

Oral Session I
Tuesday, June 5th 2018, 9:00 - 10:10 am

9:00 - 9:10 am

Warm Up Talk

*Mahmuda Afrin Badhan, University of Maryland
College Park*

9:10 - 9:30 am

Characterizing Exoplanet Meteorology

Arthur Adams, Yale University

In the last 15 years observations of exoplanetary atmospheres have expanded greatly with both transmission spectra and broadband photometry, the latter of which now often encompass at least one full planetary orbit. We have seen a parallel advance in the sophistication of theoretical models applied to these data, which now often take into account molecular chemistry, large-scale circulation, and cloud formation/dynamics. Still in question is the appropriateness of using very complex physical models to data which can suffer from low signal-to-noise and potential uncharacterized instrumental noise sources.

We have approached modeling atmospheres from two perspectives. In one we present an analysis of all available full- and partial-phase light curves from Spitzer's IRAC with a model that considers only the *minimum* number of physical processes reasonably motivated by current data. We demonstrate that in many cases this simple model captures phase offsets and amplitudes for both circular and eccentric exoplanets.

Our second approach modifies an existing 3D circulation model, which offers a comprehensive framework to test physical processes which contribute most strongly to observables. Our current work considers planets on eccentric orbits, and examines how properties such as eccentricity and rotation rate affect the phase photometry under a baseline set of assumptions for surface conditions.

Both approaches aim to address questions of characterizing instrumental responses with respect to model capabilities, with an eye for future observations with the James Webb Space Telescope.

9:30 - 9:50 am

Exoplanet Characterization with JWST: Evolved Climates and Observational Discriminants of the TRAPPIST-1 System

Andrew Lincowski, University of Washington

The seven-planet TRAPPIST-1 M dwarf system provides an unprecedented opportunity to study terrestrial exoplanet evolution with near-term facilities such as the James Webb Space Telescope (JWST) and ground-based observatories. Since M dwarf planets likely suffer extreme volatile loss during the host star's protracted super-luminous pre-main-sequence phase, the TRAPPIST-1 planets may have highly-evolved and possibly uninhabitable atmospheres. Here we use a versatile, 1D terrestrial-planet climate model with line-by-line radiative transfer and mixing length convection (VPL Climate) coupled to a terrestrial photochemistry model, to simulate environmental states for the TRAPPIST-1 planets. We present the climatic effects, self-consistent atmospheric compositions, and observational discriminants of post-runaway, desiccated, 10-100 bar O₂- and CO₂-dominated atmospheres, with and without interior outgassing, as well as more Earth-like compositions. We include the radiative and observational impact of realistic aerosols. Our simulations show a broad range of surface temperatures, most of which are not habitable, though we also present possible habitable environments. Using these simulated environments, we compare the two most prevalent ways to characterize terrestrial atmospheres: primary and secondary eclipse spectroscopy. We assess all available JWST instruments and modes and determine the best methods to probe each TRAPPIST-1 planet atmosphere for the compositions we simulated. These results can inform JWST observation planning and data interpretation for the TRAPPIST-1 system, and for M dwarf terrestrial planets in general.

9:50 -10:10 am

Tracing the Origins of Nitrogen Bearing
Organics Toward Orion KL with ALMA

*Brandon Carroll, Harvard-Smithsonian Center
for Astrophysics*

A comprehensive analysis of a broadband 1.2 THz wide spectral survey of the Orion Kleinmann-Low nebula (Orion KL) has shown that nitrogen bearing complex organics trace systematically hotter gas than O-bearing organics toward this source. The origin of this O/N dichotomy remains a mystery. If complex molecules originate from grain surfaces, N-bearing species may be more difficult to remove from grain surfaces than O-bearing organics. Theoretical studies, however, have shown that hot ($T=300$ K) gas phase chemistry can produce high abundances of N-bearing organics while suppressing the formation of O-bearing complex molecules. In order to distinguish these distinct formation pathways we have obtained extremely high angular resolution observations of methyl cyanide (CH_3CN) using the Atacama Large Millimeter/Submillimeter Array (ALMA) toward Orion KL. By simultaneously imaging $^{13}\text{CH}_3\text{CN}$ and CH_2DCN we map the temperature structure and D/H ratio of CH_3CN . We will present updated results of these observations and discuss their implications for the formation of N-bearing organics in the interstellar medium.

Oral Session II
Tuesday, June 5th 2018, 10:30 - 11:50 am

10:30 - 10:50 am

Decomposition of Amino Acids in Water with
Application to Enceladus and Europa
Ngoc Truong, Cornell University

Amino acids, the building blocks of proteins, are key biosignatures in the search for life. However, amino acids can also be synthesized from abiotic processes and preserved in a range of primitive materials such as carbonaceous chondrite meteorites. Therefore, the first step in using amino acids as biosignatures is to distinguish between primordial synthesized amino acids and the one generated from active production within the ocean. In this study, we calculate the decomposition timescale of amino acids in water under a wide range of conditions that could happen on Enceladus or Europa's oceans, such as water temperature, pH, redox states, minerals catalyst with the application to this purpose. In consideration of the possible presence of life within the ocean of Enceladus, we expand the work to the decomposition of amino acids concentrated in mineral chimneys. In all cases, we reported a relatively short lifetime of most amino acids (except Gly, Ala, Val, Glu), suggesting that: if any amino acids can be detected on Enceladus or Europa, their origin should come from active production rather than primordial synthesis. For amino acids concentrated in pore spaces of chimney structures, their lifetime is shorter than their free dissolved amino acids in the ocean, and for most amino acids in this study, even much shorter than the plausible timescale of Enceladus's ocean. Thus, for the beginning of life on Enceladus, even if accumulation mechanisms are efficient enough to concentrate prebiotic molecules into pore spaces of chimney structures for a substantial amount of time, polymerization of peptides and nucleic acids face a challenge that thermal decomposition could destroy them before polymerization conditions are obtained. Any models considering the production of amino acids (both abiotic and biotic production) should take into account the effect of the decomposition process.

10:50 - 11:10 am

Cometary Delivery of Cyanide to the Early
Earth for Prebiotic Synthesis
Zoe Todd, Harvard University

Impact delivery of organic material has been postulated to be potentially important for the origin of life on Earth. The inner terrestrial planets underwent a period of Late Heavy Bombardment (LHB) shortly after the formation of the Solar System, which could have delivered substantial amounts of water and organics to the Earth. Delivered material could potentially include amino acids, lipids, nucleobases, and simpler feedstock organics. Of these feedstock molecules, recent experiments especially emphasize HCN (Patel et al. 2015, Xu et al. 2017). Here, we consider the amount of cyanide delivered by impacts on the early Earth and estimate the concentration of cyanide in prebiotic aqueous reservoirs (e.g. lakes and oceans) from this source. The steady state concentration of cyanide in aqueous bodies purely from impacts exceeds micromolar levels at pHs from 4-6 in the global ocean at low temperatures, and could reach millimolar levels for local lake scenarios. Millimolar concentrations of cyanide have been used in laboratory experiments for synthesizing molecules of interest, and it has been postulated that micromolar concentrations would be sufficient. Shortly after an impact, local concentrations of cyanide are likely to be much higher (tens of millimolar), which could create particularly favorable circumstances for prebiotic synthesis. We conclude that impact delivery is a potentially significant source of this molecule, and could be responsible for seeding the Earth with enough cyanide for the origins of life. We note that these are lower limits as additional cyanides are likely to form due to impact chemistry.

