – with FT-ICR MS analysis underway – suggests that naled ice contains inputs from diverse water sources across core depth and location in the forefield. Nevertheless, certain microbial and DOM profiles differ from those in both spring and fall meltwater. These findings support the use of naled ice as a tool for accessing and studying subglacial winter conditions.

δD, $\delta'^{18}O$, and $\Delta'^{17}O$ Variations in Hydrothermal Minerals of the Miocene Geitafell Central Volcano, Iceland

Afrid Abdaly Sheik,[1] *David Zakharov,*[1] *Mark H Reed,*[2] *and Elizabeth A. Bell*[3]

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Geothermal energy systems, active volcanism, and associated hydrothermal circulation are key drivers of Earth's heat and fluid transfer, ore deposit formation, and the sustenance of subsurface microbial ecosystems. Understanding the coupling between magmatism, meteoric water infiltration, and mineral alteration is essential for constraining the physical and chemical evolution of magmatic hydrothermal systems and its role in supporting life. The 6 Ma Geitafell central volcano in SE Iceland provides a well-exposed setting to investigate these processes, with intrusive complexes, host basalts, and a well-characterized meteoric water source ($\delta D = –60 \pm 10$ ‰, $\delta'^{18}O = –8 \pm 1$ ‰, $\Delta'^{17}O = +0.030 \pm 0.01$ ‰).This study maps δD, $\delta'^{18}O$, and $\Delta'^{17}O$ in altered minerals from intrusive and surrounding basaltic rocks to reconstruct the hydrothermal alteration history. Petrography and cathodoluminescence imaging of quartz, combined with sampling up to 4 km from the intrusion, constrain thermal gradients. Whole-rock $\delta'^{18}O$ values range from –6.3 ‰ to +2.0 ‰ with $\Delta'^{17}O$ between –0.048 ‰ and –0.013 ‰. Epidote and garnet have $\delta'^{18}O$ between –6.9 ‰ and +0.4 ‰ and $\Delta'^{17}O$ from +0.005 ‰ to +0.030 ‰, consistent with water–rock exchange at ~150–500 °C and water–rock ratios ≥ 1.5. Quartz $\delta'^{18}O$ ranges from –2.3 ‰ to +7.6 ‰ with $\Delta'^{17}O$ from –0.021 ‰ to +0.019 ‰, corresponding to ~130–477 °C. Isotope disequilibrium in quartz–epidote pairs, supported by SIMS $\delta^{18}O$ variations (–4.1 ‰ to +6.3 ‰) across 100–500 µm, reflects episodic low-temperature quartz precipitation. Gabbroic intrusions contain clinopyroxene and plagioclase with $\delta'^{18}O$ from –1.8 ‰ to +4.7 ‰ and $\Delta'^{17}O = –0.020$ ‰, indicating isotopic overprinting by fine-grained replacement in the presence of meteoric water. These results document a magmatic–meteoric hydrothermal system with high fluid flux and prolonged isotopic exchange, providing constraints on heat transfer, mineral alteration pathways, and potential subsurface habitats in volcanic–hydrothermal environments.

Quantifying Planetary Origin of Life Potential: Connecting Global Climate to Local Wet Dry Cycling on Volcanic Islands

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The chemical evolution within "warm little ponds" is a critical factor in theories for an origin of life, particularly regarding the synthesis of RNA via wet-dry cycles [1, 2]. Large-scale climate heavily influences the appearance, frequency, and timing of such cycles. This work investigates this connection by modeling the chemistry of freshwater ponds on volcanic islands, tracking organic concentrations from sources like meteorites and atmospheric haze against sinks like seepage and UV destruction [2]. To determine the influence of global planetary parameters, we drive our pond chemistry model with climate data from ExoPlaSim, a general circulation model. We specifically test how varying a planet's obliquity impacts local precipitation and temperature, which in turn controls the frequency of wet-dry cycles and the stability of organics. Our results show that obliquity's control over stellar flux distribution leads to dramatic variations in pond organic concentrations. Through this work, we aim to develop the Origin of Life Index (OLI) to quantify these effects across latitudes and obliquity scenarios with future plans of expanding to include similar investigations of other planetary scenarios, ie, varying eccentrcity and rotation rates.

References:

[1] Pearce, B. K. D., et al. 2017, PNAS, doi: 10.1073/pnas.1710339114
[2] Damer, B., & Deamer, D. 2020, Astrobiology, 20, doi: 10.1089/ast.2019.2045

Explorations of ~40 kyr biomarker records from Loktak Lake, India: Insights to Indian summer monsoon dynamics

Abigail Santis,[1] Bronwen Konecky,[1] Jack Hutchings,[1] Choudhurimayum Pankaj Sharma,[2] Yengkhom Raghumani Singh,[3] Aubrey L Hillman,[4] and Mark B Abbott[2]

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The Indian Summer Monsoon (ISM) plays a significant role in atmospheric circulation and precipitation dynamics across the Indian Ocean and subcontinent, and provides >70% of annual precipitation to the billions of people living in the monsoon domain. Existing records of ISM variability during the late Quaternary come predominantly from marine sediments and speleothems, with few lake records and sparse coverage prior to the Last Glacial Maximum. Lipid biomarkers in lacustrine sediment serve as valuable tools for reconstructing paleoenvironmental information throughout time. Here we present new ~40,000 year biomarker records of climatic and environmental change from Loktak Lake in the Imphal Basin of India (24.5593° N, 93.8147° E), the largest freshwater lake in NE India. We purified samples to target a variety of biomarkers including n-alkanes, fatty acid methyl esters (FAMEs), and polycyclic aromatic hydrocarbons (PAHs). We present initial results of leaf wax hydrogen (δD_{wax}) and chain length distributions to reconstruct changes in the ISM and the lacustrine environment over time. The δD_{wax} record from C_{29} n-alkanes reveals strong millennial-scale variability at the start of the record during late MIS3, and a large shift towards more depleted values toward the end of the last deglaciation, suggesting a transition to wetter conditions toward the end of the glacial period. Leaf wax n-alkane chain length distributions suggest substantial shifts in aquatic and terrestrial ecosystems at Loktak Lake throughout the record corresponding to fluctuating lake levels. We utilize these initial results to improve our knowledge of environmental changes at Loktak Lake, and compare with other records from the region to further understand monsoonal dynamics across the Indian subcontinent.

Spatial and Temporal Variability in Groundwater Oxidation-Reduction Chemistry and Microbiological Function

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More than 1 million wells across the Lower Peninsula of Michigan provide access to clean drinking water in the form of shallow groundwater in the Glacial Drift, Saginaw, and Marshall aquifers. Near the central part of the state, groundwater recharge captures young (decades-old) groundwater, potentially influenced by recent conditions at the land surface. As flow progresses towards the Great Lakes, groundwater from the same aquifers bears mean ages of 10's of thousands of years before present [1, 2]. These parcels of water are imprinted by the subsurface environment while microbial processes influence the in situ reduction-oxidation (redox) chemistry of the water as it travels. 42 groundwater wells of various ages and locations were sampled to understand how redox chemistry and microbial metabolism changes across this continuum. Water parameters, including dissolved oxygen, oxidation-reduction potential (ORP), pH, and conductivity, were measured on-site using an EXO3s Sonde probe. Major nutrients and redox-sensitive metals, such as Fe and Mn, were determined using ion chromatography and inductively coupled plasma mass spectrometry, respectively. Additionally, the abundance and oxidation state of iron and sulfur compounds were assessed through colorimetric analyses. Microbiological analyses, including 16S rRNA Amplicon sequencing and shotgun metagenomic analysis was performed using Illumina Sequencing. Preliminary results showed a range of redox conditions in both young and old groundwater. Young groundwater showed dissolved oxygen concentrations ranging from oxic to anoxic, potentially related to local geochemistry and subsurface microbiological activities. Additionally, ferrous iron and total sulfide measurements showed little to no correlation with groundwater age. Amplicon sequencing of the 16S rRNA gene showed a positive correlation between putative iron and sulfur cycling organisms and sulfate concentrations. These results imply that microbial metabolisms are more clearly linked to redox conditions than groundwater age.

References:

[1] Wen T., Castro M. C., Hall C. M., Pinti D. L. and Lohmann K. C. (2016) Constraining groundwater flow in the glacial drift and saginaw aquifers in the Michigan Basin through helium concentrations and isotopic ratios. *Geofluids* 16, 3–25.

[2] Ma L., Castro M. C. and Hall C. M. (2004) A late Pleistocene-Holocene noble gas paleotemperature record in southern Michigan. *Geophys. Res. Lett.* 31.

Local and diagenetic restructuring of carbonate geochemistry shapes Early Triassic carbon cycle instability

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Our understanding of Earth history heavily relies upon carbonate geochemical records, but it is often challenging to decipher the extent to which they reflect global paleoenvironmental patterns. This is especially true within the Early Triassic, which records substantial carbon cycle instability during the protracted recovery from the end-Permian mass extinction. As conventionally interpreted, these unusually large and rapid $\delta^{13}C_{carb}$ excursions are commonly linked to seawater $\delta^{13}C_{DIC}$ variability, interpretations of which rely on the faithful preservation of globally representative $\delta^{13}C_{carb}$ values. However, both local variations in seawater chemistry and the ubiquity of early marine diagenesis in shallow-water carbonates may appreciably impact preserved carbonate geochemistry, and disentangling these signatures is crucial for understanding observed Early Triassic carbon cycle instability. Here, we leverage a carbonate geochemical framework to decipher potential local and diagenetic influences on geochemical records from the Great Bank of Guizhou (south China), a carbonate platform that forms the backbone of Early Triassic chemostratigraphic records.

During the Induan, $\delta^{13}C_{carb}$ values vary by up to 5‰ from the platform top to the basin, with this gradient largely disappearing after the early Olenekian. Calcium isotope records reveal comparable patterns: $\delta^{44/40}Ca$ values vary by 1‰ across the platform in the Induan, consistent with the preservation of aragonite to primary (or partially neomorphosed) calcite sediments. Subsequently, $\delta^{44/40}Ca$ values increase towards inferred Triassic seawater $\delta^{44/40}Ca$ values in the early Olenekian, driven by early marine diagenetic resetting that would have influenced associated $\delta^{13}C_{carb}$ records. These results suggest that the Guizhou $\delta^{13}C_{carb}$ records may reflect a combination of local, facies-related controls (Induan), and early-marine diagenetic resetting (Olenekian), with this shift likely driven by the development of significant platform-to-basin architectural relief in the early Olenekian. These findings collectively underscore the importance of deconvolving facies-specific and diagenetic signatures in carbonate geochemical records prior to inferring global palaeoceanographic trends.

Diagenetic or Not: Addressing the Effects of Diagenesis on Carbon Isotopes in PETM Planktic Foraminifera from Walvis Ridge with Secondary Ion Mass Spectrometry

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The magnitude of the global, negative carbon isotope excursion (CIE) during the Paleocene-Eocene Thermal Maximum (PETM; ca. ~56 Ma) varies within and between different sedimentary archives. The excursion has been linked to a rapid release of isotopically light carbon into the atmosphere and oceans, which resulted in widespread warming and ocean acidification. This has made it challenging to estimate the size of the CIE in the global dissolved inorganic carbon (DIC) reservoir, as mechanisms like dissolution and diagenesis could have artificially lowered the magnitude of the CIE in the marine record. Here, we employ Secondary Ion Mass Spectrometry (SIMS) on planktic foraminifera from ODP Site 1263 at Walvis Ridge in the southeast Atlantic to characterize the effects of diagenesis on the $\delta^{13}C$ record. SIMS allows us to perform multiple $\delta^{13}C$ measurements within a single foraminiferal shell while avoiding material potentially compromised by poor preservation, providing detailed information on the stratigraphic signature of the CIE as well as inter- and intra-shell variability. Our results not only capture the CIE in our samples but also reveal distinct differences in the stratigraphic record depending on where in the shell the $\delta^{13}C$ was measured. Our analysis spots fall into three shell location categories- inner wall, outer wall, and exterior ornamentation, called muricae. We find that the shell wall tends to follow the bulk $\delta^{13}C$ record, while the muricae deviate from the bulk, particularly after the peak-CIE and in the recovery. We also observe a reversal in the offset between inner wall and muricae $\delta^{13}C$, where before and after the CIE the wall tends to be lighter than muricae, while during the event the opposite is true. This calls into question which part of the shell reflects the surface ocean CIE at the time of growth and which part has been compromised by diagenesis.

