ExplOrigins Colloquium 2022

Thursday, Feb. 17th

5:00pm – 6:00pm: Poster Session

Molecular Sciences and Engineering Atriums 3 & 4

Friday, Feb. 18th

10:00am – 3:45pm: Oral program

Physical location: IBB, 1st floor, Suddath Room

Attendee link: https://primetime.bluejeans.com/a2m/live-event/ftkwuzsp

YouTube Stream: *youtube.com/watch?v=4-fhkaUmuD4*

Georgia Tech

Schedule

February 17th, 2021

Molecular Sciences and Engineering (MoSE) Atriums 3 and 4
5:00 – 6:00 PM: **Poster Session**

February 18th, 2021

Attendee link: https://primetime.bluejeans.com/a2m/live-event/ftkwuzsp
10:00 AM – 10:10 AM: **Introduction and Welcome**
10:10 AM – 11:00 AM: **Morning Session One: Clathrates, Cubesats, and Characterization**

1. Abigail Johnson
   Bacterial Clathrate-Binding Proteins in the Deep Subsurface Biosphere: Implications for Gas Clathrate Stability and Habitability
2. William Rawson
   Virtual Super-Resolution Optics with Reconfigurable Swarms (VISORS): a Two-CubeSat Formation-Flying Telescope for Coronal Observation
3. Kimberly Faye Meyberg
   Characterization and Thermal Analysis of Metal Phosphites and Their Role in Astrobiology

11:00 AM – 11:05 AM Break
11:05 AM – 12:00 PM: **Morning Session Two: All About Mars**

1. Emily Hughes
   Geochemical and Mineralogical Evidence Against Hydrothemal Conditions in Eridania Basin, Mars
2. Abigail Russ
   Modeling the behavior of mud flows on Mars
3. Grace Fanson
   Testing the Hypothesis of Ancient Volcanism in Arabia Terra, Mars

12:00 PM – 1:00 PM Lunch
1:00 PM – 2:00 PM: **Keynote Plenary: Dr. Amy Mainzer**
Don't Look Up: Near-Earth Asteroids and Comets
2:00 PM – 3:05 PM: **Afternoon Session: Inside Cellular and Molecular Evolution**

1. Kavita Matagne
   Molecular Memory at the Emergence of Life
2. Jay Haynes
   Experimental Predictions of Ribosomal Evolution
3. Brooke Rothschild-Mancinelli
   Using the S. cerevisiae mitochondrial ribosome as an orthogonal evolvable translation system
4. Anthony Burnetti
   The Dual Origins of Phototrophy Reveals the Importance of Evolutionary Priority Effects in Major Transitions

3:05 PM – 3:15 PM: Astrobiology Certificate Ceremony
3:15 PM – 3:45 PM: Discussion and Debrief

Plenary Speaker

Dr. Amy Mainzer

Title: Don't Look Up: Near-Earth Asteroids and Comets

Biography:

Dr. Amy Mainzer is a professor of planetary science at the University of Arizona. Before that, she was a Senior Research Scientist at NASA's Jet Propulsion Laboratory. Her research interests include asteroids and comets, particularly those that approach the Earth; instrumentation for remote sensing; and applications of remote sensing for monitoring invasive species on Earth.

Prof. Mainzer is the principal investigator of NASA's Near-Earth Object Wide-field Infrared Survey Explorer (NEOWISE) mission, an Earth-orbiting space telescope that is searching for Earth-approaching asteroids and comets. She is also the lead of NASA's Near-Earth Object (NEO) Surveyor mission, which will carry out a comprehensive survey of asteroids and comets using a dedicated space telescope. The NEO Surveyor mission has entered its preliminary design phase and is scheduled for launch in March 2026.

Prior to joining the Jet Propulsion Laboratory in 2003, she designed and built the fine guidance sensor for NASA's Spitzer Space Telescope as an engineer at Lockheed Martin. The sensor she built was used daily by the observatory to initialize its pointing system throughout its mission from 2003 until its end in 2019.

Prof. Mainzer serves as the science curriculum consultant, on-camera host, and executive producer of the PBS Kids series Ready Jet Go!, a TV show aimed at teaching physical science and Earth science to kids ages 3-8, and she served as the science consultant for the Netflix movie Don't Look Up. Prof. Mainzer is the Past Chair of the American Astronomical Society's Division for Planetary Sciences, the world's largest professional society of planetary scientists. She serves as the chair of NASA's Planetary Science Advisory Committee and is a member of the NASA Advisory Council Science Committee.