11:10 - 11:30 am
Simulations of Methane on Mars Using
Curiosity Data
Amber Britt, Fisk University

The presence of methane in the Martian atmosphere has been a photochemical mystery particularly with regard to claims of high concentrations (24 ± 10 ppb) and significant temporal and spatial variations using ground based measurements (Mumma et al. 2009). Since the launch of NASA's Curiosity mission local surface abundances of methane have been measured and their presence indicates a localized source seeing as though the atmospheric lifetime of methane in the Martian atmosphere is relatively short (~300 years). In addition, the measured variance in surface methane concentrations indicates a seasonal variance. We investigate the temporal and transient signals measured by Curiosity Using a 1D photochemical model. We show successful modeling of the temporal variations in surface methane concentration and a successful buildup of methane to the highest reported Curiosity measurement (~9.34ppbv). However, we find the breakdown of methane at this magnitude takes 100 times longer than the observational timescale.

References:

M. J. Mumma et al. (2009) *Science*, 323, 1041-1045.

11:30 - 11:50 am
RISE UP: Robotic Exploration beneath the Ross
and McMurdo Ice Shelves
*Justin Lawrence, Georgia Institute of
Technology*

The NASA-funded RISE UP program (Ross Ice Shelf and Europa Underwater probe) is a three-season project to observe ice-ocean interactions and conditions beneath McMurdo Sound, the McMurdo Ice Shelf (MIS), and the Ross Ice Shelf (RIS) in Antarctica. In addition to traditional water column sampling and profiling methods, these observations are being made via the AUV/ROV Icefin, designed to conduct basal ice and benthic surveys through 30 cm boreholes in remote locations. During the 2017-19 austral summers, and in cooperation with the Antarctica New Zealand Ross Ice Shelf Programme (PI Christina Hulbe), RISE UP will provide insight into these largely unmapped and uncharacterized sub-ice environments.

RISEUP aims to autonomously characterize habitability and sample under-ice environments on broad spatial scales via robotic platforms. By combining data from Icefin's sensors with CTD profiling, nutrient sampling, cell counts, and DNA extractions, we are mapping observations from the vehicle to the biologically relevant environmental parameters that support life. Across the gradient of field locations from the front of the RIS to the grounding zone, we can trace circulation, ice mass balance, nutrient flux, and sub-shelf biodiversity while refining the sensors autonomous vehicles can use to link environmental processes and habitability. Here, we present the results of this complementary water column sampling from the first season of RISE UP beneath the McMurdo and Ross Ice Shelves.

Oral Session III
Tuesday, June 5th 2018, 1:00 - 2:10 pm

1:00 - 1:10pm

Warm Up Talk

Zach Duca, Georgia Institute of Technology

1:10 - 1:30 pm

Assessing new biogenicity criteria of
microfossils with high-
resolution imaging techniques

*Lara Maldanis, Brazilian Synchrotron Light
Laboratory*

Microfossils are morphological biosignatures of microorganisms preserved in the geological record and comprise the oldest direct record of life on Earth. Their study can provide us a view into the planet early biosphere, a reason for which they are also important analogues for the search for past-life signatures outside Earth. However, due to the micrometric size and the chemical composition (highly dense and homogeneous rocks), most of the oldest described microfossils of Earth are very controversial and still debated, especially because of the difficulty to differentiate true biogenic structures from diagenetically formed pseudofossils and/or later contaminations in these ancient and very geochemically altered Precambrian rocks. The use of micro-analytical imaging techniques based on different physical phenomena has been proposed as a potential approach to overcome these limitations, exploring both the morphology and chemical composition of the samples in its geological and paleoenvironmental context.

Here I will present some challenges of using X-ray imaging to study microfossils, and also some results of 3D Ptychography, micro-CT and Confocal Laser Scanning Microscopy in different Cambrian and Precambrian microfossils immersed in rock matrix. Through complementary data, these techniques allowed a 3D multi-scale analysis with both chemical and morphological information of the controversial and the well-preserved structures. Together, this non-destructive approach can largely contribute for establishing more robust biogenicity criteria, which could be applied to the investigation of controversial and/or unique samples, such as the oldest microfossils of Earth, samples collected

from Martian meteorites or, in in the near-future, Mars return missions.

1:30 - 1:50 pm

Planetary Image Analysis using Advanced
Artificial Intelligence Techniques - An example
with crater detection

Ebrahim Emami, University of Nevada, Reno

Deep Convolutional Neural Networks(CNN) have recently achieved great success in the field of Artificial Intelligence. Such networks can now solve some of the challenging computer vision tasks with an error rate lower than human! Unlike the conventional classification techniques based on feature engineering and classification, CNNs learn both features and classification models during training. These advancements in Artificial Intelligence have been applied to many other fields of technology for object recognition. To a limited extent, these techniques have also been employed for planetary image analysis. In this work, we put one step forward, by evaluating the effectiveness of CNNs for crater detection on Lunar images. Craters are the most dominant landmarks on many celestial bodies and the detection of craters has various applications in planetary science. Due to the enormous and growing amount of planetary data, large scale manual crater detection is laborious and impractical and autonomous crater detection approaches are desired. In this work, we evaluate the performance of our customized Region-based Convolutional Neural Network (Faster R-CNN) in crater detection. Using this network, we achieved to detect 92% of craters on our test site images captured by Lunar Reconnaissance Orbiter. Furthermore, we investigate the performance of the state-of-the-art deep CNNs on lunar crater classification. VGGNet, GoogLeNet, and ResNet have been among the most popular and successful deep CNNs proposed in the past few years and employed in our experiments.

1:50 - 2:10 pm

The Breakthrough Listen Search for Intelligent Life: the first SETI results and other future science.

J. Emilio Enriquez, UC Berkeley/ Radboud University Nijmegen

the study of astrophysically powered radio emission from stars targeted by our program.

The Breakthrough Listen (BL) Initiative is the largest campaign in human history on the search for extraterrestrial intelligence. The work presented here is the first BL search for engineered signals. This comprises a sample of 692 nearby stars within 50 pc. We used the Green Bank Telescope (GBT) to conduct observations over 1.1-1.9 GHz (L-band). Our observing strategy allows us to reject most of the detected signals as terrestrial interference. During the analysis, eleven stars show events that passed our thresholding algorithm, but detailed analysis of their properties indicates they are consistent with known examples of anthropogenic radio frequency interference. This small number of false positives and their understood properties give confidence on the techniques used for this search. We conclude that, at the time of our observations none of the observed systems host high-duty-cycle radio transmitters emitting at the observed frequencies with an EIRP of 10^{13} W, readily achievable by our own civilization. We can place limits on the presence of engineered signals from putative extraterrestrial civilizations inhabiting the environs of the target stars. Our results suggest that fewer than $\sim 0.1\%$ of the stellar systems within 50 pc possess the type of transmitters searched in this survey. This work provides the most stringent limit on the number of low power radio transmitters around nearby stars to date. We explored several metrics to compare our results to previous SETI efforts. We developed a new figure-of-merit that can encompass a wider set of parameters and can be used on future SETI experiments for a meaningful comparison. We note that the current BL state-of-the-art digital backend installed at the Green Bank Observatory is the fastest ever used for a SETI experiment by a factor of a few. Here we will describe the potential use of the BL backend by other groups on complementary science, as well as a mention the ongoing and potential collaborations focused in particular in

Poster Session I
Tuesday, June 5th 2018, 3:30 - 5:30 pm

Poster 1

Atmos: A 1-D Coupled Climate-Photochemical
Model to Simulate Exoplanet Atmospheres
*Mahmuda Afrin Badhan, University of Maryland
College Park*

Upcoming observatories, including NASA missions such as JWST, will provide transit spectroscopy data needed to constrain abundances of species in exoplanet atmospheres with unprecedented accuracy. It will also increase the number of smaller, cooler planets for which we have such information. Interpreting the observed signals will require reliable atmospheric modeling tools that simulate both physical and chemical processes, especially for those cooler planets, where equilibrium chemistry does not necessarily dominate. The Virtual Planetary Laboratory's "Atmos", a coupled 1-D climate-photochemical modeling tool, has been validated for modeling of early Mars, Archean (~4-2.5 billion years ago) and modern Earth atmospheres. These codes have also been used to simulate rocky exoplanets, including simulations that have helped define the habitable zone. In recent years, we have extended our modeling capabilities to other environments such as Titan, sub-Neptune worlds, and hot-Jupiter exoplanets. Mixing ratio profiles of gases and photochemical hazes are derived from Atmos. For rocky planets in the habitable zone, we also obtain temperature structures. These can be fed into radiative transfer models to generate spectra for different types of exoplanets. The spectra can then be used with future mission simulators to self-consistently determine the potential for retrieval of spectroscopic signatures with upcoming space-borne instruments. Here I will highlight the present modeling capabilities of Atmos, show results from our recent work simulating solar system and exoplanet atmospheres, and discuss how these simulations can help interpret results from JWST. Atmos is now publicly available on Github, and this release presently contains our most stable and well-validated templates.