Constraining the Temporal and Environmental Window for Waulsortian Mound Growth: Geochemical Signals from the Tournaisian Carbon Isotope Excursion

Kayla McCabe and Selva Marroquín

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The Tournaisian Carbon Isotope Excursion (TICE) is one of the largest positive $\delta^{13}C$ excursions of the Phanerozoic (~7‰) and marks a major disruption to the global carbon cycle during the early Mississippian. A carbon cycle perturbation of this magnitude likely influenced biological, sedimentological, and geochemical processes across the Earth system. Previous studies have documented increased marine anoxia, shifts in reef-building communities, and the emergence of deeper-water microbial carbonate buildups (i.e., Waulsortian mounds) during this time. Yet despite broad interest, the temporal and geochemical feedbacks linking shifts in biological, carbonate sedimentation (i.e. Waulsortian mounds), and the TICE remain unresolved. Our data are the first to establish that mound emergence occurred in a discrete interval within the TICE, offering new insights into carbon cycle dynamics during the early Mississippian.

Here we present new $\delta^{13}C$ data from the Funeral Mountains of southern California that document the full duration of the TICE for the first time at this site. We find that Waulsortian mound development is stratigraphically restricted to the rising limb of the TICE and terminates before the brief return to lower $\delta^{13}C$ values that define the double-peaked structure of the excursion. Mounds are absent from both underlying and overlying beds, indicating that their formation was confined to a narrow window of elevated $\delta^{13}C$ values. Comparisons with other mound-bearing sections across most of North America reveal similar temporal restriction to the TICE, supporting the idea that mound development was potentially influenced by broader oceanographic conditions. Together, these results provide the foundation for establishing global carbon cycle Earth system feedbacks between the TICE, ocean geochemistry change (e.g. redox), and sedimentological shifts (e.g. deep water carbonate mounds).

Exploring Marine Nitrogen Cycle Feedbacks in Phanerozoic Hothouse Climates

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Nitrogen (N) couples atmospheric chemistry and biosphere evolution over deep time via marine biogeochemical N-cycling. Hence, modeling the marine N-cycle over Earth history may provide context for long-term biosphere evolution. Biogeochemical N-cycling rates are strongly dependent on temperature, yet the response of the marine N-cycle to Phanerozoic climate variability has not been fully resolved in extant N-cycle models for Earth history, especially at high temperatures. To fill this gap, we apply Earth-system box model of the N and phosphorus (P) cycles to account for effects of marine redox chemistry, pH, and global mean surface temperature (GMST) on biogeochemical rates over the Phanerozoic. To capture N-cycle variability at higher resolution, we impose independent forcings for state variables including GMST, marine pH, atmospheric pO_2, and paleogeography.

Our findings suggest that a hyperactive "hothouse N-cycle" in eutrophic, redox-stratified oceans may have characterized the warmest periods of the Phanerozoic. High GMST and pO_2 enhance biogeochemical rates of crustal P weathering, N_2 fixation, primary productivity, and nutrient recycling. Rapid regeneration of nitrogen oxides in the surface ocean supports intense denitrification in deep anoxic waters on longer timescales, while N_2 fixation ultimately balances this sink and sustains high [N] near the surface. The modeled ratio of N_2 fixation vs. incomplete water-column denitrification, which qualitatively controls marine $\delta^{15}N$ through time, responds strongly to GMST and shows trends in reasonable agreement with the sedimentary $\delta^{15}N$ record over the Phanerozoic.

Our results imply that the marine biological N-cycle is strongly amplified under hothouse conditions. Consequently, its interactions with the atmosphere intensify, both by increasing emissions of the greenhouse gas and ozone-destroying agent N_2O (leading to climate warming feedbacks and increased UV irradiation of surface ecosystems) and by sequestering N into the geosphere over deep time (leading to a decrease in atmospheric pN_2 and diminished climatic stability).

The Influence of Iron on Cyanobacteria Activity in a Precambrian Ocean Analog

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Cyanobacteria have been major primary producers throughout Earth's history and were ultimately responsible for the Great Oxidation Event (GOE) that occurred roughly 2.4 billion years ago. It is estimated that the first cyanobacteria may have preceded the GOE by at least half a billion years and one reason for the delay between their origin and the oxygenation of Earth's atmosphere may have been due to the limited availability of nutrients in the Archean Oceans. Ferruginous conditions persisted throughout the Precambrian Oceans, but they were redox stratified with Fe^{2+} titrated from surface waters as insoluble Fe^{3+} oxides due to oxygen production by ancient cyanobacteria. Because of this, it is possible that Fe limitation could have occurred in the surface ocean despite ferruginous conditions at depth. Here, we investigate the role of Fe in photosynthetic activity among cyanobacteria in a ferruginous Precambrian Ocean analog, Deming Lake (Itasca State Park, MN, USA). Deming Lake is characterized by a subsurface chlorophyll maximum layer (SCML) that corresponds to a maximum of photosynthetic cells at the base of the redoxcline. Because the SCML occurs where Fe concentrations increase, Fe may play a role in its formation. To determine how Fe impacts Deming Lake's SCML and early photosynthetic activity, we measured Fe uptake and photosynthetic activity in response to Fe additions across Deming Lake's redoxcline. We found that Fe additions led to an increase of intracellular Fe at all experimental depths and that it increased photosynthetic activity among *Pseudanabaena* and taxa rich in the pigment phycoerythrin at the SCML. Additionally, the isotopic composition of particulate and intracellular Fe at the SCML is consistent with biological Fe uptake. Lastly, we conducted metagenomic sequencing and found that *Pseudanabaena* lack transporters for Fe^{2+}. Together, this suggests that some cyanobacteria may be susceptible to Fe limitation under ferruginous conditions.

Ancient Lakes as Archives of Earth's Oxygenation and Alkalinity Through Time

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The widespread oxygenation of Earth's atmosphere fundamentally transformed the global carbon (C) and nitrogen (N) cycles. Although N-evolution through time is well documented in marine settings, lacustrine environments remain underexplored, despite their importance as shallow, transient systems that may have experienced oxygen fluctuations earlier than oceans. We compiled sedimentary carbon ($\delta^{13}C_{org}$) and nitrogen ($\delta^{15}N$) isotopes from modern anoxic ($n = 27$) and oxic ($n = 152$) lakes to determine how water column oxygen conditions may have impacted geochemical signals preserved in the rock record. For the entire modern lake dataset, the average and standard deviation for $\delta^{15}N$ is +2.9 ± 3.2‰ and -25.99 ± 3.77‰ for $\delta^{13}C_{org}$. Modern lake sediments exhibiting very negative (< -32‰) or positive (> -16‰) $\delta^{13}C_{org}$ values are characteristic of anoxic water columns, reflecting anaerobic metabolic processes that are often amplified by eutrophication. Within-site $\delta^{15}N$ variability typically falls within ~5‰ as observed within a single anoxic lake; however, both modern and ancient alkaline lakes exceed this range. Consistently high $\delta^{15}N$ values (> +10‰) in alkaline lakes (pH > 9) are preserved in both modern and ancient records, supporting previous studies of $\delta^{15}N$ as a robust proxy for past lake alkalinity. Unlike the marine record, in the ancient lacustrine record ($n = 27$ geologic units) the increase in $\delta^{15}N$ from the Archean (+0.1 ± 2.7‰) to the Cenozoic (+7.0 ± 1.4‰) coincides with the appearance of new enzymes involved in oxygen-dependent N-metabolic pathways. Lacustrine $\delta^{15}N$ signatures provide a powerful proxy for reconstructing past oxygen conditions and alkalinity, providing new insight into Earth's history that is not preserved in the marine record.

Dissolved O_2 Seasonality Impacted the Emergence and Diversification of Ediacaran Fauna

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The Ediacaran fauna emerged in a poorly-oxygenated surface ocean. There has been considerable debate surrounding potential links between environmental O_2 availability and increased biological complexity during the Ediacaran, but progress towards understanding these links has been complicated by the nature of our geochemical and fossil records. Geochemical proxies used to reconstruct Ediacaran O_2 record environmental conditions over timescales that exceed the lifetime of individual organisms, but dissolved O_2 in the Ediacaran surface ocean would have also varied on seasonal timescales. This may have placed important constraints on the regions in the surface ocean where Ediacaran fauna could persist and thrive over their lifetimes. Moreover, the magnitude of seasonal O_2 variations may have had distinct regional patterns, acting as a spatial environmental driver of biological stress and/or innovation.

To investigate this, we used cGEnIE, a 3D marine biogeochemical model, to simulate the spatial and temporal distributions of dissolved O_2 in the Ediacaran surface ocean. We modeled a range of Ediacaran atmospheric pO_2 estimates and continental configurations. We then quantitatively compared the distribution of fossils at sites in the Avalon, White Sea, and Nama assemblages to dissolved O_2 from our simulations to statistically evaluate the impacts of latitudinal and seasonal O_2 variability on taxonomic abundance and morphological diversity. We find that sites in low latitudes experience more consistent O_2 availability year-round and have higher taxonomic abundances than high-latitude sites. Additionally, fossils with high surface area-to-volume ratios (SA/V) in their body plans are strongly correlated with high-latitude sites experiencing highly seasonal O_2, suggesting that specific morphological characteristics enabled some Ediacaran fauna to thrive under short-term O_2 stress. We thus argue that environmental O_2 availability in space and time played a key role in early animal evolution.

Reconstructed Ancient Nitrogenases Preserve Canonical Isotopic Signatures Over 2 Billion Years

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Nitrogen isotope fractionation signatures have been preserved and recorded in the rock record for over 3 billion years. Of these signatures, some are the product of biological nitrogen fixation, specifically by the enzyme Mo-nitrogenase. Ancient nitrogen fixation signatures have been interpreted using the isotopic signatures of extant organisms, but it remains unclear how billions of years of biochemical evolution may have affected nitrogenase fractionation. In this study, we measure the N-isotope fractionation of ancestrally reconstructed Mo-nitrogenases in the biomass of the model nitrogen-fixing bacteria, *Azotobacter vinelandii*. The reconstructed ancestors in this study span most of the evolutionary timeline of Mo-nitrogenase, with the oldest ancestor dating back to the Great Oxidation Event (~2 billion years old). The results of this study suggest that the biological nitrogen fixation isotopic values of Mo-nitrogenase are robust to evolutionary change and have remained consistent since its early evolution.

Poster Presentation Abstracts

Session 1

Influence of Land Distribution on the Climate of Synchronously Rotating M-Dwarf Exoplanets

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With JWST and future telescopes' potential to characterize M-dwarf exoplanets, we must identify the geologic properties that determine habitability and their resulting observable signatures. Our current knowledge of the geologic processes, particularly silicate weathering, and their potential effects on habitability on a M-dwarf rocky exoplanet is limited. The silicate weathering cycle is a fundamental process that stabilizes Earth's climate over geologic timescales by modulating atmospheric pCO2. However, it is unclear whether this process will have the same effect on M-dwarf planets. We aim to investigate the influence of continental weathering on the climate and habitability of synchronously rotating M-dwarf planets. We use ExoPlaSim, a 3D global circulation model, to explore how the distribution and size of landmasses affect the long-term climate of TRAPPIST-1e. Ocean-dominated planets with a large dayside continent are more habitable than land-dominated planets with a dayside inland sea and are more sensitive to changes in atmospheric pCO2. A continent or inland sea centered on the nightside of an ocean- or land-dominated planet does not have a significant impact on the overall climate state. Understanding the processes that affect habitability, and climate is crucial for accurately predicting the characteristics of observed exoplanets with next-generation telescopes.