Poster Presentations: Thursday, February 17th

Colin Burnett: *Aerobraking Ring for Large Scale Mars Transportation*

Colin Burnett[1], James Wray[2], John Dec[2]
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Currently NASA operates 8 missions on the surface or in orbit around Mars. While these missions have sent back tremendous amounts of data that have given us key insights into the planet's past and present, the next step in exploration of the red planet is to send human explorers. NASA and many private companies, most notably SpaceX, have manned missions to Mars as a top priority goal for the coming decades. The biggest challenges are the detrimental effects interplanetary space travel on the human body, mainly from radiation exposure and zero-g conditions. This poster proposes a transportation system that will be able to cut Mars transit times and provide artificial gravity for astronauts to reduce radiation exposure and lessen the atrophy of microgravity.

The design is a structural ring which 8 SpaceX Starships attached. The ring is spun up in transit to Mars to provide Astronauts with 1/3g artificial gravity within the Starships. The front face of the ring will have retractable Kevlar sheets that act as a variable aerobraking surface to circularize the rings orbit before the starships are deployed and descend to the Martian surface. These Kevlar sheets can be angled to reduce the angular velocity of the ring with every drag pass. Once the design is finalized and the structures overall lift and drag coefficients for its different configurations are determined, aerobraking simulations will be run using NASA's General Mission Analysis Tool (GMAT) with the Mars Global Reference Atmospheric Model. Structural analysis will be done on the ring structure and preliminary starship models, and thermal analysis will be done on the Kevlar and the ring structure.

Camille Butkus: *Graphite Hydrogenation as a Source of Abiotic Methane on Exoplanets*

Camille R. Butkus[1], Sasha O. Warren[2], Edwin S. Kite[2], Santiago Torres[3], Smadar Noaz[3], Jennifer B. Glass[4]
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[2]Department of the Geophysical Sciences, University of Chicago
[3]Department of Physics and Astronomy, University of California Los Angeles
[4]School of Earth and Atmospheric Sciences, Georgia Institute of Technology

Atmospheric methane at low levels is a promising biosignature gas that will be detectable in exoplanet atmospheres with the James Webb Space Telescope. On Earth, methane is produced by microbial methanogenesis in anoxic environments and thermal breakdown of organic matter, with very small fluxes from abiotic pathways including serpentinization and mantle outgassing. Previous studies on abiotic methane production focus on processes that occur on Earth and other silicate worlds with oxidizing atmospheres and low carbon abundance. Exoplanets with a graphite-rich crust, a reduced mantle redox state, and either water- or hydrogen- rich atmospheres may have favorable conditions for abiotic formation of methane gas. The goal of this study is to establish the kinetics of graphite hydrogenation as a potential source for abiotic methane production on exoplanets. Chemical engineering literature from the 1970s-1980s includes extensive studies on the reaction of graphite with molecular and atomic hydrogen to yield methane. Experiments were generally conducted at temperatures of 175-1000°C, with the maximum methane yield and formation rate at 300-900°C. Nickel, a common crustal element on Earth and likely also on terrestrial exoplanets, was found to be an effective catalyst for the graphite-hydrogen reaction. There are two rate limiting steps in this reaction: the breaking of carbon-carbon bonds and dissociation of molecular hydrogen. Atomic hydrogen, which can be produced by photodissociation of water vapor, readily reacts with graphite to produce methane, eliminating one of the rate-limiting steps. Molecular hydrogen accreted from the nebula or from serpentinization may also contribute to hydrogen rich exoplanet atmospheres. To rule out false positives for life detection via gaseous biosignatures on exoplanets with different elemental abundances than Earth, alternative abiotic methane production pathways should be considered. A carbon-rich planetary crust (including trace nickel catalyst) and an atmosphere rich in molecular hydrogen or atomic hydrogen produced by photodissociation of water vapor, may produce favorable conditions for the abiotic production of methane. Ongoing collaborative work will place constraints on the planetary significance of this reaction.

Bryce Clifton: *Achieving Multiple Rounds of DNA and RNA Copying in Concentrated Amide Solutions: Circumventing the Product Inhibition Problem*

Bryce E. Clifton[1,2], Adriana Lozoya-Colinas[1,2], Martha A. Grover[1,3], and Nicholas V. Hud[1,2]
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Nucleic acid replication in the absence of cellular machinery remains a major focus of origins of life research (Szostak, 2012). Although it has been demonstrated that a template nucleic acid strand can direct the synthesis of a complementary strand by organizing activated monomers or oligomers as reactant substrates, continuous synthesis of both strands is impeded by product inhibition, the so-called Product Inhibition Problem (Adamala and Szostak, 2013; He et al., 2017; He et al., 2019; von Kiedrowski, 1986; Szostak, 2012) Essentially, the resulting template-bound product strand is thermodynamically favored to remain template bound, inhibiting exchange with substrates for subsequent copying. Furthermore, while the strands can be separated with heat, the product strand will preferentially reassociate with the template strand upon cooling.