Poster 2

On the Formation of C₂H₅NO Isomers in the
Interstellar Medium
*Seyedsaeid Ahmadvand, University of Nevada,
Reno*

Peptide bonds are essential for the formation of life on Earth. Formamide, the first molecule with a peptide bond, was detected in the north region of Sagittarius B2 (Sgr B2(N)). Acetamide and N-methyl formamide (C₂H₅NO isomers) were detected consequently in the same region of the interstellar medium (ISM) via low energy content rotational emissions. To investigate the formation of C₂H₅NO isomers, radical-molecule reactions: NH₂ + C₂H₄O (acetaldehyde, vinyl alcohol, and oxirane) and CH₂ + NH₂CHO are computationally studied based on the reaction exothermicity and the presence of precursors in Sgr B2(N). Density functional theory (DFT) and coupled cluster quantum mechanical methods are used for the geometry optimizations, vibrational analysis, transition state search, and calculation of energy. Among the studied reactions, the spin-forbidden reaction of CH₂ (T) + NH₂CHO (S) is the kinetically favorable (barrier-less) reaction for the formation of acetamide. The latter reaction is also the only reaction, which leads to the formation of N-methyl formamide, however, this formation is not kinetically favorable at low temperatures in gas phase. G3 (MP2, CCSD(T)) composite method needs to be done to confirm DFT results and compensate for the zero point energies and dispersion interactions. Eventually collision theory and Nahoon Kida kinetic model will be used to obtain the rate constants and matching them with the abundance of detected species in the ISM, respectively.

Poster 3

Self-Assembly of Nucleobases Analogues: Quantum Mechanical and Molecular Dynamics Study

Asim Alenaizan, Georgia Institute of Technology

Cyanuric acid and triaminopyrimidine are nucleobases analogues that form noncovalently stacked, hexameric plates in aqueous environment. They have been proposed as potential prebiotic alternatives of the canonical nucleobases in extant DNA and RNA, in order to circumvent the challenge that the monomeric canonical nucleobases do not pair in water. However, the structure and dynamics of these assemblies and their underlying noncovalent interactions, in particular hydrogen bonding and stacking, have not been explored. This research applies a variety of quantum and classical computational methods to study the self-assembly of these systems. Molecular dynamics simulations using the General Amber Force Field indicate that these systems form stable helical structures at ambient temperature and pressure. Symmetry adapted perturbation theory applied to a two-plate model system reveals the physical origin for the stability of the helical system, showing that it balances the noncovalent forces in the system, especially exchange repulsion and dispersion.

Reference: Cafferty, B. J.; Gallego, I.; Chen, M. C.; Farley, K. I.; Eritja, R.; Hud, N. V. *Journal of the American Chemical Society* 2013, 135, 2447-2450.

Poster 4

Subsurface Aquifers and Caves Environments as Models for Astrobiology *Adrim Barry Sosa, University of Florida*

Cave ecosystems may have features similar to those found on Mars or Ocean Worlds, making them attractive analogues to inform the search for life outside Earth. Environments in the subsurface are protected from many of the stresses that preclude habitability on extraterrestrial surfaces, such as lethal fluxes of UV and ionizing radiation, extreme temperature oscillations, and the absence of liquid water. In Earth's subsurface, microbial interactions with the lithosphere provide energy sources that support diverse microbial communities in air and water-filled caves. There is a growing body of evidence that chemosynthetic processes can form the basis of subterranean food webs. Florida has one of the most extensive karstic underwater cave systems in the world; however, the microorganisms inhabiting the subsurface aquifer are largely unexplored. Caves underlying West-Central and North Florida have a variety of geochemical gradients and conditions relevant for metabolisms expected in extraterrestrial environments, such as lithotrophic sulphide-oxidation and methanogenesis. To fully understand the limits and constraints of life in dark subsurface environments, new observations are required to reveal their nature and biogeochemical contributions. Knowledge of how to seek, identify, and characterize life and life-related chemistries in subsurface ecosystems is relevant to efforts that search life beyond Earth.

Poster 5

Geochemical and Geophysical Gradients from a Meteoroid Impact Result in a Unique Pattern of Microbial Distribution.

Manish Baviskar, Lamar University

Meteoroid impacts are considered as some of the most crucial events in the planet's history. While the initial effect of meteoroid impact is catastrophic, after a certain period of time novel bacterial species develop within the unique environment of the impact crater. The Marquez crater is a buried and complex 58 million years old meteoroid impact crater neighboring the city of Marquez in Texas, USA, whose geophysical and geochemical gradients influence microbial diversity. The purpose of this project was to determine the microbial distribution around the Marquez crater based on cultivable heterotrophs (aerobes, anaerobes, and yeast and molds), chemotrophs (iron reducing bacteria) and indicator bacteria. Included in this analysis was the evaluation of the distribution and levels of microbial contaminants generated by the nearby human activity using indicator bacterial counts as per EPA guidelines. Results show that the population of cultivable heterotrophic aerobes vary significantly with the spatial distribution, gradually decreasing from the outer edge of the crater to its center. On the contrary, cultivable chemotrophs, heterotrophic anaerobes, and yeast and molds, follow opposite distribution patterns.

Poster 6

The Influence of Positive Ions During Laboratory Simulations of Titan's Haze Formation

Jennifer Berry, University of Colorado - Boulder

Titan, one of Saturn's moons, is the only other planetary object in our solar system with a thick nitrogen atmosphere. Surrounded by a haze, it is possible that astrobiologically relevant chemistry is occurring in Titan's atmosphere. Titan's haze formation is initiated by energetic electrons and UV photons leading to a complex series of ion-neutral and radical reactions that result in high molecular weight hydrocarbons and nitrogen containing species. A long history of laboratory and modelling studies of ion-neutral reactions and haze particle composition exist, but there has been little experimental work on the role of ions on haze production. Here, we use an Aerodyne/Tofwerk Atmospheric Pressure interface Time-of-Flight Mass Spectrometer (APi-ToF-MS) to measure the ion chemical composition and relative abundance during the formation of haze analogs initiated by irradiating CH₄ in N₂ by a deuterium lamp. The instrument's high resolution ($R > 7000$) allows us to detect multiple ions at the same unit mass, leading to clear identification of hydrocarbons and nitrogen containing compounds with the same nominal mass. Families of C_xH_y⁺, C_xH_yN_w⁺, C_xN_w⁺, and H_yN_w⁺ are detected with increasing saturation at higher masses during the irradiation of CH₄/N₂ mixtures. The statistical deconvolution method of Positive Matrix Factorization (PMF) was used with the APi-ToF-MS data to pull out different factors that are related to the progression of haze formation during irradiation. Nitrogen incorporation into compounds could hold significance in determining the prebiotic chemistry occurring on Titan, as these compounds could be precursors to amino acids and nucleobases.