Nano-phases formed at redox interfaces in a sulfidic spring

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Colloids, small reactive solids in aqueous media, play a large role in the chemical and physical composition of ecosystems. Through the transport of nutrients, transport of sorbed organic matter, and serving as electron acceptors/donors, colloids influence organisms in groundwater ecosystems. Zodletone, an artesian euxinic spring in western Oklahoma, is a natural laboratory where we can study the composition of colloids, including transported colloids and nanophases formed at the redox interface of deep, reduced, S-rich waters with the surrounding meteoric groundwater. Zodletone acts as an analog site for early Earth and potential extraterrestrial ecosystems due to its combination of low oxygen and high sulfur content, and extremophilic organisms. Our research objective is to examine the distribution, mineralogy, chemistry, and textural relationships of colloids collected from groundwater wells at the Zodletone spring site. By examining the mineral components of this colloidal system using x-ray diffraction (XRD), scanning electron microscopy (SEM), and transmission electron microscopy (TEM), we have characterized the bulk colloidal composition and have begun to investigate individual particles and groundwater chemistry. Silicates (quartz, feldspars, and clays) and carbonates are present in all sediment and colloid samples; whereas sulfides, elemental sulfur, and sulfates are only present in the spring water impacted sediments and colloid samples. This suggests that the sulfides and sulfate minerals, pyrite, gypsum, and barite are formed through interactions at the euxinic-oxic interface and/or are transported with the spring water. Future work will clarify the abundance, mineralogy, and chemistry of groundwater colloids and groundwater chemistry across the site in relation to other biogeochemical and hydrological processes.

Reconstructing Historical Water Quality in Lakes Impacted by Coal Mining in Southern Vigo County, IN, Using Diatom Analysis

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Abandoned coal pits have a complex impact on water quality and aquatic life as they develop and are associated with unhealthy conditions such as elevated heavy metals. Fox and French Lake were part of the Chieftain No. 20 mine, which operated from 1933 to 1969, and Paint Mill Lake is a man-made reservoir with no mining association. Diatoms fossilized in the sediment can be analyzed to reconstruct historical water quality, ecological changes, and climate change in lake systems. We will be studying how the abandonment of coal pits, climate change, and how human use has affected the lakes' environmental conditions since their formation. Sediment cores were collected from the sites and divided into individual sub-samples for quantitative diatom and geochemical analysis on an X-ray fluorescence machine. Low-resolution counts were performed on the Fox Lake core, and our results show that the bottom of the core is dominated by species indicative of low to moderate nutrient availability, while the upper core is characterized by species of nutrient rich habitats. Our findings suggest that the lake had poor productivity and water quality after the mine's abandonment and has shifted to a productive, nutrient rich lake as people altered the surrounding landscape.

Nitrate Loss from a Drained Agricultural Watershed in Central Indiana: Effects of Crop Type and Hydrologic Flow Path

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Application of nitrogen (N) fertilizer in intensive agricultural systems has become a routine practice to increase crop productivity. Since growing crops can utilize a fraction of the N fertilizer applied, an appreciable amount of residual N can remain in the soil and become available for loss through surface runoff and subsurface leaching specially in the form of nitrate. This study was conducted in 2017-2018 at an agricultural field in the School Branch Watershed in Central Indiana (Brownsburg) under corn-soybean rotation. The amount of nitrate leaving the field through surface runoff and via sub-surface tile drainage was monitored in 2017 (corn year) and in 2018 (soybean crop). The rate of N fertilizer application was 150 kg N/ha during the corn year and 1.8 kg N/ha (as starter) during soybean. Surprisingly, nitrate flux was higher during the soybean (12.5 kg N/ha/yr) than during the corn year (3.1 kg N/ha/yr). The distribution of rainfall during those two seasons may have contributed to this unexpected result. The 2017 growing season was relatively dry (rainfall: 40 % below normal) which likely impeded N uptake by the corn crop. As a result, a significant amount of residual N fertilizer may have remained in the soil after corn harvest. Then, this residual N was leached out when normal precipitation returned during the fall of 2017 and winter/spring of 2018. These results illustrate the role of rainfall distribution on N loss from agro-ecosystems and underscore the need for long-term monitoring (over several years) to establish the effect of farming practices on N export.

Seasonal Uptake and Regeneration of Reduced Nitrogen in Western Lake Erie

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Lakes globally, including Lake Erie, are experiencing shifts in their winter conditions as the climate warms. Due to a historical lack of sampling in winter, the impacts of winter regime shift on seasonal patterns in nitrogen (N) cycling and phytoplankton communities is unknown. Changing winter conditions in Lake Erie may be impacting the availability of reduced forms of N, including ammonium and urea, for microbial communities. To examine shifts in cycling of inorganic and organic forms of reduced N in Western Lake Erie, whole community water column samples were collected using the City of Toledo Wastewater Treatment Plant's offshore raw intake line. We measured whole community rates of respiration, ammonium uptake and regeneration, and urea uptake and regeneration using 15N additions from December 2024-August 2025. We concentrated our study in Western Lake Erie to complement previously measured summer rates of N uptake and regeneration, particularly during cyanobacterial blooms. We report N uptake and regeneration rates under multiple notable conditions, including during under-ice diatom blooms and storm events. These are preliminary results from a larger project to document monthly N uptake and regeneration rates for two years to understand how N cycling varies between seasons.

How does the arctic lake morphology control freeze-thaw timing?

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Thermokarst lakes (TLs) are key indicators and drivers of Arctic climate change; their presence signals permafrost degradation, impacting landscape stability and altering hydrologic and ecological systems. TL morphometric characteristics vary greatly across the region, which has implications for climate change. However, scaling relationships between TL parameters such as area, perimeter, circularity, and depth, remain poorly constrained. These characteristics are thought to exert control over lake ice phenology, including the timing and duration of ice on/off periods, which influence biogeochemical processes such as methane emissions. While methods exist to predict the timing of lake freezing and thawing, simple empirical models based on temperature thresholds do not explicitly account for differences in lake morphology. Further, the role of lake morphology in controlling freeze-thaw timing is unquantified; especially in the Arctic Coastal Plain (ACP) on Alaska's North Slope, which features key infrastructure and economic resources. We aim to better constrain morphometric scaling relationships and identify morphology's influence on lake ice timing and duration.

We leverage existing lake inventories to extract morphometrics and constrain the size distribution of TLs in the ACP. We apply a deep learning model to identify the timing of ice on/ice off conditions using SAR polarimetric data. Using this spatially extensive, multi-year dataset we quantify the relationship between lake morphometrics and the timing of ice on/off conditions. Finally, we compare these direct observations to ice thickness estimates from the ERA5 climate reanalysis product and accumulated degree day of thaw and freezing models. Our analysis highlights important scaling relationships between lake morphometrics in Northern Alaska and their influence on lake ice conditions. This motivates a larger circumpolar study of TLs over the spectrum of permafrost landscapes to identify persistent TL morphometrics relationships and their influence on lake ice conditions, with implications for the role of TLs in accelerating future climate change.

Phylogenetic Insights into Nutrient Limitation: Mapping the History of Iron, Nitrogen, and Phosphorus Scavenging in Microbes

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Primary production on Earth, and thus the scope of the biosphere, is by the availability of key elements, including iron, nitrogen, and phosphorus. Geological studies and models have attempted to determine which of these nutrients was most likely limiting to the biosphere on a global scale through Earth history, but while it is possible to estimate the flux or abundances of specific elements on Earth at different points of Earth history, it is more challenging to assess which elements were specifically limiting to the biosphere given biological stoichiometry. Here, we use a phylogenetics approach to reconstruct the evolutionary history of nutrient scavenging genes as a means of identifying patterns in nutrient limitation over Earth history. We conducted a literature search to identify genes related to scavenging of iron, phosphorus, and nitrogen from the environment. Genes related to nutrient scavenging were grouped by substrate specificity (ferrous iron, ferric iron, nitrogen, and phosphorus) and mapped across bacterial and archaeal lineages to identify when gene deletions, duplications, horizontal gene transfers, and losses occurred. By reconstructing the changing availability of different nutrients over Earth's history, we aim to provide new insights into how evolving environmental conditions have shaped the adaptations and metabolic capabilities of microbes through deep time. Our results show slight differences in the relative timing for the emergence and rise of different nutrient scavenging genes over time, potentially revealing shifting nutrient demands as the Earth became more oxidized. Investigating the interplay between nutrient availability and metabolic evolution is key to understanding microbial responses to environmental change across deep time.

Calcium isotope fractionation in hypersaline lake microbial carbonates

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Calcium isotope ratios in sedimentary archives are a useful tracker of long-term changes in seawater chemistry. Calcium isotopes in evaporitic carbonates have been applied to constrain the calcium-to-alkalinity ratio (Ca:ALK) of seawater and, by extension, past ocean pCO_2 and pH[1]. However, the use of Ca isotopes in paleoenvironmental reconstructions requires a detailed understanding of the isotope fractionation mechanisms affecting sedimentary archives. For evaporitic settings in particular, experimental studies demonstrating Ca isotope behavior are limited. Therefore, alkaline lake environments provide natural systems where the relationship between $\delta^{44}/^{40}$Ca in carbonates and parent solution chemistry can be evaluated. Previous studies of Ca isotope fractionation in Mono Lake carbonates support the predicted behavior, showing that the magnitude of isotopic fractionation during calcium carbonate precipitation depends on the ratio of Ca to CO_3^{2-} in the parent solution[2]. Here we present preliminary Ca isotope results from microbial carbonates collected in high-altitude hypersaline lakes of the Argentine Puna (Laguna Negra, Laguna Diamante, and Carachi Pampa). These lakes span a broad range of Ca:ALK ratios and pH, offering a natural test of the predicted relationship between carbonate Ca isotope fractionation and solution stoichiometry. Initial data indicate variability in $\delta^{44}/^{40}$Ca across lake systems. Understanding the controls on Ca isotope fractionation may provide new insights into the relationship between the isotopic composition of carbonate minerals and paleoenvironmental conditions. Ongoing work will expand this dataset to further resolve the influences of Ca:ALK, microbial mediation, and local hydrologic conditions on Ca isotope behavior.

Increased soil greenhouse gas emissions from the combined use of cover crops and no-tillage in producer-managed fields

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The use of cover crops offers multiple benefits for agroecosystems, but is still an underutilized practice. Its combination with no-till (CCNT) is increasingly promoted to enhance system-level effectiveness. However, its impact on soil greenhouse gas (GHG) emissions remains a topic of debate. Existing studies are predominantly based on researcher-managed settings and often fail to assess all three major GHGs of carbon dioxide (CO_2), nitrous oxide (N_2O), and methane(CH_4). To address these knowledge gaps, this study conducted a 30-month field monitoring under producer-managed settings to quantify soil GHG emissions under CCNT compared to no-tillage (NT) alone. Results showed that CCNT increased soil global warming potential (GWP) by 15.2% relative to NT. CO_2 was the dominant contributor, accounting for 91.69% of the total GWP. On average, daily fluxes of CO_2, N_2O, and CH_4 under CCNT were elevated by 16.2%, 32.3%, and 55.6%, respectively. Meteorological factors explained 85.3% of the CO_2 flux increase and 46.1% of the N_2O flux increase associated with CCNT. Furthermore, two types of CCNT practices differed in their GHG emission responses, although both approaches reduced nitrogen losses. These quantitative results, derived from actual production systems, provide informed decision-making among local producers regarding cover crop adoption. Moreover, this field-based evidence offers a robust empirical foundation for future modeling efforts aimed at assessing the ecological benefits of cover crops under varying climatic and soil conditions.

Selective accelerated solvent extraction method optimized for the sequential extraction and chromatographic separation of sedimentary plant wax and fire biomarkers

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Understanding past climate and ecological changes requires distinguishing between anthropogenic versus natural drivers, a challenge that paleoenvironmental and archaeological studies have increasingly addressed over the last two decades via multi-biomarker analyses. Accelerated solvent extraction (ASE) is a widely used technique in these fields, combining high temperatures and pressures with solvents to efficiently extract organic compounds from environmental matrices, including sediments and soils. Here we present an optimized selective ASE method for the sequential extraction and chromatographic separation of biomarkers commonly used for sedimentary paleoenvironmental and paleoclimate reconstructions. We show that our method can be used successfully to extract, separate, and purify *n*-alkanes, *n*-alkanoic acids, and polycyclic aromatic hydrocarbons (PAHs) with more consistent PAH recovery while maintaining uniform sample-to-sample variability in *n*-alkyl lipid yields, and significantly higher *n*-alkanoic acid yields. We demonstrate the utility of our new method with new downcore lacustrine sediment samples from Lago Caranã, eastern Amazonia, a site with a well-documented history of anthropogenic fire during the late Holocene. The new PAH record from Lago Caranã is largely different from the previously published charcoal influx record from the same sediment core, but shows local fire histories that reflect the replacement of non-edible eudicots with edible monocots, driven by pre-Columbian Indigenous land management. Ultimately, our selective ASE method represents a valuable tool for high-throughput biomarker analyses in paleoenvironmental and geoarchaeological research.