Here, we report a possible solution to the Product Inhibition Problem, demonstrating multiple rounds of nucleic acid replication upon slow heat cycling in various concentrated chaotropic amide (e.g., formamide) and amidine (e.g., guanidinium chloride) solutions, focusing on one aqueous solvent system rich in urea and acetamide (UAcW) (Lozoya-Colinas et al., 2022). Unified by the shared effect of slowing nucleic acid reassociation, these solutions promote the binding of substrates over product binding under a variety of conditions, including salt concentration, chaotrope composition, and water activity; and under various hydration/dehydration schemes and temperature cycling rates. Likewise, template-product duplexes exhibit decreased thermodynamic stabilities under the conditions reported, requiring accessible and less extreme temperatures to separate duplexed templates, which would otherwise degrade labile nucleic acids like RNA. We report DNA and RNA templates and substrates of various lengths can form stable assemblies and undergo copying under these conditions.

The conditions we observe that support nucleic acid replication were likely abundant on the prebiotic Earth in environments that underwent fluctuating water activity due to evaporation, such as warm ponds and lakes on sunlit terrestrial surfaces. Driven by various environmental cycles, including day/night and wet/dry cycles, these environments could accumulate high concentrations of chaotropes, owing to their low volatilities relative to water. Moreover, the hygroscopic nature of these compounds could provide a means of local rehydration to accommodate subsequent prebiotic processes without dilution effects, which would be expected in bulk water environments. Lastly, we highlight the relevance of these prebiotically plausible amides and amidines to other central prebiotic reactions in an evaporating pond model (Burcar et al., 2016; Forsythe et al., 2015; Menor Salván et al., 2020; Miller et al., 1976). Our findings demonstrate the importance of solvent properties on controlling prebiotic processes and may present environmental constraints on the conditions in which life originated on Earth and where life may be found on other planets.

References:

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Claire Elise Elbon: *Diversity of Heme Copper Oxidases in a Hypersaline Analogue for Ocean Worlds*

Claire E. Elbon[1], Benjamin Klempay[2], Avishek Dutta[2], Margaret M. Weng[3], Alexandra Pontefract[3], Jeff S. Bowman[2], Britney E. Schmidt[4], Christopher E. Carr[1], Jennifer B. Glass[1], and The Oceans Across Space and Time Team
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Hypersaline brines on Earth provide excellent analog sites for understanding habitability on remnant and relict ocean worlds (Europa, Enceladus, Mars, etc.). Biology faces many challenges under hypersaline conditions such as osmotic stress, high or low temperatures, low water activity (aw, inversely related to salinity), and oxygen and energy limitations. Halophilic, or "salt-loving" microbes dominate hypersaline brines with specific enzymatic adaptations to these challenging conditions. The heme-copper oxidase (HCO) enzyme superfamily comprises both nitric oxide reductases (NOR; reducing nitric oxide to nitrous oxide as part of denitrification) and cytochrome c oxidases (COX; oxygen reduction in the final step of oxygenic respiration). HCO transmembrane proteins originated as ways for organisms to cope with toxic gases: nitric oxide and oxygen. The free energy released by reduction of oxygen and nitric oxide is used by all COX enzymes and many NOR enzymes to create cellular ATP via proton transfer pathways. Studying the HCO superfamily can provide insight into the evolutionary history of microbial enzymes that play key roles in planetary scale redox reactions.

There are four types of COX: type A1 (aa3), type A2 (caa3), type B (b(o/a)3), and type C (cbb3). Within the catalytic subunit I, all HCOs contain six highly conserved histidines that play crucial roles in orientation of a low and high-spin heme, as well as ligation of the non-heme metal in the active site. The four types of COX are distinguished by differences in hemes present in the complexes, energetics of catalytic subunit I (COX1), organization of COX genes on the operon, and key amino acids for proton transfer. Type A2 COX1 contains a tyrosine-serine motif for proton transfer whereas type A1 COX1 contains a glutamic acid that plays the role of the YS motif. Cyanobacteria of the class Oxyphotobacteria have only been found to contain type A2 COX. The root and evolutionary history of the HCO superfamily remains highly disputed due to multiple lateral and horizontal gene transfer events that have occurred. There remain many unknowns as to how HCOs in halophilic microbes are adapted to the selective pressures in hypersaline conditions.

Here, we used shotgun metagenomic assembled genomes (MAGs) at solar salterns in San Diego, CA to probe for HCOs at a range of salinities, and to explore the diversity and potential adaptations of HCOs under hypersaline conditions. We performed basic local alignment searches on MAG-mapped metatransciptomic reads from multiple time points of a single NaCl-dominated site (aw ~ 0.84) to determine the active HCOs.