Poster 7

Cell Survival in the Antarctic Dry Valleys
Julie Bevilacqua, Georgetown University

The Dry Valleys of Antarctica were once thought to be “sterile,” but despite the harsh conditions, they harbor robust microbial communities. The Dry Valleys have been identified as one of the best Martian analog environments on Earth because of the extreme cold, low levels of precipitation, and high rates of sublimation. Such conditions, which parallel those on Mars, provide intense obstacles to life in the Dry Valleys, and the study of life existing at its limits on Earth can offer insight to the kind of mechanisms that could be used for survival on Mars. In order to understand this mode of survival, an analysis of the microbial populations of the Dry Valleys is necessary to characterize the communities that are capable of enduring such conditions. To this end, samples were sterilely collected in December 2016 from multiple sites in the region. DNA was extracted utilizing a polyezymatic treatment to increase yields from varying cell types. Results suggest not only a high level of compositional diversity across the Valleys, varying with depth, but also pathways associated with stress response. These findings have implications for understanding life in extremely cold and arid environments. The analysis of microbial community composition and metagenomics lends insight to the mechanisms utilized by terrestrial microbes, thereby shedding light on potential features of life on Mars.

Poster 8

Iron: Primordial Cofactor for the Translation System
Marcus Bray, Georgia Institute of Technology

The ubiquity of ferrous iron (Fe^{2+}) in life, despite its toxicity and insolubility, may stem from conditions of the ancient Earth, when Fe^{2+} was abundant and labile. Indeed, biochemistry had access to Fe^{2+} for over a billion years before oxygen rose to levels sufficient to precipitate iron as rust, reducing its bioavailability and increasing toxicity. Today, Mg^{2+} is an essential cofactor that serves diverse structural and functional roles in life’s oldest macromolecular machine, the translation system. Given its likely importance in early biochemistry, and previous results showing successful Mg^{2+} -to- Fe^{2+} substitutions in other biochemical systems, we tested whether Fe^{2+} can serve as a ribosomal cofactor under anoxia. In vitro translation reactions in which the type and concentration of divalent cation could be manipulated were designed and run under anoxic conditions. Protein production was then assayed as a proxy for ribosomal functionality. We determined that Fe^{2+} can associate extensively with the ribosome and support translation of active protein at up to 80% of rates with Mg^{2+} . Our result is remarkable given the enormous number of diverse roles that divalent cations play in translation and suggests that Fe^{2+} can mediate diverse biochemical functions previously thought unique to Mg^{2+} . Given that the translation system originated and matured when Fe^{2+} was abundant, these findings suggest that Fe^{2+} played a role in early ribosomal evolution and that role may be retained in extant microbes living in anoxic niches.

Poster 9

Evaluation of Biogenicity in Rocks Related to
Brazilian Paleozoic Glacial Events

*Flávia Callefo, Institute of Geosciences -
University of Campinas*

Microorganisms play a significant role in mineral precipitation. In this work we describe the activity of microorganisms in sedimentary structures and mineral formation during the glacial period of the Gondwana supercontinent recorded by the “Itu rhythmites”. The Itu rhythmites has been considered a varve-type deposit that present alternating dark laminae (clay/silt-size sediments) and light layers (sand/gravel-size sediments). The rock succession is of Permian to Carboniferous age and located in the Paraná Basin, Brazil. Earlier studies focused on abiotic processes of structure formation. In our contribution, we use different analyses to describe MISS (microbially-induced sedimentary structures) and biominerals, such as biogenic magnetite. Some sedimentary structures as wrinkle structures, ripple marks and soinoial desiccation cracks can be interpreted as fossil microbial mats. Petrological, geochemical and magnetic analyses on the samples reveal a variety of microscopic textures such as mat fabrics and oriented grains. The geochemical signals support the interpretation as microbial structures. Therefore, we offer a new depositional model that considers the participation of microorganisms in the formation of laminae. We also suggest that the iron minerals found in these samples have a strong indication of biogenic origin. It is important to emphasize that the analytical techniques that have being applied for the terrestrial samples on this work in order to test their potential biogenicity, may contribute directly to the analysis of extraterrestrial samples, by in situ and ex situ methods. The results and interpretations obtained so far can be used for studies of structures resembling MISS on Mars, or on meteorites.

Poster 10

Genetic Basis Underlying de Novo Origins of
Multicellularity in Response to Predation
Kimberly Chen, Georgia Institute of Technology

The evolution of multicellularity is a Major Transition that sets the stage for subsequent increases in biological complexity. However, the genetic mechanisms underlying this major transition remain poorly understood. Here, we used the unicellular alga *C. reinhardtii* to generate de novo origins of multicellularity under predation. Outcrossed populations of *C. reinhardtii* were subjected to selection by the filter-feeding predator *Paramecium tetraurelia* in the laboratory. After 50 weekly transfers, two of five experimental populations evolved multicellular structures not observed in any of the three unselected control populations. To uncover genetics underlying multicellularity, we isolated DNA from 24 isolates from the two experimental populations and one control population (8 from each population) and performed Illumina whole-genome sequencing to identify mutations occurred in those evolved isolates. Our results show that the multicellular isolates from the two experimental populations exhibit distinct genetic signatures from each other. We identified the mutations that arose in each evolved isolates and found that the multicellular isolates in each experimental population shared a number of mutations together. Currently, we are conducting tetrad analysis and bulked segregant analysis to determine the number of and the actual loci that contribute to the multicellular phenotypes. This is the first step towards understanding the dynamics and mechanistic basis of the evolution of complexity.

Poster 11

Using Isotopes to Constrain Amino Acid Synthesis on Meteorite Parent Bodies

Laura Chimiak, California Institute of Technology

Meteorites contain a variety of molecules required for terrestrial life, including sugars, alcohols, nucleobases, and amino acids. These compounds have been isolated from uncontaminated samples of meteorites and analyzed for their carbon, hydrogen, and nitrogen isotope signatures. These data suggest at least some components of these prebiotic molecules and/or their precursors are derived from the interstellar medium. Prior measurements of meteoritic organics have been restricted to averages of isotope ratios across all atoms in a molecule (e.g.: all carbon atoms for a $\delta^{13}\text{C}$ measurement). This limitation makes it challenging to relate isotopic measurements to specific moieties and reaction mechanisms and therefore has prevented us from reaching clear conclusions about the precursors and synthetic pathways of meteoritic organics. We have developed a method using the Q-Exactive Orbitrap GC to measure site-specific isotope ratios in amino acid derivatives. Using this method, we measured alanine from produced from Strecker synthesis under various conditions and found a -6‰ equilibrium isotope effects on the amine carbon and up to a -50‰ kinetic isotope effect on the carboxyl carbon. We will compare our results to a sample from Murchison meteorite.

Poster 12

Lumps, Bumps, and Depressions: Europa's Surface Shallow Hydrology

Chase Chivers, Georgia Institute of Technology

Europa, Jupiter's innermost icy moon, has a wealth of diverse geologic features marking the surface of its 20-40km thick ice shell that indicate a constantly active world over its lifetime. In particular, small, elliptically-shaped disruptions of the surface called pits, domes, and small chaos (collectively named lenticulae) may point toward potential habitability and recent geologic activity, but how they're formed on Europa's surface is not well understood. Current models suggest either warm ice upwelling to the near surface or saucer-shaped pockets of liquid water, called sills, disrupting the brittle crust. So far, the sill model has proved most promising due to better thermodynamic requirements, but how the sill deforms the surface to the observed morphology is still unclear. To test current hypotheses on lenticulae formation, we survey lenticulae characteristics to measure topographic relief and geological context using high-resolution imaging data from the Galileo spacecraft. Analysis on relative size, geometry, distribution and a Fourier analysis component, which decomposes the long- and short-wavelength topography present, allows us to constrain whether shallow subsurface water is the cause of these features. We examine whether the shallow hydrological system on Europa might be a possible niche for life by mediating the exchange between the surface and ocean.