Impact of hydrothermally processed digestate on methane production by anaerobic digestion

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In the United States, 34 billion gallons of wastewater are treated every day. Wastewater treatment involves removing toxic elements from water systems through both microbial treatments and through removing biosolids. These biosolids are further utilized in a process called anaerobic digestion (AD). In AD, biosolids are decomposed by anaerobic microorganisms, producing biogas and digestate. The waste digestate can be used as fertilizer, but the majority is sent to landfills or incinerated, which represents a significant financial burden to treatment plants that utilize AD. The only financial return is through selling produced methane.

The patented hydrothermal technology known as Honeyshyne™ (HS) can dissolve biomass into water using only heat, oxygen, and pressure. A large percentage of the carbon from processed biomass is converted into soluble form and is therefore more readily bioavailable to microorganisms. We hypothesized that when HS is used to process digestate, the resulting soluble product can be returned to the AD system, potentially producing more biogas. We investigated two scenarios: one where pre-AD solids were processed by HS and another where nutritionally depleted post-AD solids were processed by HS. We set up anaerobic vessels using live inoculum from the pre- or post-AD environment, introducing dissolved organics produced by HS to experimental groups and water to controls. Vessels were incubated at 37°C for 35 days, monitored for gas pressure, biogas and microbiome composition. We found that pre-AD solids processed by HS resulted in a 27% increase in biogas production, while post-AD solids processed by HS resulted in a 473% increase in biogas production. Our research demonstrates that the HS process could provide dual benefits to AD systems by increasing biogas production, adding value, and minimizing costs by reducing waste solids. This preliminary study indicates that combining HS technology with the AD industry could provide both economic and environmental benefits.

Investigating Impact-Induced Freeze-Thaw Cycles on the Surface of Titan

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Impact-induced melt ponds that interact with biomolecule precursors on Titan's surface could assist in creating conditions for rich prebiotic chemistry for hundreds of thousands of years. Exposure of these prebiotically complex melt pools to the extremely low temperatures on Titan's surface, followed by additional impacts that reheat the ice, allows for freeze-thaw cycles (FTCs) to be possible. These FTCs may be analogous to wet-dry cycles as a mechanism for polymerizing information molecules such as RNA (Monnard, Ziock, 2008). We aim to understand how polymerization, prebiotic chemistry, and complexification of biomolecules could be conceivable on Titan with FTCs as a driving force. We created a *Python*-based Monte Carlo model named *O*verlap *R*ecognition and *A*nalysis of *C*raters from a *L*ocation-Based *E*ntry *S*imulation (ORACLES) to understand the frequency of potential FTCs on Titan. Our code pulls crater sizes from a distribution of impactor sizes and frequencies (Artemieva and Lunine, 2005) and impact locations from a distribution that considers leading/trailing hemisphere and equatorial biases (Hedgepeth et al., 2020). To calculate where the most overlaps could occur, we employed the Haversine formula (de Mendoza y Rios et al., 1796). ORACLES is applicable to any mapped or modeled celestial body and can be extended to any point in its history. We are currently running thousands of simulations to understand the likelihood of different FTC quantities occurring anywhere on Titan for multiple eras since its formation. Additionally, we have run preliminary experiments with an ultra-high-performance liquid chromatography (UPHLC)-Orbitrap mass spectrometer, and we were able to confirm the detection of complex oligomer standards. These detections are essential groundwork for the analysis of our FTC experiments in the lab. To summarize, we present our initial ORACLES results throughout Titan's history while establishing the viability of this model for future applications and our preliminary UPHLC isomeric and oligomer detections.

How Much Information is in a Biosignature?

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Fossilized lipid biomarkers provide crucial evidence for reconstructing the history of life on Earth, but their interpretation can be complicated by uncertainties in production and diagenesis. Biomarkers carry information through their chemical structure and isotope ratios [1]. We define three types of information that can be inferred from structure alone: topological complexity [2], biosynthetic pathway complexity, which is adapted from a graph complexity metric [3], and genetic information [4]. A lipid's topology reflects its biological function; pathway complexity captures the enzymes required for its biosynthesis; genetic information refers to the DNA sequences encoding these enzymes.

Using an information-theoretic framework, we analyze publicly available databases [5-7] to quantify and compare these three information channels and explore their interrelationships. For a curated set of biomarker lipids, we identify all known biosynthetic pathways, assess the taxonomic distribution of genes involved, and estimate the total amount of biological information (in bits) that can be retained in the fossil record. This quantitative approach offers a new perspective on the interpretation of biomarker signals, both on Earth or elsewhere.

References:

[1] Hayes JM, Freeman KH, Popp BN, Hoham CH. Org. Geochem. 16(4):1115–1128 (1990).
[2] Böttcher T. J. Chem. Inf. Model. 56(3):462–470 (2016).
[3] Green C. J. ACM 20(3):378–384 (1973).
[4] Adami C. Phys. Life Rev. 1(1):3–22 (2004).
[5] Caspi R, Billington R, Keseler IM, et al. Nucleic Acids Res. 48(D1):D445–D453 (2020).
[6] NCBI Resource Coordinators. Nucleic Acids Res. 52(D1):D34–D43 (2024).
[7] Szklarczyk D, Kirsch R, Koutrouli M, et al. Nucleic Acids Res. 51(D1):D638–D646 (2023).

High-Confidence Detection of RNA Precursors with UHPLC–Orbitrap MS

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One leading hypothesis for the origin of life proposes that it began with self-replicating RNA, potentially forming in pond environments on early Earth [1-4]. Testing this idea in laboratory simulations requires analytical methods capable of detecting and distinguishing RNA's molecular building blocks with precision. In prebiotic chemistry experiments, these compounds often occur in complex reaction mixtures, making it essential to use tools with exceptional sensitivity, resolution, and structural specificity. Current approaches such as gel electrophoresis, nanopore analysis, AFM, NMR, TOF-MS, and HPLC have advanced our ability to detect the building blocks of RNA but often fall short in resolution, sensitivity, or structural confirmation. This study develops and optimizes a UHPLC Orbitrap MS protocol designed for high-confidence detection and separation of nucleobases, nucleosides, nucleotides, and short RNA oligomers in the context of prebiotic chemistry experiments. Key chromatographic and mass spectrometric parameters were systematically evaluated, including column and solvent selection, elution gradient, ionization mode, and collision energy, with the goals of achieving complete separation of closely related analytes, sharp and symmetrical peak shapes, and efficient analysis within approximately 30 minutes. The resulting optimized method achieves clear separation and ultra-sensitive detection for all targeted analytes, including four nucleobases, four nucleosides, ten nucleotides, and three RNA oligomers (dimer, trimer, tetramer). The optimization process also underscored persistent challenges in LC–MS analysis of phosphorylated compounds, including phosphate–metal interactions with stainless steel hardware that can cause peak tailing, and ion suppression effects may reduce signal intensities for highly phosphorylated species such as ATP and ADP. The method provides a robust analytical framework for RNA building block detection in complex mixtures and will support future efforts to unravel chemical pathways that may have led to life's emergence.

References:

[1] Goodman, H. M., & Rich, A. 1962, PNAS, 48, 2101–2109, doi: 10.1073/pnas.48.12.2101

[2] Gilbert, W. 1986, Nature, 319, 618, doi: 10.1038/319618a0

[3] Pressman, A., et al. 2015, Current Biology, 25(19), R953–R963, doi: 10.1016/j.cub.2015.06.016.

[4] Damer, B., & Deamer, D. W. 2020, Astrobiology, 20, 429–452, doi: 10.1089/ast.2019.2045.

Understanding the triple O-isotope composition of cherts

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Cherts is a diagenetic rock that originates from marine silica precipitation and recrystallization to form more stable quartz. Numerous studies have explored the oxygen isotope composition of cherts across the geological scale in pursuit of oceanic temperature reconstructions, hinting that Archean seawater might have had temperatures close to 100 °C. In recent years, the advent of triple O-isotope measurements that allow precision of $\Delta'^{17}O$ better than ±0.01 ‰ has sparked a new wave of detailed investigations of cherts. We will present a summary of our previous studies that focus on cherts from Archean to Cenozoic. Here we make a distinction between cherts that originated in sensu stricto sedimentary ways and those that originated due to replacement of protoliths (i.e., silicification). We rely on petrography, electron microprobe mapping, bulk triple O-isotope measurements and microscale SIMS $\delta^{18}O$ and $\delta^{30}Si$ measurements to improve the accuracy of our interpretations. Collectively, these show the importance of sample selection, original silica sources, recrystallization and impurity of the analyte. In addition, the isotope effects of diagenesis of modern seafloor-drilled cherts with $\delta^{18}O$ values between +30 to +35 ‰ correlate with the age of the oceanic lithosphere, prompting a new way to interpret the low $\Delta'^{17}O$ values. We also show the results of hydrothermal water-rock interaction in silica saturated Archean seawater and its bearing on the $\delta'^{18}O$-$\Delta'^{17}O$ of greenstone-hosted cherts. New triple O-isotope data for ~2.2 Ga cherty layers from Kona Dolomite (Upper Peninsula, MI) will be discussed in this presentation.

Sulfide Variation in the 3.2 Ga Deltaic Sediments of the Moodies Group

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Atmospheric oxygen levels increased rapidly 2.4 billion years ago during the Great Oxygenation Event (GOE), yet oxygen production likely began long before, producing local "oxygen oases" around microbial communities [1]. The 3.2-billion-year-old Moodies Group on the Kaapvaal Craton in South Africa contains marine deltaic sediments deposited 800 million years before the GOE, along with previously reported "microbially induced sedimentary structures" [2, 3]. We are examining these sediments for further evidence of biosignatures, with the end goal to test the hypothesis that oxidative photosynthesis existed at this time.

Drill cores from the Moodies Group consist of coarse-grained sedimentary rocks that contain dark finer-grained layers referred to as "crinklies" [4]. Micro X-ray fluorescence (µXRF) and Raman spectroscopy show the finer-grained laminations contain abundant heavy mineral grains [5], although the most abundant grains throughout the core samples is quartz. Raman spectroscopy also shows concentrated masses of fossil organic matter (kerogen) in these crinklies. Redox sensitive grains such as pyrite have been identified throughout the rock. If there was free oxygen available at the time of deposition, these detrital grains may contain rims of oxidation products. Initial analyses have not identified Fe-oxide rims around detrital pyrites but reflected light microscopy does reveal multiple stages of growth on the detrital pyrites. Raman spectroscopy also shows peak shifts across detrital pyrite grains, but more work is required to determine the cause of these shifts. This likely elemental difference from core to rim may give insights into the original host rock of these detrital grains as well as diagenetic history, such as the reduction of iron oxides into iron bearing sulfides or later sulfide precipitation. A portion of the grain population contain abundant inclusions that may give insight into grain provenance.

References:

[1] Olson, S. L., Kump, L. R., and Kasting, J. F. (2013). Chemical Geology 362: 35-43.
[2] Homann, M., Heubeck, C., Airo, A., and Tice, M.M. (2015). Precambrian Research 266: 47-64.
[3] Noffke, N., Eriksson, K. A., Hazen, R. M., Simpson, E. L. (2006). Geological Society of America 34: 253-256.
[4] Heubeck, C., Engelhardt, J., Byerly, G. R., Zeh, A., Sell, B., Luber, T., Lowe, D. R. (2013) Precambrian Research 231: 236-262.
[5] Zawaski, M. J., Tice, M., Shapiro, R. S., Czaja, A. D., Orrill, B. (2023) Presented at the Lunar and Planetary Science Conference, 2023.
[6] Pisapia, C., Humbert, B., Chaussidon, M., Demoisson, F. & Mustin, C. (2010) The American mineralogist, vol. 95, no. 11-12, pp. 1730-1740.