The HCOs actively transcribed were COX-type involved in aerobic respiration. Abundant type A1 COX transcripts mapped to metagenomic genomic bins (MAGs) from halophilic Cyanobacteria and Euryarchaeota. Interestingly, COX1 in the cyanobacteria bins had top hits to type A1 HCO in haloarchaea, with the characteristic glutamic acid instead of the tyrosine-serine motif. Yet the operon structure in these MAGs was type A2, with two other COX subunits matching halophilic cyanobacterial type A2. We also found type B COX transcripts that mapped to Euryarchaeota (Halobacteria) and Bacteroidetes MAGs with type B operon organization. The two most transcriptionally active COX1 HCOs were a type A1 and type B from a halophilic Cyanobacteria bin and Bacteroidetes bin, respectively. Our data suggest that cyanobacteria in hypersaline environments use a hybrid A1-A2 COX for aerobic respiration, and Bacteroidetes use type B COX for aerobic respiration. Additionally, dependent on the genus, halophilic archaea use type A1 or type B COX for aerobic respiration. Future steps include structural homology modeling of detected HCO sequences and phylogenetic analyses to determine if COX genes were transferred from haloarchaea to halophilic cyanobacteria.

Rebecca Guth-Metzler: *RNA and the Goldilocks Zone: Where Mg^{2+} concentration is just right*

Rebecca Guth-Metzler[1,2], Ahmad Mohyeldin Mohamed[1,2,3], Elizabeth T. Cowan[1], Moran Frenkel-Pinter[1,2,3,4], Roger M. Wartell[1,2,5], Jennifer B. Glass[2,6,7], and Loren Dean Williams[1,2,3,6]

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To RNA, divalent metals (M^{2+}) are a double-edged sword: promoting folding but catalyzing cleavage. We investigated whether these opposing behaviors achieve balance at some metal concentration using life's most abundant M^{2+}, magnesium (Mg^{2+}). We show that too little Mg^{2+} accelerates RNA cleavage by minimizing folding, a means of cleavage protection. Too much Mg^{2+} accelerates RNA cleavage by over-riding protection. The in-between "Goldilocks zone" of Mg^{2+} is "just right". Our experiments and simulations follow the expectation that only RNAs that fold have Goldilocks zones. Additional requirements for RNA Goldilocks zones are that the protection via folding should slow RNA cleavage by half or more and the folding should be cooperative. Goldilocks zones can be tuned through RNA sequence offering a potential mechanism for chemical and biological evolution by fitting some RNAs to their surroundings while degrading others. Ultimately, the average Goldilocks zone of modern RNA may reflect the M^{2+} conditions of its origin, and the advantage of a Goldilocks zone perhaps caused RNA to win out over competing polymers on early Earth.

Emma Johnson: *SWAM: A Submersible Water Activity Sensor*

Nathan Daniel[1], Anthony Limiero[1], Emma Johnson[1], Chad Pozarycki[2], and Christopher Carr[3]
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Jennifer Kim: *Minimization of the Ribosome*

Jennifer Kim[1], Kavita R Matange[1], Loren Dean Williams[1]
[1]School of Chemistry and Biochemistry, Georgia Institute of Technology
The ribosome is an essential macromolecular translation machine composed of ribosomal RNA (rRNA) and ribosomal proteins (rProteins). At the core of the ribosome are universal rProteins that are conserved across all three domains of life. The ribosome expanded over time and structurally recorded its evolution. Thus, the ribosome can be interpreted as a molecular fossil that provides a record of the biochemical processes that led the evolution of life today. Ultimately our goal is to minimize the *E. coli* ribosome by using a protease cocktail to digest parts of the ribosome. Accessing the activity of this minimized ribosome could reveal which proteins are critical for its function. Information about the structure and function of the ribosome could provide insight into the history and development of biology on Earth. Here we focused on digesting the *E. coli* ribosome using a serine protease called Proteinase K, along with various concentrations of ions. In addition, we test for an inhibitor of Proteinase K which would allow us to assess the activity of these minimized ribosomes. An ideal candidate is one that completely

inhibits further ribosomal digestion while being compatible with the assay. By structurally probing the *E. coli* ribosome, we hope to learn more about its evolution and the origin of life.