Poster 13

Linking Legacy Metabolites to Potential Organic Matter Preservation in an Antarctic Cryoencapsulated Hypersaline Brine
Luoth Chou, University of Illinois at Chicago

The McMurdo Dry Valleys (Antarctica) is an ideal analog for astrobiological investigations of icy worlds. Lake Vida, located in Victoria Valley, contains an anoxic and aphotic ice-sealed brine that has been isolated for millennia and currently hosts active microbes at -13°C . Cold environments can preserve organic material over long timescales which may inundate the total organic carbon pool with legacy signatures, masking modern organic signals. We use metabolomics to elucidate the biogeochemical processes that contribute to the survivability of the active microbial community and determine whether a legacy signal was present in Lake Vida brine (LVBr). Analyses of the extractable dissolved organic matter (DOM) of LVBr was performed using gas chromatography-mass spectrometry (GC-MS) and multidimensional GC-time of flight-MS. Results revealed the presence of legacy metabolites deriving from a previous ecosystem that occupied the ancient open Lake Vida. The metabolome of LVBr also contains oxidized sulfur-bearing organic compounds (sulfones and sulfoxides) of unknown origin. To the best of our knowledge, this study is the first to report on these compounds in the metabolome of an astrobiologically-relevant environment. Here, we speculate on the origin of these compounds, including biologically-mediated and abiotic reaction mechanisms. Oxidized sulfur-bearing compounds persist in global ocean water columns as part of the refractory DOM. Thus, their presence in LVBr may be attributed to a preserve legacy signal from a previous ecosystem. These findings have significant implications for interpreting the origins of organic material recovered from cold, cryoencapsulated brines on Earth and other bodies, such as Mars or Europa.

Poster 14

Coenzymes, Viruses and the RNA World
Wolfgang Francisco Cottom Salas, Universidad Nacional Autónoma de México

The results of a detailed bioinformatic search for ribonucleotidyl coenzyme biosynthetic sequences in DNA- and RNA viral genomes are presented. No RNA viral genome sequence available as of April 2011 appears to encode for sequences involved in coenzyme biosynthesis. In both single- and double-stranded DNA viruses a diverse array of coenzyme biosynthetic genes has been identified, but none of the viral genomes examined here encodes for a complete pathway. Although our conclusions may be constrained by the unexplored diversity of viral genomes and the biases in the construction of viral genome databases, our results do not support the possibility that RNA viruses are direct holdovers from an ancient RNA/protein world. Extrapolation of our results to evolutionary epochs prior to the emergence of DNA genomes suggest that during those early stages living entities may have depended on discontinuous genetic systems consisting of multiple small-size RNA sequences.

Poster 15

Multicellularity in Wild Yeast an Adaptive Trait
in Environments with Nutrient Fluctuation

*Quinn Dickinson, Georgia Institute of
Technology*

Multicellularity in yeast is a trait that has been shown to be adaptive when dealing with the production of common goods, such as enzymes that break down sucrose into usable forms. Wild yeast exist in environments where nutrient availability fluctuates, leading to feast famine cycles whereby at least two different conditions are selected for, growth and starvation. Because of this, it is hypothesized that multicellularity could be a trait adapted for survival during famine cycles. To test this, a wild champagne strain of yeast was used as it showed a multicellular phenotype after starvation. With this strain, competition experiments were performed under various starvation conditions between unicellular and multicellular forms of this strain. Random spore analysis and tetrad dissections were used to determine the frequency of multicellular forms and illumina sequencing was used to determine potential genetic causes of multicellularity. Currently additional work is being done to determine the cause of multicellularity, the mechanism by which it provides adaptive benefits to starving cells and a computational model of the maintenance of unicellular and multicellular forms over evolutionary time scales.

Poster 16

The Effects of Salts on Prebiotic Reactions of
Peptides

Rio Febrian, Saint Louis University

In this project, we probe the effects of salts on prebiotically relevant reactions. The synthesis of biopolymers is one of the main challenges to the origin of life because in aqueous systems, hydrolysis is typically favorable. Given that salts were likely ubiquitous on the Prebiotic Earth, we seek to understand their effects on the kinetics of condensation and hydrolysis. We report preliminary studies concerning the effects of salts on the polymerization of glycine via wet-dry cycles.

Poster 17

Nano-Spectroscopic Approaches to Origins of
Life at Mineral-Organic Interfaces

*Narangerel Ganbaatar, Tokyo Institute of
Technology, Earth-Life Science Institute (ELSI)*

It is strongly supported that mineral surfaces played an important role as adsorbing platform of amino acids and also as catalysts for their abiotic polymerization to form peptides, which were one of the main components of the first self-replicating system. Understanding the mechanism behind the adsorption of simple amino acids on mineral surfaces is a topic of great interest not only in the field of prebiotic evolution but also in many other branches of material sciences. Among various clay minerals, pyrite (FeS_2) is one of the most favored minerals as it possesses a highly reactive surface to drive molecular adsorption. Recent theoretical studies suggest that amino acids adsorption on pyrite surface depends on its surface structure. However, these results have not been tested experimentally. In the present work, through quantitative force analysis with atomic force microscope (AFM) in which a single amino acid residue was mounted on the tip apex of AFM probe, we were able to find adsorption sites of amino acids on pyrite surface. Our results of Raman spectroscopic studies and force measurements with a chemically modified AFM probe demonstrated for the first time that pyrite provided higher adsorption probabilities of amino acids for the chemical reactions at surfaces.

Poster 18

Impact Craters on Titan: The Search for Life in
Titan's Craters

*Joshua Hedgepeth, University of Western
Ontario*

Saturn's moon Titan is one of the most dynamic bodies in the solar system as the only moon with a thick atmosphere. Titan's landscape is therefore not visually dissimilar from Earths, with an active hydrological cycle like Earth. However, the atmosphere of Titan is composed of organic rich molecules, and rather than rain water it rains liquid methane because of low temperatures ($\sim 94\text{K}$). This does not meet traditional criteria for a habitable world. However, a new analysis by Neish et al. (2018) shows how life could still find a way.

The heavy organics in Titan's atmosphere have the potential to form more complex structures that more closely resemble life when introduced to liquid water. While not stable on the surface, large volumes of water ponds form in fresh impact craters. These only last on the order of 100k of years, but the speed at which life could progress in this primordial soup is not known. Therefore, Titan's impact craters offer a unique opportunity to study how life transitions from prebiotic chemistry to life.

It is essential to have a complete assessment of Titan's crater population if we ever hope to investigate this further. Larger craters produce larger melt ponds, and fresher (less eroded) craters increase the ease of finding biomolecules in the ice. Here we have compiled the depth (to assess the erosion) and diameter (to determine melt pond sizes) of all known craters on Titan, and we use it to produce a list of the best craters to study.