Preservation of Depositional Marine Sedimentary Sulfur Isotope Records Under Thermal Alteration

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The sedimentary sulfur record is critical for interpreting the evolution of marine environments because the burial of reduced species impacts global climate through the drawdown of CO_2 and buildup of O_2 levels. Sedimentary $\delta^{34}S$ records are used to reconstruct changes in ocean chemistry, which can be influenced by microbial activity in deep time and thermal alteration during burial. Therefore, it's important to assess whether sedimentary $\delta^{34}S$ archives record original values or diagenetically altered signals. The microbially-mediated reduction of sulfur allows the species to react with iron to form pyrite or with organic matter to form organic sulfur. This process occurs in anoxic environments when other respiration processes are unavailable to organisms. Thus, the deposition of reduced sulfur in the sedimentary record can indicate periods of anoxia in marine environments through time. However, it remains unclear whether original depositional $\delta^{34}S$ signals are retained after later stage burial, diagenesis, and/or metamorphism, and whether preservation of $\delta^{34}S$ differs between organic and pyrite sulfur. This is important to distinguish as all sediments have undergone some degree of heating and compaction during the lithification process. This study assesses the effects of heating on the sulfur isotope record in sedimentary pyrite by measuring the $\delta^{34}S$ of pyrite along a thermal gradient in a field setting. Samples were collected within a single bed perpendicular to an igneous intrusion into the Pierre Shale in the Raton Basin, NM, where heating decreased with distance from the dike. We collected SIMS data on individual pyrite grains, along with external heating constraints (e.g. Rock Eval pyrolysis and vitrinite reflectance) and bulk $\delta^{34}S$ records for pyrite and organic sulfur. This work supports our interpretations of measured $\delta^{34}S$ values of thermally altered sediments, future studies on settings with wider degrees of thermal alteration, and development of correction models for reconstructing depositional $\delta^{34}S$.

Biofilms in Serpentinization-Associated Extreme Environments: Implications for Habitability and Life Detection.

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Serpentinization occurs when ultramafic rocks interact with water, forming serpentine minerals, hydrogen, and methane, which support microbial life. This process takes place in subduction zones, mid-ocean ridges, and ophiolites, playing a role in Earth's history and possibly in early life evolution. This project examines three serpentinizing systems across different environments: (i) The Lost City Hydrothermal Field (LCHF), located on the Mid-Atlantic Ridge, is a submarine hydrothermal system crucial for studying ultramafic-hosted microbial life. (ii) The Prony Hydrothermal Field (PHF) in New Caledonia is unique for its combination of submarine and intertidal sites that discharge alkaline, hydrogen- and methane-rich fluids. (iii) The Santa Elena Ophiolite (SEO) in Costa Rica features terrestrial hyperalkaline springs with high methane concentrations.

Bacteria thriving in these extreme environments form thick biofilms, where cells are embedded within a self-produced matrix of Extracellular Polymeric Substances (EPS). EPS, composed of polysaccharides, proteins, enzymes, extracellular DNA (eDNA), and lipids, play a crucial role in microbial interactions with their surroundings. Given that serpentinization-associated environments serve as compelling analogs for astrobiological studies due to their prevalence in the solar system, microbial biofilms may provide valuable insights into habitability and biosignature detection in extreme terrestrial and extraterrestrial settings [1].

Considering this, we aim to: (i) investigate EPS biosynthesis potential in LCHF, SEO, and PHF by analyzing biosynthetic gene clusters (BGCs) and (ii) compare microbial biofilm communities and metabolisms across these serpentinizing systems using metagenomic and microscopy. Preliminary data reveal BGCs involved in exopolysaccharide biosynthesis in LCHF and SEO, with compositions and abundances dictated by physicochemical conditions. LCHF and SEO favor the production of sphingan exopolysaccharides, which demonstrate stability at high pH and temperatures (100–150 °C) while exhibiting strong selectivity for calcium. These findings highlight the adaptability of microbial communities and the role of EPS in shaping biosignatures within serpentinization-driven ecosystems.

References:

[1] Gonzalez-Henao, S., & Schrenk, M. O. (2025). An astrobiological perspective on microbial biofilms: their importance for habitability and production of detectable and lasting biosignatures. *Applied and Environmental Microbiology*, e01778-24.

Diagenesis of Proteins from Microbes (and Cows) in Tree Resin

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Because microbes do not often leave behind informative body fossils, identifying individual microbial taxa in the fossil record is a difficult task, entire communities or microbiomes even more so. For microbes, molecular fossils – cellular biochemical constituents preserved (but also chemically altered by diagenesis) in a range of geologic archives – can be our best set of clues to the biological past. Amber (fossil tree resin), is a geologically-durable archive that can preserve delicate biological structures, and potentially also biopolymers from microbial biomass trapped within. 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 bovine serum albumin, cyanobacterial biomass and soil in tree resin to understand protein diagenesis in fossil resins. In diagenetic experiments, the total number of identified peptides decreases over time, while the 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.

What's on the Menu? Tracing Microbial Metabolisms and Nutrient Flow from the Surface to Subsurface via Compound-Specific Isotope Analysis of Amino Acids

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Stable isotopes record information about the chemical and physical processes in an environment. In macroecology, isotopic analysis of biomass has traditionally been used to distinguish photosynthetic pathways, identify food sources, and map food web interactions. At the compound-specific level, isotopes of lipids and amino acids can also be used to study biochemical processes in organisms. For microbes, the carbon, nitrogen, and hydrogen isotopes of amino acids can provide insight into nutrient and water sources, trophic dynamics, central metabolic pathways, and routes of carbon and nitrogen fixation or assimilation.

In this study, we use cultivation-based experiments to constrain the isotopic signatures of microbial amino acids. By growing microbes with distinct metabolic capabilities on various C and N sources, we aim to identify unique isotope patterns associated with different metabolisms. The microbes and substrates span a range of aerobic and anaerobic metabolisms, including chemoautotrophy via the Wood–Ljungdahl pathway, C1 metabolisms, and heterotrophy using sugars and organic acids. While carbon source and metabolism influence $\delta^{13}C$ values, we also expect shifts in $\delta^{2}H$ values due to differences in fluxes between intracellular hydrogen pools such as NAD(P)H. For nitrogen, isotopic effects during uptake and assimilation can vary depending on the nitrogen source (e.g., organic vs. inorganic) and concentration.

We then apply this triple-isotope framework to environmental samples from three subsurface ecosystems: (1) Mammoth Cave, Kentucky, (2) Paradox Basin, Utah, and (3) the Deep Mine Microbial Observatory, South Dakota. Our goal is to understand how microbial metabolisms, nutrient cycling, and food web structures change with depth. Ongoing analysis will allow us to compare these patterns across depths and environments, revealing how subsurface microbial metabolisms shift with geochemical context. These analyses will help us interpret how metabolic strategies vary with changing environmental conditions and provide new insights into subsurface microbial ecology and biogeochemical cycling.

Why is pyrite in shallow marine sediments so isotopically heavy?

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The $\delta^{34}S_{pyr}$ bulk composition is a function of two major variables: (1) ambient $\delta^{34}S_{H2S}$, 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. Pyrite potentially forms intermittently over time in marine sediments during multiple stages of early diagenesis. Samples deposited in shallow shelf settings in a variety of locations display the greatest complexity, with multiple pyrite textures and subpopulations in $\delta^{34}S_{pyr}$. The history of these complex processes can be evaluated using a combination of petrographic (SEM) and isotopic analysis of individual pyrite grains using secondary ion mass spectrometry (SIMS). We compare modern sediments from both the Po River delta and off the coast of Milos deposited in shallow marine settings above wave base to comparable Pleistocene deposits from southern Italy. All samples contain a significant population of framboidal pyrite with a minimum $\delta^{34}S_{pyr}$ value ~ -55‰, despite having bulk $\delta^{34}S_{pyr}$ values ranging from -38 to +5‰. Distributions of framboidal pyrite in modern sediments can be bimodal or exhibit skewed distributions (toward ^{34}S-enriched values) that mirror distributions during 'baseline' bulk samples in the Pleistocene record. However, ^{34}S-enriched outliers in the Pleistocene record contain significant populations of non-framboidal pyrite (euhedral or overprinted textures) that compose distinct and ^{34}S-enriched modes and account for the 'heavier' bulk $\delta^{34}S_{pyr}$ values. When bimodal distributions exist in the rock record with second ^{34}S-enriched modes primarily composed of non-framboidal pyrite, we hypothesize a second pulse of pyrite formation after burial produced the 'heavy' mode and represents early diagenetic processes. However, the existence of 'heavy' tails or bimodal distributions of framboids found in modern sediments deposited above wave base (i.e., in 'open system' conditions) requires an alternative explanation.

Prebiotic Chemistry Insights for Dragonfly: Thermodynamics of Amino Acid Synthesis in Selk-sized Craters on Titan

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Titan, Saturn's largest moon, is a world of astrobiological interest where impacts can generate transient melt pools that may persist for several thousands of years, providing aqueous habitats in an otherwise cryogenic environment. In this study, we use Cantera models to evaluate the thermodynamic feasibility of amino acid synthesis in Titan-relevant post-impact melt pools, focusing on mixtures of hydrogen cyanide, acetylene, and ammonia. We examine the equilibrium production of twenty-one canonical amino acids across varying ammonia concentrations. Our models show that in the absence of ammonia, only proline, alanine, and beta-alanine are produced. With as little as 5% ammonia (relative to water), nearly the full amino acid suite becomes thermodynamically accessible. Higher ammonia levels do not further increase yields. Intriguingly, alanine, beta-alanine and proline appearing in the ammonia-free system suggests alternative synthesis routes beyond the classical Strecker or aminonitrile hydrolysis chemistry, warranting further investigation. The results highlight the role of acetylene, which is abundant on Titan but rare on early Earth, as a potential feedstock for prebiotic chemistry in extraterrestrial environments. Comparison with experimental kinetics (Farnsworth et al., 2024, ACS Earth and Space Chemistry, 8(12), 2380-2392) indicates that while equilibrium predicts near-complete conversion, observed rates yield partial products over weeks. However, estimated equilibration timescales are far shorter than melt pool lifetimes, supporting the plausibility of equilibrium being approached on Titan. These results provide testable predictions for NASA's Dragonfly mission. DraMS, the onboard mass spectrometer, will be capable of detecting amino acids, enabling direct assessment of whether post-impact aqueous alteration is another source for molecular complexity on Titan. More broadly, our findings expand the landscape of prebiotic chemistry to include pathways unique to non-Earth environments, offering new perspectives on the universality of life's building blocks.

Session 2

Low Resolution Paleolimnological Analysis of Lake Amatitlán, Guatemala Using Diatom Fossil Assemblages

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Lake Amatitlán is situated in the central highlands of Guatemala, near the country's capital, Guatemala City. The lake has been reported to suffer from eutrophication, enhanced siltation, and toxic contamination. Additionally, in 1976, Guatemala was struck by a magnitude 7.5 earthquake, resulting in thousands of casualties and over a billion dollars in economic losses. Diatom fossil assemblages preserved in lake sediments can be analyzed to understand how ecosystems and water quality change throughout time. In 2024, two sediment cores were collected from the lake. Performing a low-resolution diatom analysis of one of these cores presents a unique opportunity to assess how human activity, eutrophication, toxic pollution, and earthquakes have impacted the ecology of this lake system. Results indicate large shifts in biodiversity at the hands of both natural and anthropogenic phenomena.

Holocene Reconstruction of Eutrophication and Hypoxia in Lake Erie

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Lake Erie, the most ecologically dynamic of the Laurentian Great Lakes (LGLs), has undergone significant biogeochemical shifts throughout the Holocene. Recurring hypoxia and eutrophication reflect both natural climate variability and, more recently, anthropogenic nutrient loading. Understanding this long-term evolution is critical for anticipating the lake's response to ongoing environmental stress. In July 2024, piston and multi-cores from Lake Erie's Central and Eastern Basins were collected aboard the R/V *Blue Heron* to reconstruct past nutrient and redox conditions using multi-proxy sediment analyses. Two key intervals were emphasized: (1) the mid-Holocene Thermal Maximum (~8–5 ka BP), when climate-driven productivity potentially caused episodic hypoxia, and (2) the Anthropocene (last ~200 years), characterized by widespread, persistent oxygen depletion linked to nutrient enrichment. The targeted basins represent distinct hydrological and biogeochemical regimes on Lake Erie, allowing assessment of both spatial and temporal patterns in lake response to climate and anthropogenic stressors. Organic geochemical proxies (C/N ratios, $\delta^{13}C$, $\delta^{15}N$) and total organic carbon (TOC) offer insights into productivity and organic matter sources, while trace elements—such as Mo, V, Fe, and Mn—are used to infer redox conditions. To strengthen chronological resolution, paleomagnetic secular variation (PSV) curves were applied, improving age models where radiocarbon dating is limited. Preliminary results depict increases in $\delta^{15}N$ and Mo concentrations in late Holocene sediments, likely reflecting agricultural and oxygen stress in the Anthropocene. Sedimentological features provide further context: distinct black bands (~4.7-7.6 ka BP) align with rising lake levels and shifting redox conditions, while decreased total inorganic carbon (TIC) (~4 ka BP) indicates the end of a low-stand with increased terrestrial input, and potential basin isolation. By comparing long-term trends, this work will clarify how climatic and anthropogenic forces shaped eutrophication and hypoxia in Lake Erie, providing a paleoenvironmental framework to guide lake management and enhance our understanding of ecosystem resilience.