Jordan McKaig: *Solid-State Nanopore Targeting of Translation Machinery as a Biosignature*

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Life is commonly defined as a chemical system capable of Darwinian evolution. This implies a mechanism to store heritable information, and further implies a mechanism to translate this information into the cellular machinery required for maintenance, growth, and reproduction. In all known life, this function is performed by the ribosome, an ancient structure composed of RNA and proteins. Life beyond Earth, even if ancestrally or chemically distinct from life as we know it, may utilize a similar structure due to balancing the energetic costs of assembling translation machinery with the complexity required for such a machine. Thus, we propose that cellular machinery could function as a biosignature, agnostically of the lifeform's origin or physiochemical basis. We demonstrate that ribosomes can be detected using solid-state nanopore instrumentation, a single-molecule detection technology of particular interest for future long-duration interplanetary missions searching for evidence of extraterrestrial life, particularly on Ocean Worlds. Furthermore, we show that it is possible to identify informational polymers (e.g. DNA, RNA) and differentiate them from the translational apparatus (e.g. ribosomes) and potentially other cellular components. Performing these experiments revealed multiple caveats and considerations for future directions, which include optimizing buffer, pore size, and detecting ribosomes specifically within cellular lysate.

Vahab Rajaei: *Combinatorial Explosion vs. Compression: What Can We Learn From Multicomponent Systems?*

Vahab Rajaei[2,3], Moran Frenkel-Pinter[1,2,3,4], Kavita Matange[2,3], John T Costner[2,3], Adelaide Robertson[2,3], Anton S. Petrov[1,2,3], Jessica C. Bowman[2,3], Loren Dean Williams[1,2,3]
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Adelaide Robertson: *Life Without a Membrane?*

Adelaide Robertson[1], Brooke Rothschild-Mancinelli[1], Loren Dean Williams[1]
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The plasma membrane, a universal feature in all domains, is an essential component of cells. The plasma membrane has many different functions, such as regulating cell transport and maintaining cell structure. This project focused on using a top-down approach to see if life can survive in a container without a membrane. An unconventional method of creating low melt agarose gels was used to facilitate the growth of *E. coli*. The *E. coli* strain used contained plasmids that encoded lysozyme and phospholipase C. Lysozyme is under the control of an arabinose-induced pBAD promoter and phospholipase C is under the control of an

IPTG-induced trc promoter. Arabinose and IPTG were able to easily diffuse through the gels, delaying colony growth when the two inducers were combined.

Tyler P Roche: *Prebiotic Reactivity of Noncanonical Nucleobases*

Tyler P. Roche[1], Pranav J. Nedumpurath, David M. Fialho, Gary B. Schuster[1], and Nicholas V. Hud[1]

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To understand the origins of life we must understand how the first molecules of life were formed. RNA is generally considered a central molecule of life, involved in transmitting information from DNA to make proteins. RNA is made up of three types of molecules, or subunits: phosphates, sugars, and nucleobases. The nucleobases adenine (A), guanine (G), cytosine (C), and uracil (U) are considered the “canonical” nucleobases, meaning that they are standard in modern life. However, early life or chemistry could have used non-standard, or “noncanonical” nucleobases before settling on those that are used today. In our study, we tested a selection of putative prebiotic noncanonical nucleobases to see how they reacted with common molecules in a model “primordial soup.” We carried out these reactions in different ways, including in wet or dry conditions, or with more acidic or basic solutions. We show that some of these nucleobases react more easily than others, and in a predictable way. These results show that noncanonical nucleobases can be much more reactive than the canonical nucleobases, making them better candidates for incorporation into early versions of RNA.

Oral Presentations: Friday, February 18th

Morning Session One: Clathrates, Cubesats, and Characterization

10:10-11am

Abigail Johnson: *Bacterial Clathrate-Binding Proteins in the Deep Subsurface Biosphere: Implications for Gas Clathrate Stability and Habitability*

Abigail M. Johnson[1], Manlin Xu[1], Dustin Huard[3], Raquel Lieberman[3], Sheng Dai[2], Jennifer B. Glass[1]
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[3]*School of Chemistry and Biochemistry, Georgia Institute of Technology*

Gas clathrates, high-pressure habitats that naturally occur on continental shelves and in permafrost, host microbial communities unique from other subsurface ecosystems. Gas clathrates are a natural gas resource and can also serve as Earth analogs for habitability elsewhere in our solar system, such as Mars and Titan. This research tests whether bacteria living in gas clathrates employ a strategy like that of cold-water fish that express ice-binding proteins to inhibit the growth of ice crystals. We have identified bacterial Clathrate-Binding Proteins sequenced from gas clathrate-bearing sediments based on their similarity to ice-binding proteins. In this study, we synthesized the proteins and tested their effect on methane clathrate. A methane clathrate shell was formed on a treatment droplet at 5 MPa and -10˚C. We found that the proteins alter clathrate morphology and inhibit clathrate formation. Significantly less methane clathrate formed in the presence of CBPs relative to negative controls (cytochrome, PBS), as measured by gas consumption. The bacterial proteins discovered in this study may aid in maintaining habitable environments for bacteria in these high-pressure clathrate systems.