Poster 19

Alarmones as Vestiges of a Bygone RNA World
*Ricardo Hernandez-Morales, Universidad
Nacional Autónoma de México*

All known alarmones are ribonucleotides or ribonucleotide-derivatives that are synthesized when cells are under stress conditions, triggering a stringent response that affects major processes such as replication, gene expression and metabolism. The biological distribution of some alarmones in all living beings suggests that they are very ancient molecules that may have been present in cellular systems prior to the divergence of the Archaea, Bacteria and Eukarya domains. Their chemical structure, wide biological distribution, and functional role in highly conserved cellular processes strongly suggest that these modified nucleotides are molecular fossils of an epoch in the evolution of chemical signaling and metabolite sensing during which RNA molecules played a much more conspicuous role in biological catalysis and genetic information

Poster 20

Stepping Back in Time: Selecting *Escherichia coli* with an 'Ancestral' Tryptophanyl-tRNA Synthetase
*Jessica Hobson, University of North Carolina,
Chapel Hill*

The evolution of the genetic code and codon-dependent protein translation connects pre-biotic chemistry and the origin of life. We believe aminoacyl-tRNA synthetases (aaRSs) played a central role in the development of the genetic code. aaRSs activate amino acids and attach them to the appropriate tRNAs, thus enforcing the rules of the genetic code. Previously, we used structural superimposition of aaRS homologs to identify conserved catalytic cores, termed Urzymes, for both Class I and II aaRSs. We showed Urzymes increase amino acid activation and tRNA aminoacylation rates by 10^9 - and 10^6 -fold over the uncatalyzed rates, respectively. To further investigate primordial protein translation, we now seek to select *Escherichia coli* mutants that are able to survive when the native Tryptophanyl-aaRS (TrpRS) is replaced with its Urzyme. We are replacing TrpRS with a series of five successively less active TrpRS mutants in order to select *E. coli* strains adapted to progressively less functional TrpRS enzymes. The final mutant TrpRS will be replaced with the Tryptophanyl-Urzyme. We hypothesize this gradual decrease in catalytic efficiency will allow us to select *E. coli* with background mutations that enable it to tolerate the decreased catalytic efficiency of the Urzyme. Demonstrating the *in vivo* activity of an Urzyme would provide strong support for our hypothesis that Urzymes are close approximations of ancestral aaRSs and outline a novel selection method that can be applied to other ancestral gene reconstructions.

Poster 21

Co-factor driven evolution of dynamic peptide libraries

Ankit Jain, CUNY Advanced Science Research Center

Proteins are an indispensable component of the modern biological metabolic machinery. A key part of understanding and emulating their function is to converge them into their minimalistic components. Considering the complexity that has evolved over billions of years this seems to be a non-trivial task. However, if an approach is to be formulated, for in vitro evolution that could potentially rival in natura evolution a co-factor driven formation of peptidic materials is to be sought. Recently, Pappas et al. showed that library of dipeptides can be used for dynamic evolution of nano materials. In this work we modified this approach to amplify peptide sequences which assemble selectively on binding with specialized co-factors. The co-factors that we chose for this work were porphyrin derivatives and highly relevant biomolecules such as RNA, DNA and ATP. Among porphyrins, we chose specifically three derivatives, Hemin (natural) TMPyP, Fe-TMPyP (synthetic). Rationale for selecting these derivatives was to eventually create functional peptidic assemblies that could partake in various photo-physical phenomena, endogenous to the porphyrin systems. We selected seven dipeptides for our dynamic library, allowing each set to evolve in solution with thermolysin and respective Co-factor. The results of evolving libraries and their consequences would be presented in the talk.

This approach has been developed as an in vitro auxiliary driven library which can further be used for finding binders of more complex molecules such as RNA and DNA expanding the significance of the approach into possible pre-biotic investigation.

Poster 22

Self-Assembled Biomaterial Nanostructures as Catalysts and Biomarkers of “Life”

Tony Jia, Tokyo Institute of Technology, Earth-Life Science Institute (ELSI)

The initial emergence of life is believed to have been governed by the ability for a system to develop machinery capable of replication and metabolism. Modern extant life utilizes biopolymers such as DNA and proteins, respectively, for these purposes. Early cellular life likely did not have access to large amounts of these long biopolymers due to the general inability for prebiotic systems to easily replicate these molecules, but replication and metabolism are still necessary features of life. One area of recent interest is the possibility of using supramolecular self-assemblies to assist in or catalyze these essential reactions. These self-assemblies can be assembled from simple small molecules, short oligomers such as short peptides, or even minerals and mineral surfaces; all of these components would have likely been readily available on the early Earth (much more readily available than longer biopolymers). The resulting structures, whether they are nanofibers, uniform sheets, crystalline structures, or phase-separated compartments, potentially give rise to novel emergent properties that the smaller individual components cannot and also may be a novel, nontraditional biomarker that we should consider for future life detection missions. Here, we study the self-assembly properties and resulting supramolecular structures of various prebiotically relevant supramolecular systems, including short tripeptides, peptide/nucleic acid coacervate droplets, hydrogels, polyesters, and mineral surfaces. We then probe the ability of these systems, as well as systems that emerge from combinatorial chemical evolution studies, to perform prebiotically relevant functions, including assisting in scaffolding, binding, concentration, replication, and catalysis.

Poster 23

Potential Direct Feeding of Anaerobic Oxidation of Methane by Methanogenesis in the Sulfate-Reduction Zone of a Coastal Wetland System
Sebastian Jian Krause, University of California, Los Angeles

Methane has been proposed as a promising bio-signature, and recent discoveries have inspired ongoing research about the nature of methane cycling in astrobiologically relevant environments. The methane emitted from wetlands, Earth's largest natural source, comes primarily from biological methanogenesis by diverse groups of archaea, and is the last step in carbon catabolism of organic matter. In anoxic marine sediments, methane can be efficiently metabolized by a process called Anaerobic Oxidation of Methane (AOM), whereby a microbial consortium of methanotrophic archaea and sulfate-reducing bacteria oxidize methane to bicarbonate. This imparts a unique geochemical trend in sediments called the Sulfate-Methane Transition Zone (SMTZ). Sulfate reduction coupled to organic matter degradation is energetically more favorable than methanogenesis when utilizing hydrogen and acetate. Thus, sulfate reduction tends to suppress methanogenesis above the SMTZ when competing for these substrates. But methanogenesis can co-exist in the presence of non-competitive substrates, such as methionine, methanol, and methylated amines, which are particularly abundant in organic-rich sediments. Here I will present my proposed research to investigate the relationship between methanogenesis and AOM above the SMTZ in the Carpentaria Salt Marsh Reserve, a coastal wetland located about 80 miles north of Los Angeles, CA, USA, using radioactive labeled non-competitive substrates, state of the art technology in biogeochemistry, microscopy and molecular techniques. The results will identify substrates, anaerobic metabolisms, and biogeochemical trends associated with methane in anoxic environments, which will improve our understanding of methane as a potential bio-signature in extraterrestrial environments.

Poster 24

Sunlight Driven Reactions of SO₂ with Organic Molecules
Jay A. Kroll, University of Colorado Boulder

In examining the planetary conditions required for habitability, a clear understanding of planetary climates systems is vital. Aerosol formation plays a vital role in the climate and is tied to feedback loops that can cool or warm the planet. As such, understanding the chemical mechanisms that lead to aerosol seeding molecules is important for understanding larger scale climatic responses in planetary atmospheres. Sunlight is the largest energy source in the Earth's atmosphere and acts as a driver of a wide variety of chemical processes. Recent work in the Vaida lab has shown that sulfur dioxide, when excited with UV light available in the solar spectrum, is incredibly reactive with a wide range of organic molecules including saturated alkanes. This photochemical reaction leads to formation of aerosol seeding molecules. I have undertake a study to measure the rate constants for the reaction of photochemically excited sulfur dioxide with a series of alkanes ranging from methane (1 carbon atom) to n-nonane (9 carbon atoms). I will present on the effect of chain length on the reaction rate and the effect of branched and ringed structures of alkanes on the reaction. I will also discuss the photochemical mechanism for the reaction that leads to aerosol seeding molecules.

Poster 25

An Investigation of Carbonaceous Chondrite Meteorites via Raman Spectroscopy
Amy LeBleu- DeBartola, University of Central Florida

Many carbonaceous chondrite meteorites have been found to have Amino Acids present, and may be a significant vehicle for the delivery of amino acids to planetary bodies. It is theorized that certain subtypes of carbonaceous chondrites are more likely to have amino acids due to the amount of thermal processing they received. Thin slices from several meteorites were analyzed using Raman spectroscopy to discover information about the heating they underwent in high spatial detail. This has implication for the type and complexity of organic molecules that can be formed and not reprocessed.