Reconstructing Reactive Iron Geochemistry along a South Atlantic Transect: Implications for iron delivery and ocean productivity

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International Ocean Discovery Program (IODP) Expeditions 390 and 393 drilled seafloor sediment cores from five locations within the south Atlantic Gyre. The sites were aligned off the coast of Brazil, along a transect at the ~-30° S latitude line on the western side of the Mid-Atlantic Ridge. S and sin sediments, collected ranging ranged in age from about 6.6 Ma (U1559) nearest to the Mid-Atlantic Ridgespreading center to about 61.2 Ma (U1556), furthest from the ridge were collected. This study focuses on the distribution of the different reactive iron species minerals that include iron carbonates (e.g., Fe^{2+} such as siderite), iron oxides (e.g., Fe^{3+} such as ferrihydrite) (ferrihydrite and (oxyhydr)oxides crystalline and easily reducible), and iron magnetite, and iron sulfides (acid volatile sulfides and pyrite) (Fe^{2+} and Fe^{3+} such as magnetite), and pyrite. The relative distribution of reactive iron can provide information about the redox state of the seafloor and possibly iron delivery to the central gyre and its potential influence on marine primary productivity. Gyres are typically nutrient-poor, low productivity areas/regions that do not deliver an abundance of nutrients and organic matter to the ocean floor. However, iron, a limiting nutrient for marine life, could be transported with wind-blown dust carrying bioavailable iron minerals such as ferrihydrite. However, iron (in the form of wind-blown dust), a limiting nutrient for marine life, found in iron minerals such as ferrihydrite, could be delivered. The iron in oxides, carbonates, and magnetite, and sulfides were sequentially extracted using wet chemical procedures from sediments collected from at sites U1560, U1558, U1583, U1559, and U1556. The focus of this study is to use iron speciation to both reveal how hydrothermal activity has influenced the samples through time and draw conclusions about possible redox conditions. Initial results indicate that crystalline iron oxides are the dominant iron species across all sites in the South Atlantic Transect during beginning in the Miocene and peaking in the Plio-Pliestocene. Magnetite was the next most abundant form of iron and had peaks through the different sites also during the Miocene. Iron carbonates and sulfides were at trace to negligible amounts through all time periods in all five sites. Iron distributions will be compared with other redox sensitive metals, such as aluminum, to have a better understanding of spatial distribution as well as sources of iron dust. The increase in bioavailable iron coincides with the southern hemispheric glaciation and the global drawdown in atmospheric CO_2 concentrations through the Pleistocene. An expansion of arid regions and intensified wind belts during glaciation potentially contributed to elevated iron delivery.

Plant-derived pentacyclic triterpenoid hydrocarbons: Sedimentary Distributions at the Pliocene Gray Fossil Site, Tennessee, USA

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The early Pliocene is the interval of geologic time when the Earth last had atmospheric CO_2 concentrations of ~425 ppm comparable to present levels. The Gray Fossil Site (GFS) is a paleosinkhole lake in-fill deposit from the early Pliocene (4.5-4.7 Ma) in east Tennessee, one of few records for this epoch from North America. The distribution of hydrocarbons in GFS sediments affords a unique insight into the depositional paleoenvironment and post-depositional diagenetic processes. Among the GFS hydrocarbon constituents, plant-derived pentacyclic triterpenoids (PDPTs) comprise compounds representative of progressive diagenetic stages, augmenting and consistent with prior studies. The suite of PDPTs includes aliphatic, aromatic, and A-ring degraded derivatives with oleanane, ursane, and lupane structures. The dominance of PDPTs as contributors of terrestrial organic matter to the GFS deposit attests to the prominence of angiosperms in Pliocene southern Appalachia. An angiosperm-dominant environment, rather than the mixed angiosperm-gymnosperm modern flora, is indicative of a warmer and wetter climate in the early Pliocene.

Filtered geochemical constraints on the environmental drivers of early animal extinction

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The latest Ediacaran period represents a critical geobiological transition with the emergence of the Ediacaran fauna, and their abrupt disappearance before the Cambrian "explosion." A major open question is: *what caused this transition?* To evaluate potential causal relationships between environmental and biotic change, this research will analyze the sulfur isotopic composition (δ^{34}S) of carbonate-associated sulfate (CAS) and radiogenic strontium isotopic ratios (^{87}Sr/^{86}Sr) from carbonates across the Ediacaran-Cambrian (E-C) boundary, in Nevada and Mongolia.

While the $\delta^{34}S_{CAS}$ proxy has been widely applied to reconstruct global ocean redox changes throughout Earth's history, a growing body of work suggests the fidelity of bulk rock $\delta^{34}S_{CAS}$ as a primary record of seawater sulfate can be compromised during early and late diagenesis (e.g., by sulfate reduction, or oxidation of reduced sulfur phases). To mitigate this, X-ray Fluorescence Microscopy (XFM) and calcium isotopic ratios ($\delta^{44/40}$Ca) will be used to screen data prior to analysis of δ^{34}S values.

Preliminary data from X-ray Absorption Near-Edge Structure (XANES) analyses show that multiple phases of sulfur (e.g., CAS, organic sulfur, pyrite) are disseminated throughout Ediacaran-Cambrian carbonate samples. Micro-XRF maps indicate that some, but not all, CAS is co-located with reduced sulfur phases, which may have implications for reconstructing primary S-isotope signals. Additionally, CAS appears to be concentrated in the matrix of carbonate samples suggesting a diagenetic influence. Between 82 to 20% of $\delta^{44/40}$Ca values in Nevada, and 87 to 65% in Mongolia, meet the threshold of being the likeliest to have preserved primary δ^{34}S (i.e., more positive than a $\delta^{44/40}$Ca cutoff value between −0.5 and −0.9‰ relative to coeval seawater (0.4‰)). Highly variable $\delta^{44/40}$Ca values within this cutoff range may indicate transient diagenetic conditions and thus non-primary δ^{34}S values.

Exploring rainfall variability in Central America using biomarkers: New results from Laguna Lachuá, Guatemala

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Interannual precipitation variability in Central America is driven by both its unique topography and complex interactions between several coupled ocean-atmosphere climate phenomena. Here we share initial biomarker data from new, annually varved sediment cores from Laguna Lachuá (15° 54'50"N, 90° 39'49" W), a karstic lake located in the lowland humid forests north of Guatemala's largest mountain chains. These sediments offer a unique opportunity to examine past climate extremes preserved at very high temporal resolutions. We analyzed leaf wax *n*-alkane average chain length (ACL) and compound-specific hydrogen (δ2H) compositions. In this presentation we provide a detailed examination of the upper ~200 years of sedimentation, comparing biomarker and lithological data against meteorological station data, in order to characterize recent regional rainfall and ecological variability. We then use this foundation to contextualize initial results from downcore analyses spanning the late Holocene.

A Novel Technology for Processing of *Chlorella vulgaris* for Continuous Biofuel Production

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The burning of fossil fuels has been the primary energy source since the Industrial Revolution causing many adverse effects to health and the environment. Microalgae-derived biofuels offer an alternative without the risk of competing with human dependent resources (e.g. arable land) and is sustainable, ensuring energy independence while closing carbon loops. Unfortunately, the complexity of microalgal cell walls and the logistical difficulties of harvesting cells from water is an economic pain-point that prevents commercialization of microalgae use for biofuels. Current methods that exist disrupt algal cell wall structures but are expensive, use or generate toxic chemicals, or require pure biomass feedstocks.

A novel technology known by its' industry name, Honeyshyne™ (HS), presents a unique process that is simple, does not use or produce toxic chemicals, and efficiently can dissolve solid biomass into water without needing a pure biomass feedstock. HS technology was used for the first time to process the microalgae *Chlorella vulgaris*, successfully disrupting the cell wall and releasing free fatty acids (FFAs). The FFAs were extracted from the HS liquid using solvent exchange and chemically converted into fatty acid methyl esters (FAME). The resulting product was a range of C6 and C18 saturated and unsaturated FAME molecules confirmed by Gas Chromatography - Flame Ionization Detector (GC-FID) and were successfully used to run a small diesel model airplane engine.

The efficacy of combining HS technology with microalgae will need to be tested by a robust technical economic analysis investigating cultivation, harvesting, processing, extraction, and production of biofuels. In this study we show our initial steps to mixotrophically grow *C. vulgaris,* concentrate to ~3% solids, processed by HS, and determine the FFA and FAME yield. Water-soluble 'waste' products from the lipid extraction will be reused as media to cultivate sequential batches of *C. vulgaris* for continuous lipid harvesting.

Preservation of Fe(III)-oxyhydroxides in Near-Saturated Martian Brines

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Satellite and rover data collected from recent Mars missions shows a high abundance of iron-bearing materials on the surface of Mars, including poorly crystalline Fe(III)-oxyhydroxide phases such as ferrihydrite. In terrestrial systems, ferrihydrite is a key component in influencing soil reactivity, nutrient availability, and microbially mediated redox reactions. Understanding the long-term preservation of ferrihydrite in extreme extraterrestrial environments such as Mars may help in better evaluating the degree of potential habitability in Mars' history. The persistence of these crystalline iron phases in Mars' cold, arid conditions may be due in part to the formation of near-saturated salt brines, which hinder the effect of aqueous alteration over long-term exposure. Near-saturated brines formed via deliquescence on the surface are likely rich in sulfate, perchlorate, and chlorides. Based on this knowledge, we hypothesize that high sulfate/perchlorate brine chemistry has a strong influence on the long-term persistence of ferrihydrite on the surface of Mars. To test this, we reacted lab-synthesized 2-line ferrihydrite with near-saturated and diluted solutions of NaCl, $CaCl_2$, $MgCl_2$, $MgSO_4$, $NaNO_3$, Na_2SO_4, Na_2CO_3, $NaClO_3$, and $NaClO_4$ for 30 consecutive days, then analyzed the solids with x-ray diffraction (XRD) and Raman spectroscopy. We found that ferrihydrite remained stable against phase transformation in near-saturated sulfate and perchlorate brines and exhibited minor transformation to goethite, hematite, lepidocrocite, and akaganéite in the remaining saturated brines and all the diluted brines. In addition, ferrihydrite preservation is also strongly influenced by drying state prior to brine exposure with freeze-dried ferrihydrite exhibiting little to no phase transformation. This suggests that ferrihydrite formed in cold, arid conditions before contacting highly saturated brines. These findings may have significant implications for the formation, cycling, and bioavailability of iron species on Mars.

Constraining the Possible Metabolic Pathways of Neoarchean Filamentous Microorganisms

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The remains of Earth's earliest life provide a window into an enigmatic period in our planet's history. Preserved in only a few Archean units, these rare fossils come from a time before the initial oxygenation of Earth's atmosphere, when the planet's biosphere was entirely microbial. Though their morphologies are often simple, and their preservation is often poor, such fossils have broad implications for our understanding of the origin and early evolution of life on our planet, as well as the potential development of life elsewhere in the universe.

For 2.5 billion years, chert from the Tsineng Member of South Africa's Gamohaan Formation has preserved the remains of such microscopic organisms. When first described, these filamentous microfossils were interpreted as photosynthetic, based on their morphological similarities to modern cyanobacteria. However, more recent depositional estimates place the unit below the ocean's photic zone, calling into question the organisms' access to light. While the fossils are similar in appearance to some cyanobacteria, they are also morphologically comparable to extant chemosynthetic (sulfur-cycling) bacteria like *Beggiatoa*, that do not utilize light in their metabolism. This research will provide depositional context for the Tsineng Member and its fossils, helping to constrain the potential metabolism of the fossil microbes by determining the environment in which they lived. This will be done using silicon isotope measurements to differentiate between terrigenous and hydrothermal silica. Additionally, by measuring sulfur isotope ratios of authigenic sedimentary pyrite grains, it will be possible to search for direct evidence of biological sulfur cycling among the Tsineng microfossils.