William Rawson: *Virtual Super-Resolution Optics with Reconfigurable Swarms (VISORS): a Two-CubeSat Formation-Flying Telescope for Coronal Observation*

William Rawson[1], E Glenn Lightsey[1], Farzad Kamalabadi[2], Simone D'Amico[3], John Sample[4], Hyeongjun Park[5], Doug Rabin[6], Adrian Daw[6], Phil Chamberlain[7]
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[5]*New Mexico State University*
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[7]*Laboratory for Atmospheric and Space Physics*

Virtual Super-resolution Optics with Reconfigurable Swarms (VISORS) is a National Science Foundation (NSF) space physics mission which will detect and study fundamental energy-release regions in the solar corona. The VISORS mission, which was selected from the 2019 NSF CubeSat Ideas Lab, will image the solar corona in the extreme ultraviolet (EUV) spectrum at a resolution of approximately 0.15 arcseconds from Low Earth Orbit (LEO) to observe coronal features on the scale of 100 km. To accomplish this objective, VISORS will use a pair of formation flying 6U (30 cm x 10 cm x 20 cm) CubeSats: one of which carries the observatory optics and the other contains the detector. This distributed instrument approach allows the use of a photon sieve with 40-meter focal length to achieve diffraction-limited image resolution, which is beyond the manufacturing limits of conventional mirror-based optics onboard a single spacecraft. VISORS will serve as a proof of concept for this distributed instrument approach by capturing and downlinking at least one image during its six-month minimum mission lifetime. Succeeding in this goal will achieve the highest resolution imaging of the solar corona to date and also demonstrate several key technologies to the mission including photon sieve optics, inter-satellite link, Guidance, Navigation, and Control (GNC) algorithms for precise formation flying, and miniaturized satellite propulsion. The VISORS mission was intentionally selected by NSF to push technology development for future CubeSat formations and to provide unique opportunities to students with 9 educational institutions collaborating with engineers and scientists from the Laboratory for Atmospheric and Space Physics and NASA Goddard Space Flight Center. VISORS is planned to be launch-ready by 2024, near solar maximum.

Kimberly Faye Meyberg: *Characterization and Thermal Analysis of Metal Phosphites and Their Role in Astrobiology*

Kimberly Faye Meyberg[1], Heather Abbott-Lyon[1]
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The conspicuous role of phosphorus in life as we know it is demonstrated in various biomolecules and metabolic processes critical to the formation and sustainment of life. However, the route by which phosphorus was incorporated into prebiotically-relevant molecules in early Earth conditions remains uncertain. Phosphate, the most prevalent species of phosphorus preserved in the geological record for early Earth, is insoluble and unreactive with organics in aqueous environments. Additionally, the most abundant biogenic elements, carbon, nitrogen, hydrogen, oxygen, and sulfur, can be found in a volatile phase under terrestrial conditions, except for phosphorus. This suggests that minerals must have been the main sources of phosphorus on the early earth. One possible solution is that phosphite, a reduced phosphorous species, contributed reactive phosphorus to the early Earth and facilitated phosphorylation of biomolecules. Plausible sources of phosphite include meteoritic corrosion products and iron redox geochemistry in Archean oceans. Here, we present the synthesis, characterization, and thermal analysis of four divalent and trivalent metal phosphites, $CaHPO_3$, $MgHPO_3$, $FeHPO_3$, and $Fe_2(HPO_3)_3$. Characterization methods included ^{31}PNMR, infrared spectrometry (FTIR), thermogravimetric analysis (TGA), and powder x-ray diffraction (XRD). Oxidation events were observed in temperature scans for calcium and iron phosphites, and preliminary kinetic analysis of isothermal data for $CaHPO_3$ suggests two competing chemical processes, oxidation and polymerization of phosphite and phosphate, were occurring. Additionally, the compounds were heated to variable temperatures from 200-600°C in a tube furnace under a nitrogen purge to facilitate the formation of oxidation and polymerization products, which were identified using ^{31}PNMR. The results of this study suggest that geochemical modeling of metal phosphite minerals is complicated by the occurrence of competing chemical processes. Additionally, these

data will aid in the analysis of organophosphates formed from phosphonylation of prebiotically-relevant molecules via metal phosphites.