Poster 26

Cultivation of *Bacillus subtilis* in Spaceflight Alters the Mutational Spectrum in the rpoB Gene
Joshua Leehan, University of Florida

In contrast to the classical view that mutations are random, a growing body of evidence indicates that exposure to environmental stress in microbes can alter both the mutation rate and the mutagenic spectrum, thus increasing the supply of mutational outputs in a phenomenon dubbed Stress-Induced Mutagenesis (SIM). The human spaceflight environment presents its own unique set of physical stressors, including cosmic radiation, microgravity, vibration, electromagnetic fields, and altered atmospheric compositions. Numerous studies have explored microorganisms' physiological responses to spaceflight exposure. However, very few studies have asked whether microbial exposure to spaceflight might lead to SIM. The effect of *Bacillus subtilis* exposure to the human spaceflight environment on growth, mutagenic frequency, and spectrum of mutations to rifampicin resistance (Rif^R) was investigated to determine if the human space flight environment leads to SIM. *B. subtilis* cells were cultivated in Biological Research in Canister-Petri Dish Fixation Units (BRIC-PDFUs) on two separate missions to the International Space Station (ISS), dubbed BRIC-18 and BRIC-21, with matching asynchronous ground controls. No statistically significant difference in either growth or in the frequency of mutation to Rif^R was found in either experiment. However, nucleotide sequencing of the rpoB gene from Rif^R mutants revealed dramatic differences in the spectrum of mutations between flight (FL) and ground control (GC) samples, including two newly discovered rpoB alleles in the FL samples (Q137R and L489S). The results strengthen the idea that exposure to the human spaceflight environment causes unique stresses on bacteria, leading to alterations in their mutagenic potential.

Poster 27

Guided Polymerization of Mononucleotides by Lipid Bilayers Studied by Molecular Dynamics Simulations

Dylan Malenfant, McMaster University

One model for the generation of RNA-like polymers on the prebiotic Earth uses wet-dry cycles in warm little ponds. This process may be facilitated by amphiphilic molecules. When these ponds are dried, the constituents are confined into thin, highly concentrated films. Nucleotides were reported to form pre-polymers – stacks of ~10 monomers at the characteristic 3.4 Å distance [1,2]. Heating under dry conditions can then fuel the formation of phosphodiester bonds and the creation of RNA polymers. To examine this model with atomistic detail, we used Molecular Dynamics (MD) simulations. Monomers of adenosine and uridine monophosphate, were studied in both low- and high-concentration regimes corresponding to 1.5 and 50 mol% in contact with a 128-lipid 1,2-dimyristoyl-sn-glycero-3-phosphatidylcholine (DMPC) bilayer. We found the lipid bilayer to strongly suppress diffusion perpendicular to the membranes, leading to two-dimensional organization of the monomers. The drying process was modelled by continuous removal of water molecules from the simulations. Dehydration was found to organize the monomers with a preference for a 5'-to-2' bonding scheme instead of 5'-to-3' at a ratio of approximately 1.5:1. This shows that a lipid bilayer alone is not efficient in forming RNA. Simulations which also included ammonium chloride led to a preference for the 5'-to-3' bonding scheme observed in RNA polymers. Previous experiments and current simulations thus suggest that wet-dry cycling is a promising approach to generate RNA strands under prebiotic conditions.

[1] Topozini et al., 2013, PLoS ONE 8, 31285

[2] Himbert et al., 2016, Sci Rep 6, e62810

Poster 28

Community Composition and Metabolic Characterization of the Bonneville Salt Flats
Julia McGonigle, University of Utah

An 18 square mile salt flat on Mars has recently been speculated to be a remnant of the last large lake which may have potentially hosted life on the red planet. Similar large scale salt deposits exist on Earth, such as the Bonneville Salt Flats in Utah. These salt flats are a remnant of a massive lake that stretched further than the Great Salt Lake in the Pleistocene. Although these salt flats on Earth currently undergo ephemeral wet/dry cycles the salt flats on Mars no longer experience, they nonetheless represent a Mars analog and provide the opportunity to learn more about extreme ecosystems that support microbial communities on Earth.

Comprehensive microbial studies have been conducted on salt flats in other locations, but to date the only studies done at the Bonneville Salt Flats have been limited to culture-based approaches. We are using culture-independent approaches for the first time to investigate the microbial community of these salt flats. Sequencing of the 16S rRNA gene, the universal taxonomic marker for microbial species, was performed on samples collected in September 2016 from 8 pits spanning the flats in horizontal and vertical transects. Here we report diversity and species composition between pits and speculate on metabolic capability of microbial communities that inhabit the salt flats.

Poster 29

rRNA Expansion Segments of the Homo sapiens
Ribosome: Structure and Function

*Santi Mestre Fos, Georgia Institute of
Technology*

Ribosomes are molecular fossils that have been fitfully increasing in size for around four billion years. Recent growth, over the last 1 billion years, is apparent from comparing secondary and three-dimensional structures of ribosomes across different species. Organismal complexity is correlated with the size of the rRNA: ribosomes (LSU) of metazoans are larger than those of protists. Eukaryotic ribosomes are larger than those of prokaryotes. rRNA additions to the ribosome, which occur at specific sites, are known as “expansion segments” (ESs). ESs are found on the ribosomal surface and do not perturb the common core, which contains the peptidyl transfer center (PTC) and the decoding center. Recent studies indicate that ESs of Homo sapiens and Saccharomyces cerevisiae bind to a wide range of non-ribosomal proteins that are part of multiple cellular processes (2,3). Furthermore, based on different CD spectra obtained with different monovalent cations, some ESs of the human ribosome have the potential of forming G-quadruplexes (3). Based on these recent data, our goal is to determine if these ESs are truly able to form G-quadruplexes and to better understand their function by performing trafficking studies in vivo. Their significantly larger sizes in metazoans compared to those of simpler species suggests that in higher organisms the ribosome has evolved to become a direct player in a wide range of different cellular processes.

Poster 30

Investigating the transfer and survivability of
bacteria within the stratosphere using imaging
and molecular techniques

Tareq Omairi, University of Sheffield

Continuing evidence from recent studies shows numerous microbial species to possess the ability to survive and replicate in the Earth's stratosphere, despite extreme conditions of this atmospheric layer. Previous attempts to isolate and identify bacteria from the stratosphere have been met with varying levels of success. In this study, with the aim of sampling the stratosphere for bacterial cells, six stratospheric balloon launches were performed over the course of three years, from different sites around the globe. Imaging and molecular techniques were used to analyse the findings, without an overreliance on routine microbial culturing protocols to minimize contamination risks. Scanning Electron Microscopy (SEM), Energy Dispersive X-Ray Spectroscopy (EDAX), and Molecular techniques, including Single-cell amplification, were used for the analysis of the obtained isolates. Identification of numerous biological cells, in addition to the mechanism which was used to bring the cells to the stratosphere, was determined from the SEM and EDAX results, based on the sizes of the recovered cells using theoretical models from previous studies. DNA presence was detected, sequenced, and identified, using single-cell amplification and next-generation sequencing, revealing a diverse range of microorganism, with many previously isolated exclusively from deep hydrothermal vents and other extreme environments. Thus raising the question of the role of the stratospheric environment in the evolution of microbial life, and its relevance as an analogous to the surface environment of Mars. The value of the Single-cell amplification technique as a tool for analysing limited astrobiological samples, minimizing contamination risks is also demonstrated in the results.