If the Tsineng fossils are the remains of chemosynthetic, rather than photosynthetic bacteria, they would be among the earliest recorded fossil sulfur bacteria. Furthermore, such early chemosynthetic organisms could have implications for life on subsurface-ocean worlds like Europa and Enceladus where photosynthesis is impossible.

Metagenomic Insights into Antimicrobial Resistance Gene Diversity in a HAB-Impacted Freshwater Ecosystem

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Antimicrobial resistance (AMR) is a global health concern intensified by antibiotic contamination in freshwater systems. In the Western Lake Erie Basin (WLEB), harmful algal blooms (HABs) fueled by agricultural runoff and wastewater inputs may interact with AMR, amplifying ecological and public health risks. HABs have been proposed as potential reservoirs for AMR, yet the environmental factors influencing AMR diversity and persistence in freshwater ecosystems remain unclear. We used environmental metagenomic sequencing to investigate the potential interplay between HABs and AMR in WLEB from 2016 to 2020. Biomass was collected from NOAA Great Lakes Environmental Research Laboratory (GLERL) monitoring stations (WE4, WE8, WE2, WE12) during May through October and analyzed via shotgun metagenomics. Sequences were annotated with DeepARG to identify and classify AMR genes, and Kraken was used for taxonomic classification. ARG abundances were normalized to transcripts/reads per million (TPM) and further adjusted through 16S rRNA gene normalization. Our analyses showed that AMR communities were taxonomically and functionally diverse, with dominant classes including peptide, aminoglycoside, bacitracin, and multidrug resistance genes. Generalized Additive Models (GAMs) indicated that seasonal patterns and environmental variables, such as nutrient concentrations and bloom metrics, showed weak associations with variations in ARG abundance. HAB-associated taxa, particularly members of the *Proteobacteria,* were frequently linked to key ARG classes. These results suggest that AMR dynamics in eutrophic freshwater systems are influenced by a combination of biological and environmental drivers, including HAB events. However, variability in environmental parameters and the complexity of biological interactions, such as HABs, highlight the need for targeted monitoring to better resolve these dynamics. Such efforts will be critical for refining our understanding, improving predictions of AMR persistence, and guiding strategies to address resistance in aquatic environments impacted by nutrient enrichment and bloom activity.

Effects of Ammonia-Bearing Fluids on the Extent and Hydrogen Production Capacity of Ultramafic Rock Alteration: Implications for the Seafloor of Enceladus

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Aqueous alteration of ultramafic rocks has been proposed as a major process creating habitable conditions on the seafloors of icy moons, such as Enceladus. These reactions release dissolved ions into the ocean and may produce H_2 gas linked to the oxidation of Fe(II) during alteration of olivine and orthopyroxene. A key control on hydrogen generation is the host of ferric iron after alteration, which is impacted by temperature, primary rock mineralogy, and fluid composition. The alteration minerals formed by serpentinization and the fate of iron are poorly constrained for ammonia-rich alteration fluids expected on icy worlds. We performed hydrothermal alteration experiments of an ultramafic rock at 225 °C in ammonia-rich and ammonia-free fluids representative of potential fluid compositions on Enceladus and other icy bodies. Ammonia suppresses the extent of serpentinization by buffering the pH to lower values than for ammonia-free fluids. In addition, ammonia induces greater iron oxidation through a currently unidentified mechanism. This indicates that seafloor alteration processes on Enceladus may behave differently than similar environments on Earth, which are often used as a possible analog for habitability studies. Accounting for the effects of ammonia-rich ocean fluids on H_2 production is important for assessing the habitability of Enceladus and other icy bodies.

Investigating the relationship between seawater manganese and Banded Iron Formation precursors

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The Archean Ocean had a strikingly different chemistry compared to the modern ocean. Predating the Global Oxidation Event (GOE) and later evolution of silica-biomineralizing organisms, the absence of atmospheric oxygen would have led to the accumulation of oxygen-sensitive elements (i.e. reduced manganese, Mn2+, and iron, Fe2+) in an ocean where silica concentrations were at or near saturation. This unique oceanic chemistry enabled the generation of Banded Iron Formations (BIFs). Most BIFs predate the earliest accepted microfossils, making these rocks valuable records of ancient biogeochemical cycling. However, despite the abundance of Mn in the Archean Ocean, pre-GOE BIFs contain markedly low manganese.

An Fe-silicate called greenalite [Fe2+3Si2O5(OH)4] is a leading candidate for the primary precipitate of BIFs. Three hypothesized mechanisms could explain the deposition of this primary mineral (1) elevated pH, (2) oxygen-induced partial oxidation of Fe2+, or (3) hydrothermal venting of high Fe2+ and Si. The incorporation of Mn in these formation mechanisms has been underexplored, but it could elucidate which mechanism produced the Mn-deficient Archean greenalite.

We tested the influence of aqueous manganese on greenalite formed at elevated pH, hypothesizing that Mn would be incorporated into the silicate structure or as a Mn-rich accessory phase. We synthesized greenalite at pH 8 under varying manganese levels. We found that Mn was excluded from the silicate structure in all scenarios and excluded from the final mineral assemblage under most Mn2+ concentrations. Our findings suggest that Archean greenalite formation, and thus BIF deposition, could be explained by increases in seawater pH.

Investigating Continental Influences on Ocean Circulation and Oxygenation

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Marine habitability for aerobic life requires the supply of dissolved oxygen and nutrients. However, the transition to an oxygenated atmosphere and ocean on Earth was a long-term, spatially uneven process affected by physiography and both local- and global-scale changes. Ocean O2 dynamics include local O2 production and consumption as well as the global-scale circulation of dissolved O2 to the ocean interior. Continental configuration is a first-order control on planetary ocean circulation and hence nutrient transport and ocean redox. Thus, circulation patterns defined by landmasses can directly shape patterns of primary productivity and the oxygenation state of ocean basins, impacting global O2 production and habitats for aerobic life.

We use an atmospheric GCM (ExoPlaSim) and a 3D Earth system model (cGEnIE) to simulate a large ensemble of randomized continental configurations, and explore the impact of changing continental distribution on ocean oxygenation state. We find that continents drastically change the spatial patterns of upwelling and deep-water formation, which respectively control surface primary productivity and dissolved O2 in the deep ocean. Importantly, varying continental distribution alone is capable of generating widespread ocean anoxia, and poorly oxygenated ocean states are possible even under modern levels of atmospheric O2. Finally, we discuss the range of planetary landscapes most favorable to surface oxygenation.

The Impact of Inorganic Ligands on Rare Earth Element Retention in Weathering Zones: Understanding Adsorption and Mineral Nucleation on Goethite

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Rare Earth Elements (REEs) are both a resource for clean energy technology and a record of weathering processes. Their liberation during weathering can result in their accumulation in regolith via adsorption to clay and oxide mineral surfaces, potentially causing a fractionation towards heavy REEs. These weathering zones also often contain secondary minerals with distinct REE signatures. Despite a dependence on a limited number of regolith-hosted deposits for heavy REEs, the mechanisms that promote REE accumulation through adsorption or secondary mineral formation are not fully understood. For other trace elements, ligands are known to inhibit adsorption by forming aqueous complexes or enhance adsorption by altering mineral surface charge or co-adsorbing as ternary surface complexes. Inorganic ligands released during weathering of granitic or hydrothermally-altered bedrock, such as fluoride and phosphate, are especially relevant to REE-rich regolith. We hypothesize that fluoride and phosphate increase REE uptake by iron oxide surfaces by forming ternary surface complexes. However, such complexes may also be precursors to the heterogeneous nucleation of secondary REE-bearing hydrous phosphates or fluorocarbonates. This may explain the occurrence of secondary REE phases in regolith and the scarcity of adsorption-dominated regolith-hosted REE deposits. We have investigated the impact of fluoride and phosphate on Nd retention by goethite. In each sample set, we fix the initial anion concentration and vary the initial Nd concentration to understand how thermodynamic saturation state impacts adsorption and nucleation. Our results suggest that fluoride weakly enhances Nd uptake on goethite. Elevated fluoride concentration nucleates a neodymium fluoride phase. The saturation state needed to induce nucleation and the role of the goethite surface in catalyzing nucleation are under investigation. The effect of phosphate will also be presented. Clarifying REE adsorption and its relationship to heterogeneous nucleation may aid resource assessments of REE-rich regolith and improve REE-based weathering process records.

Greenland's earliest ecosystems after the last glaciation: Younger Dryas and early Holocene Leaf Wax Analysis, South Greenland

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Glaciers in Greenland are shrinking due to anthropogenic climate change, with the potential to dramatically alter local landscape dynamics. Greenland's rapid deglaciation after the last ice age provides an opportunity to observe how ecosystems on freshly deglaciated landscapes evolved through past periods of climate change. During the last deglaciation ~12,900 years ago, an influx of meltwater to the North Atlantic abruptly reversed Earth's warming trend and caused northern climates to return to near-glacial conditions for more than a thousand years. This event, the Younger Dryas (YD), and subsequent abrupt warming ~11,7000 years ago at the start of the Holocene, affected landscapes through changes in vegetation and precipitation patterns. The impacts of these climate shifts are sparsely documented in Greenland and northeast North America because ice sheets still covered much of the region's present-day land. This study analyzes a lake sediment core encompassing the past 13,000 years from southern Greenland, one of the first sectors of the island to deglaciate. Lakes incorporate and preserve materials from surrounding landscapes over time, including ancient chemical biomarkers that are highly resistant to degradation. This study uses leaf wax lipid components, specifically *n*-alkane compounds, to reconstruct terrestrial landscape dynamics through the YD into a warming climate. The chain length of *n*-alkanes can differentiate between the presence of terrestrial and aquatic vegetation in some settings, and the hydrogen isotopic composition elucidates hydrological patterns. By extracting and analyzing *n*-alkanes from distinct time points within the core, the change in landscape productivity from abrupt cooling and warming will be reconstructed. Preliminary data show changes in both *n*-alkane chain length dominance and abundance throughout the core, indicating a strong response to the changing environmental conditions. Ultimately, this study will reveal how a watershed in southern Greenland was colonized immediately after deglaciation and its response to large climate shifts.

Moisture Controls on Soil Microbial Trace Gas Dynamics

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Soil microbes are key regulators of climate-active atmospheric trace gases such as hydrogen (H_2), methane (CH_4), and carbon monoxide (CO). These trace gases are important energy sources supporting microbial survival in diverse terrestrial systems. A primary control on trace gas dynamics is soil moisture, which operates through both physical and biological mechanisms. Previous studies have examined the effect of moisture variability on individual trace gas dynamics, but a mechanistically constrained understanding of microbial processes for different gases across environmentally relevant moisture regimes is lacking. In this study, we ask (i) do soil microbes vary their trace gas preferences across soil moisture gradients? (ii) do moisture thresholds for trace gas dynamics differ among gas species?

As the first step, we experimentally determined soil moisture thresholds for H_2 and CO uptake. Three different soils were collected from Indian Ridge Marsh in Southeast Illinois and the Warren Woods forest soils in Central Michigan. We then set up incubations over a range of soil moisture levels, and measured uptake rates by analyzing headspace trace gas concentrations using gas chromatography. Our results indicate H_2 uptake rates are the highest between 15-30% saturation across all soils. While CO uptake also generally followed a similar trend, in the Michigan soils, we observed CO production in the dry range. Ongoing work aims to better constrain these moisture thresholds, in addition to identifying potential "hot spots" for the uptake of different trace gas species along soil depth profiles. And to develop quantitative models predicting consumption versus production regimes across trace gases along moisture gradients. We aim to develop quantitative models predicting consumption versus production regimes across trace gases along moisture gradients. Better constraining the balance between biological and physical constraints on trace gas metabolisms is critical for predicting microbial activity under future climate scenarios with altered precipitation regimes.