Morning Session Two: All About Mars 11:05am-12pm

Emily Hughes: *Geochemical and Mineralogical Evidence Against Hydrothemal Conditions in Eridania Basin, Mars*

E. B. Hughes[1], J. Wray[1], S. Karunatillake[2]
[1]School of Earth and Atmospheric Sciences, Georgia Institute of Technology
[2]Department of Geology & Geophysics, Louisiana State University

Abigail Russ: *Modeling the behavior of mud flows on Mars*

Abigail Russ[1], Jacob B. Adler[1], Frances Rivera-Hernández[1]
[1]School of Earth and Atmospheric Sciences, Georgia Institute of Technology

Mud volcanoes occur globally on Mars suggesting that near surface groundwater systems were common in the past on the Red Planet. On Earth, sedimentary volcanism occurs when mixtures of fluids (water and gases) and sediments erupt at the surface due to subsurface overpressure and gravitational instability of buoyant sedimentary units. If the expelled material is dominated by mud-sized grains (clay and silt), then they can form mud cones. However, due to the low pressures and temperatures of the Martian surface, the expelled mud that forms the volcanoes behave differently than they do on Earth. Specifically, mud flows created in a Mars environment chamber by previous studies have shown that bubbling and levitation of mud can happen under Mars conditions affecting the flow transport behavior, such as run out distance and resulting deposit morphology. To better understand the behavior of mud flows under Mars conditions, we created a computer model using COMSOL Multiphysics, a software that allowed us to manipulate physics components and vary parameters such as gravity, pressure, temperature, and viscosity. Our initial models showed that evaporative cooling would have a stronger effect on Mars than on Earth. We also created animations of mud flowing down a slope under 16 different parameters (a variety of Earth-like and Mars-like conditions) to begin to investigate its cohesion and rheology. In these runs, we observed that at Mars surface conditions, the flow remained in a singular lobe, but at Earth conditions, the flow often split and traveled slower.
In ongoing work, we plan to build an eruption from below the surface and incorporate the formation of an insulating icy crust and stacking of multiple solidified mud layers in COMSOL. These model improvements would help simulate a more realistic mud volcano on Mars, and would be consistent with observations from Mars chamber lab experiments and theory. These models will allow us to better assess remote sensing observations, and may even be able to better identify sites with unique paleoclimates or recycling of subsurface water.

Grace Fanson: *Testing the Hypothesis of Ancient Volcanism in Arabia Terra, Mars*

Grace Fanson[1], James Wray[1]
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Introduction:

Over 70% of the surface of Mars has been resurfaced by basaltic volcanism, which cannot be accounted for by the volcanoes directly identified thus far. This discrepancy has motivated searches to find other sources that could have contributed to this massive resurfacing.
The Arabia Terra region of Mars has been hypothesized to contain remnants of ancient volcanoes, previously thought to be impact craters. By using spectral mineral classification, we can determine the composition of the region surrounding the proposed volcanoes. Finding volcanic ash in the surrounding area would support the hypothesis of a volcanic Arabia Terra.
Research/Methods:
There are several minerals indicative of volcanic activity, including hydrated/opaline silica, glass, aluminum and other smectites, zeolites, and sulfates. To identify the minerology of Arabia Terra, we used a Map-Projected Targeted Reduced Data Record (MTRDR) from CRISM, a visible/near-infrared hyperspectral mapping instrument aboard the Mars Reconnaissance Orbiter. Through spectral analysis we have identified deposits of silica near the proposed volcanoes. Thus, this on-going research supports the claims that there could have been volcanoes in the Arabia Terra region of Mars. In the near future we will examine additional CRISM observations throughout the region, in addition to thermal inertia data that can provide an independent test of whether regional deposits are thermophysically consistent with volcanic ash
Implications/Conclusion:
The presence of large, ancient volcanoes in Arabia Terra has major implications for Mars' geological and atmospheric history, sulfur cycle, and the history of habitability on Mars.

Keynote: Don't Look Up: Near-Earth Asteroids and Comets

10:10-11am

Dr. Amy Mainzer[1]
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Earth has been impacted by asteroids and comets throughout its history with varying degrees of severity and influence on the planet. Such small bodies are frequently reservoirs of primitive, volatile-rich material left over from the solar nebula, so they can offer insight into the original conditions at the time of the solar system's formation. Moreover, by characterizing their physical and orbital properties, we can learn how they migrate throughout the solar system, and quantify the likelihood that the Earth will experience another significant impact in the future.

Afternoon Session: Inside Cellular and Molecular Evolution 2-3:05pm

Kavita Matange: *Molecular Memory at the Emergence of Life*
Kavita Matange[1]*, Moran Frenkel-Pinter*[2]*, Vahab Rajaei*[1]*, Loren Dean Williams*[1]
[1]*School of Chemistry and Biochemistry, Georgia Institute of Technology*
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Memory is the acquisition, encoding, and retrieval of information. Genetics is the primary method of molecular memory in biology. DNA and RNA are two major biopolymers that encrypt all the information necessary for cellular function and are at the heart of heredity. Beyond nucleic acids, however, there are a host of memory functions in biology. Protein conformation

and interaction are forms of memory. Amyloids, which involve specific protein conformations and interactions, can replicate indefinitely, in yeast. Both genetic and non-genetic systems constitute the memory of a cell. Given the crucial role of “memory” in Darwinian evolution, we wanted to study memory in systems that demonstrate chemical evolution. During chemical evolution, memory is demonstrated through kinetic trapping. Chemical systems at equilibrium have chemical amnesia. We believe that the complex chemical systems that transit from one kinetic trap to another, can record environmental perturbations and alter chemical trajectories. This enables the chemical systems to evolve into new chemical spaces.

Jay Haynes: *Experimental Predictions of Ribosomal Evolution*

Jay William Haynes[1,2], Kathryn A. Lanier[1,2], Anton S. Petrov[1,2], Loren Dean Williams[1,2]
[1]*School of Chemistry and Biochemistry, Georgia Institute of Technology*
[2]*NASA Center for the Origin of Life, Georgia Institute of Technology*

The translation system is the most universal and conserved cellular system. The common core of the ribosome was mature in the common ancestor of extant life around 4 billion years ago. The early evolution of the ribosome is synonymous with the origin of life. We have previously developed a detailed model of the origins and early evolution of the ribosome. We have resurrected a series of ancestral stages. Using a variety of methods including UV melting, SHAPE (Selective 2’ hydroxyl acylation analyzed by primer extension) and a new application of polymerase stalling, we have characterized these stages in vitro. We demonstrate that ancestral ribosomal forms fold into structures that are consistent with the model of ribosome origins and evolution.

Brooke Rothschild-Mancinelli: *Using the S. cerevisiae mitochondrial ribosome as an orthogonal evolvable translation system*

Brooke Rothschild-Mancinelli[1,2], and Loren Dean Williams[1,2]
[1]*School of Chemistry and Biochemistry, Georgia Institute of Technology*
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The ribosome is at the core of life processes, polymerizing amino acids into coded proteins using defined mRNA sequences as templates. Engineering the ribosome allows its use as a high-fidelity polymerization machine, creating bonds between pre-selected monomers. Our approach is to use the mitochondrion as a box to contain an orthogonal ribosome. This approach side-steps the general lethality of ribosomal mutations, because functional mitochondria are non-essential in *Saccharomyces cerevisiae*. Mitoribosomal perturbations result in mitoribosomes that have wild-type function, altered function, or loss of function. We assessed mitochondrial function by switching between fermentable and non-fermentable carbon sources in the growth media: glucose to support all growth and glycerol to select only cells with functional mitoribosomes. Cells containing functional mitoribosomes grew on glucose or glycerol while those with loss of function mutations grew on glucose only. Mitoribosome function after growth in glycerol was tracked by measuring mitoribosomal sfGFP production using a flow cytometer. We demonstrate that the *S. cerevisiae* mitochondrial ribosome makes for an *in vivo* orthogonal evolvable translation system not seen elsewhere. Our system allows more targeted evolution of the translation system that cannot be done in vitro due to the large sequence space of the ribosome.

Anthony Burnetti: *The Dual Origins of Phototrophy Reveals the Importance of Evolutionary*

Priority Effects in Major Transitions

Anthony Burnetti[1], William Ratcliff[1]
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Phototrophy – the ability of a cell to capture light energy for metabolism – is responsible for the vast majority of biomass production and metabolic flux on Earth, and its origin represents an extremely important evolutionary transition. This capability has evolved independently exactly twice in Earth's history, via chlorophototrophic and retinalophototrophic machinery.

By examining the properties of these two molecular machines in detail, and performing mathematical modeling of their properties under different environmental conditions, I find them to be remarkably complimentary in their ecological roles, suggesting that their properties are the result of ancient ecological interactions between incumbent and novel phototrophs filling initially vacant ecological niches rather than being the random results of rare, difficult innovations. While I find that it is likely that retinalophototrophy originated first, each origin of phototrophy has filled a particular niche in the tradeoff between efficiency per unit light and efficiency per unit protein infrastructure, and has suppressed the evolution of novel machineries like themselves while failing to outcompete the other.

As a "dual evolutionary singularity", phototrophy can also be used as a touchstone to understand the dynamics of major evolutionary innovations and transitions in the history of life on Earth. The example of phototrophy suggests that many of these singularities could be simpler to evolve than they seem, and could be common in other biospheres. I use this example and others to argue that the combination of 'evolutionary priority effects' in which a first-mover suppresses the origin of new lineages too similar to itself, and evolutionary ratchets in which a lineage becomes locked into using a novel trait for survival and unable to revert, together result in evolutionary singularities and many common features of the evolutionary trees surrounding them.

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