Understanding Xanthan Gum and its Applications to Soil Health & Geomorphology

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Extracellular polymeric substances (EPS) are cohesive biopolymers excreted from common microorganisms found in soils. EPS can contribute to soil crust formation, reduce erosion, improve nutrient and water retention, and potentially influence geomorphology of regions with fine-grained sediment transport. Xanthan gum is a type of EPS excreted by *Xanthomonas campestris*, that is commercially fermented and harvested. To better connect laboratory experiments using xanthan gum with field and laboratory data using naturally grown EPS, we ran experiments with lab and food grade xanthan gum to establish the accuracy of xanthan gum as an EPS proxy. Using weight percents of xanthan gum found in literature experiments, we extracted EPS from mixtures of xanthan gum, sand, and clay to see if manually made weight percents are comparable to chemically extracted weight percents. We find that using lab grade xanthan gum results in a chemically extracted EPS-soil ratio that is 50% accurate. Meanwhile, food grade xanthan gum is only 30% accurate. This study will help quantify and contextualize ongoing field and laboratory studies investigating how EPS impacts soil health and if EPS can influence the geomorphology of larger landforms on Earth and possibly Mars.

Biological molybdenum usage stems back to 3.4 billion years ago

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The biological significance of the transition metal molybdenum (Mo) lies in its ability to drive a wide spectrum of redox reactions, making it indispensable to life. Importantly, Mo-dependent enzymes catalyze a variety of key reactions that drive global biogeochemical cycles. Yet a paradox persists. While modern life ubiquitously relies on Mo, geochemical evidence suggests that its availability in early Earth's anoxic oceans was extremely limited. This apparent mismatch between environmental scarcity and biological importance poses fundamental questions of how and when early life began to harness Mo. We confront this evolutionary enigma through a comprehensive paleobiological analysis of Mo- and tungsten (W)-dependent proteins across the tree of life. By reconstructing the temporal and ecological emergence of molybdoenzymes, their transport systems, and biosynthetic pathways, we reveal that biological Mo usage originated much earlier than previously recognized, dating back to the Paleo- to Mesoarchean (~3.5–3.0 Ga). These findings challenge prevailing assumptions about trace metal availability on the early Earth and underscore the profound antiquity of Mo-based biochemistry in shaping early microbial evolution.

References:

[1] A. C. Johnson, C. M. Ostrander, S. J. Romaniello, C. T. Reinhard, A. T. Greaney, T. W. Lyons, A. D. Anbar, Reconciling evidence of oxidative weathering and atmospheric anoxia on Archean Earth. Science Advances 7, eabj0108 (2021).

Building a manganese budget for manganiferous Steel Lake, Minnesota

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Significant manganiferous deposits occur preceding the Great Oxidation Event (GOE) at 2.4 billion years ago (Gya) to Late Proterozoic. Redox-sensitive manganese has the capacity to reflect the oxidation state of its depositional environment. Manganiferous conditions are characterized by dissolved and reduced Mn in solution, and can result in the deposition of manganese enriched sediments. Steel Lake, Minnesota is a rare manganiferous aquatic system that can serve as a depositional analog to past marine conditions. It has high dissolved Mn at depth where oxygen is depleted, high Mn/Fe ratios and low sulfate content. However, to constrain the past mineral precipitation pathways, we need to know how they (Mn-mineral) precipitate, deposit, preserve or alter into different minerals. To get insights into the pathways for Mn mineral formation, we are building a Mn budget that balances the external input and output. To constrain these terms, I am to determining Mn fluxes into the lake from groundwater and surface inlets, and calculating flux from water column with sediment traps and sediment cores. Surface sediments from Steel Lake host a Fe-Mn carbonate phase and are enriched in MnO and calcite from XRD (X-ray Diffraction), XRF (X-ray fluorescence) and SEM-EDS (Scanning Electron Microscopy-Energy Dispersive X-ray Spectroscopy). In the water column Mn and Fe precipitate around calcareous but not siliceous material in SEM-EDS. This suggests that Mn carbonate rather than Mn oxides may be a major primary mineral from manganiferous conditions.

Using organic sedimentary biomarkers to reconstruct ocean temperature from past warm periods as an analog for future warming in West Antarctica

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The West Antarctic Ice Sheet (WAIS) is losing mass at an accelerating rate, associated with oceanic and atmospheric warming. Understanding the magnitude of ocean warming during past warm periods in Earth's history such as the late Pliocene and Pleistocene (~3.6 million years ago to 11,000 years ago) is important for predicting ice mass loss and sea level rise. To reconstruct ocean temperatures and their influence on WAIS dynamics over the past ~2.6 million years, I used marine sediment samples that were recovered from the Ross Sea, Antarctica. Sediments from these cores can be used to infer past environments of deposition and ice sheet dynamics, and also contain organic molecules produced by marine organisms (known as organic biomarkers), which preserve information about past oceanography and climate. Using lipid biomarkers produced by *Nitrososphaerota* (a Group of marine archaea) called Glycerol Dialkyl Glycerol Tetraethers (GDGTs), we reconstruct ocean temperatures during warm interglacial periods of the late Pliocene and Pleistocene. *Nitrososphaerota* modify their lipid membranes according to temperature and thus can be used to infer past temperatures using sedimentary lipids. Using biomarker proxies, I tested the hypothesis that ocean temperatures during the late Pliocene and Pleistocene were warmer than modern temperatures in this region. This is important because the WAIS was smaller than present during the late Pliocene, and this may have been due to ocean warming melting marine-based sections of the WAIS and raising global sea level.

Exploring Extracellular DNA and RNA as Alternative Sources of Nitrogen and Phosphorus for Microorganisms in the Deep Terrestrial Subsurface

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The terrestrial deep subsurface represents a typically extremely nutrient limited environment where microbially catalyzed reactions and generation times occur at orders of magnitudes slower in comparison to surface microbial activity. On the contrary, the fraction of bacteria and archaea biomass is disproportionately higher in the deep subsurface than the terrestrial surface and ocean combined, suggesting that microorganisms can retrieve the essential nutrients for survival in the deep subsurface. Given that inorganic phosphorus (P) and nitrogen (N) are not readily available or found in low concentrations in the deep terrestrial subsurface, the purpose of this study is to observe alternative sources of N and P for microorganisms that potentially support this growth and productivity. One proposed source of N and P is extracellular DNA and RNA. In the deep subsurface, microorganisms are known to reside in biofilms, where extracellular DNA and RNA along with proteins, lipids, and polysaccharides compose the extracellular polymeric substance. Furthermore, the nucleotide metabolism, central in all living organisms, contains the nucleotide salvage pathway by which organisms reassemble extracellular nucleic acids into their own nucleotide metabolism to save energy rather than synthesize nucleic acids. Previous research indicates that terrestrial microorganisms under nutrient stress in the rhizosphere can catabolize amino acids to acquire nitrogen and carbon (C). Little is known, however, how extracellular DNA and RNA are utilized as nutrients for microorganisms, which could potentially provide a source of N, C, and P. Using metagenomes assembled genomes (MAGs) from Sanford Underground Research Facility (SURF) previously collected by Momper et al. (2023), this study re-examines the metabolism of various MAGs using BLAST to identify and characterize genes that code for enzymes in the nucleotide metabolism to determine if microorganisms catabolize extracellular DNA and RNA as a source of N and P. Preliminary data demonstrate that genes from the nucleotide metabolism vary among bacteria and archaea. Further research is needed to identify specific genes that code for proteins that transport or catabolize nucleic acids, and if these genes are present within the MAGs from SURF. This research has the potential to further understand nutrient acquisition of microorganisms under nutrient stress and the cycling of N and P in the deep terrestrial subsurface.

Metaproteomic Analyses of Microbial Communities in Greening Arctic Tundra Soils

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Climate change is altering landscapes on a global scale and the Arctic has been shown to be particularly climate-sensitive; warming at around twice the rate of the rest of the world. This rapid warming is causing dramatic landscape changes including alterations in vegetation communities and composition and permafrost thawing. As major contributors to Arctic biomass, biodiversity, energy fluxes, and global nutrient cycling, microbes serve as an important connection between the environment and the climate. Soil nitrogen availability may be the strongest predictor of the temperature sensitivity of overall respiration rates in tundra soils. Since Arctic soils have been shown to be nitrogen limited during the growing season, understanding the fate of nitrogen resources in tundra soil is especially important in understanding energy fluxes and nutrient cycling in warming Arctic conditions. By analyzing microbial community taxa and functional assembly using 15N nitrogen incubations and metaproteomic analyses I hope to address this current lack of understanding regarding the degree to which Arctic soil microbes may influence our warming planet. Soil samples were collected and amended with one of six N substrates, in either natural isotopic abundance or 15N-labeled form, and incubated up to 7 days at in situ temperature. The subsequent proteomics analysis identified a total of 22,494 proteins across the 152-sample dataset. The majority of identified proteins were bacterial, with Proteobacteria, Acidobacteria and Actinobacteria being the three most abundant phyla. For certain peptides in the 15N incubations, progressive increases in nitrogen-15 content was observed, clearly resulting from biosynthetic incorporation of the amended 15N substrates into the microbial proteins. These preliminary results demonstrate the feasibility of the 15N-tracking metaproteomics approach in Arctic tundra soils, showing that we can recover informative community metaproteomes and quantify biosynthetic 15N incorporation into individual proteins on experimental timescales.

Deconvolving Local Influences on the Sulfur Isotopic Record of Ancient Marine Pyrite: Implications for the Steptoean Positive Isotopic Excursion

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Studies in the relationship between sedimentary facies and carbon isotope excursions in ancient successions have emphasized the need for a re-evaluation of bulk isotopic profiles as direct records of changes in global ocean chemistry and redox state. Without the consideration of localized context, which is directly related to sedimentation and diagenetic alteration, a reported isotope record and subsequent interpretation neglects the effects of compounding signals that may arise from said context. From the observation that the magnitude and behavior of the late Cambrian Steptoean Positive Isotopic Carbon Excursion (SPICE) varies across shallow and deeper water environments within discrete basins and across latitudes, it conceptually follows that a parallel bulk sulfur excursion is influenced by the same local controls. Here, we utilize bulk reduced (pyrite) and oxidized (carbonate-associated-sulfate) sulfur isotopes to broadly understand the sulfur record in phase with the SPICE in the Central Missouri Intrashelf Basin with respect to facies. *In situ* microscale SIMS and SEM analyses further contextualize depositional and mineralizing conditions affecting the pyrite signal. We report a sulfur excursion generally in phase with the SPICE and aim to determine if the signal reflects changes in ambient seawater chemistry or variations in the depositional environment (e.g., TOC loading, sedimentation rate) at this locality. As the SPICE coincides with a period of evolutionary turnover, it is essential to deconvolve local signals prior to linking these records to broad developments in the redox and compositional evolution of the global ocean that may (or rather, may not) drive changes in biota.

Effects of Orbital and Continental Configurations on Terrestrial Vegetation

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Planetary obliquity modulates climate through its influence on the spatiotemporal distribution of incoming stellar radiation and atmospheric dynamics. The implications for planetary climate and the stability of liquid water have been thoroughly investigated in the past but their overall consequences for planetary habitability are less clear. Recent work suggests that high obliquity and/or high eccentricity planets may have more productive marine biospheres than their low obliquity and eccentricity counterparts [1]. However, the effects of the extreme seasonality generated by high obliquity could affect the survival of complex organisms, especially on land where seasonal temperature variations are large compared to ocean habitats owing to the high heat capacity of water. The habitability of terrestrial environments will also be modulated by the spatial position and distribution of continents, as the latitudinal position and shape of a landmass will strongly determine its climate and, at high obliquity, the magnitude of seasonal climate variability. Previous work has not systematically investigated the effects of obliquity and continental configuration in tandem.

To address this gap, we use cGENIE-PlaSim [2], a 3D biogeochemical model coupled to an atmospheric general circulation model, to simulate the climates of Earth-like exoplanets for various obliquities and continental configurations. We include both historical continental reconstructions as well as idealized configurations. This presentation will identify the obliquity and continental scenarios most favorable to terrestrial vegetation, which is a uniquely detectable form of life on Earth and the base of Earth's global ecosystem. We will then discuss the implications of our work for the detectability of surface biosignatures (e.g., vegetation red edge) on Earth-like exoplanets.

References:

[1] Jernigan J. et al. (2023) ApJ, 944, 205.
[2] Holden, P. B. et al. (2016) GMD, 9, 3347–3361.

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