Poster 31

Exploration of Raman and Carbon Isotopic
Biosignatures on Early Earth and Mars
*Jeff Osterhout, University of California, Los
Angeles*

The search for evidence of ancient life on Mars is one of NASA's primary goals for the upcoming Mars 2020 rover mission, and the strategy is based largely on studies of fossil organic matter from the Precambrian rock record on Earth. This study seeks to address the preservation and detection of macromolecular carbonaceous matter (i.e., kerogen) and its associated carbon isotopic and Raman biosignatures by analyzing a collection of biogenic microfossils from 18 geologic units containing rocks of varying thermal maturities and spanning more than one billion years of the fossil record. Combined with optical microscopy, Raman spectroscopy and secondary ion mass spectrometry (SIMS) measurements will be made for individual Precambrian microfossils to determine their degree of thermal alteration and to reconstruct ancient microbial carbon-fixation pathways. Raman spectra will be collected using visible laser wavelength (~458 nm) to calculate their relative thermal maturity (RIP value) and will then be compared with carbon isotope values of the same fossils. Furthermore, Raman will be an essential tool of the Scanning Habitable Environments with Raman and Luminescence for Organics and Chemicals (SHERLOC) instrument on the Mars 2020 rover, which will utilize a deep-UV laser wavelength (~248.6 nm) setting to map and characterize minerals, organic compounds, and potential biosignatures in Mars rocks. Thus, the same microfossils will be analyzed here using similar deep-UV settings (~244 nm) to evaluate potential biosignature preservation. The findings of this study will improve our understanding of early life on Earth to guide the search for fossil life on Mars.

Poster 32

Microfluidic Amine and Amino Acid Pre-
Concentration for Improved Limits of Detection
Kenneth Seaton, Georgia Institute of Technology

In the search for life elsewhere in our solar system and beyond, amino acids serve as biomarkers due to their ubiquity in terrestrial biology and potential for enantiomeric enrichment. Current microchip capillary electrophoresis with laser induced fluorescence (μ CE-LIF) instrumentation quantifies amino acids with parts-per-trillion limits of detection and, using a metric of between 100-500 attomoles of valine per *E. coli* cell, could detect as low as 30-150 cells/mL. If future missions contain instruments with insufficient sensitivity, they will not detect life. Only by sending instrumentation capable of detecting one quantum of life (a bacterium) will we ever know if life exists beyond Earth. Pre-concentration is a well-studied method for enhancing system-level limits of detection, and has the additional benefit of sample clean-up, removing matrix components that can hinder analytical performance (e.g. perchlorates on Mars, high salt on Europa). Here, we present the development of a microfluidic method to achieve one-step pre-concentration, derivatization and sample clean-up of amino acids. In this μ CE-LIF design, amino acids are concentrated on the surface of a fluorescent bead material by flowing large volumes of solution over the beads. Derivatized Amino acids are then liberated by flowing a reducing solution over the beads, delivering them to the separation channel. The fully optimized system will be used to analyze Europa and Enceladus analogues, demonstrating the applicability of the device to the types of samples encountered during space flight.

Poster 33

Polymerization and Assembly of Plausible
Protopeptides

Martin Solano, Georgia Institute of Technology

Studies on the origin of biopolymers and their prebiotically plausible polymerization often rely on the spontaneous emergence of a statistical distribution of polymers with various lengths and sequences. For peptides, the expectation is that a small subset of the longer polymers would be able to fold and function similarly to extant enzymes. Our research aims to show an alternative and more plausible approach to the selection of biopolymers by probing a subset of prebiotic small molecules for properties of a dynamic combinatorial system. We utilize hydration-dehydration cycles to form and break ester bonds between short hydroxy acid terminated peptides. We show how these polymers can grow to lengths of 20+ mixed monomers in a single dry phase and disassemble following rehydration. In the presence of a small molecule guest or selective pressure, the assembled polymers are expected to form a stable host-guest complex which could then be selected out of the ensemble of polymers formed.

Poster 34

Preliminary Work towards the Development of a
Miniaturized, Portable Microfluidic Cell
Counter for Icefin

*Nicholas Speller, Georgia Institute of
Technology*

NASA has identified Europa as a priority target for future exploration missions due to the European ocean's potential past and present habitability. It is imperative that instrumentation designed to detect signs of life on distant ocean worlds, such as Europa, be able to detect biosignatures here on Earth. Earth's extreme environments, particularly Antarctica and the sub-ice shelf ocean, provide powerful Europa analogues for benchmark studies. One biosignature that is considered extremely important in the search for life is direct observation of organic particles with similar size and morphology to single celled microbes. Microbes represent the most prolific and widely distributed forms of life on Earth. Here, we present preliminary work towards the development of a miniaturized, portable microfluidic cell counter for Antarctic Ocean water analyses on Icefin, an under-ice unmanned vehicle.

The microfluidic cell counter presented is prototyped using a four inlet cross channel design employing sheathflow generated by high voltage induced electroosmotic flow. Sheath flow is characterized using fluorescent dye and a video microscope. Fluorescent polystyrene latex particles are used as cell analogues and counting is characterized by comparing computer vision analyzed videos with counts from a prototype laser induced fluorescence (LIF) optical stack detector. This breadboard optical stack was developed to reduce the footprint required for LIF and as an easily tunable model system for further miniaturization as required for portable applications. This work holds great promise for development of a portable LIF enabled cell counter for sub-ice shelf ocean water analyses.

Poster 35

Adaptive Evolution of Bacteria to High
Concentrations of Magnesium Sulfate with
Implication to Europa

Azarin Yazdani, University of Arkansas

Discovered in 1610, Europa is the 4th largest moon orbiting around Jupiter. There are plausible evidences for the existence of a global subsurface saline ocean which suggest that Europa is one of the best candidates for astrobiological explorations in Solar System. Although NaCl is the most abundant salt in Earth's seawater, geochemical models suggest that Europa's ocean is dominated by high concentrations of MgSO₄. Salinity is a limiting factor for bacterial life as the cells thrive to maintain an osmotic balance with the outside environment. The current study focuses on the adaptive strategies used by mesophilic bacteria for tolerance at high concentrations of MgSO₄ with application to Europa. Our preliminary work on *Escherichia coli* demonstrate that the adaptation of this bacteria to high concentrations of MgSO₄ is feasible over laboratory time scales.

Poster 36
-withdrawn-

Oral Session IV
Wednesday, June 6th 2018, 9:00 - 10:10 am

9:00 - 9:10 am

Warm Up Talk

Rebecca Rapf, Lawrence Berkeley National Lab

9:10 - 9:30 am

Insights into Atmospheric Methane Sources and
Sinks Using Methane Clumped Isotopes

Mojhgan Haghnegahdar, UCLA

Methane is the most abundant organic chemical and the second most important long-lived greenhouse gas in the atmosphere. It also has a significant impact on the chemistry of the troposphere and stratosphere. Methane may also be an indication of life in the atmosphere of Mars or could be a consequence of geological activities. However, there are large uncertainties in the sources and sinks of methane to the atmosphere, as well as in their variability in time and space. In general very little is known about the biological/environmental controls on the rates at which methane is produced or consumed on the Earth or Mars. Different methane sources have different isotope ratios because of variations in substrates, formation reactions, and temperatures. Isotope ratio measurements will provide useful constraints on source components and sink processes. Yet, bulk isotope ratios alone are unlikely to be diagnostic because of mixing of sources. We investigated the potential of $^{13}\text{CH}_3\text{D}$ and $^{12}\text{CH}_2\text{D}_2$, the doubly substituted mass-18 isotopologues of methane, as tools for tracking atmospheric methane sources and sinks. Our work focused on measuring $^{12}\text{CH}_2\text{D}_2$ and $^{13}\text{CH}_3\text{D}$ in methane samples from natural boreal lakes, collected in Alaska, Canada, and Siberia. We analyzed methane samples representing a diverse set of cold lakes in different geographical regions, with varying geological and ecological contexts, methane fluxes and isotopic signatures. Measurements of both $\Delta^{13}\text{CH}_3\text{D}$ and $\Delta^{12}\text{CH}_2\text{D}_2$ are now possible with the large-geometry gas-source mass spectrometer at UCLA. Most our samples are far from clumping equilibrium, but resemble laboratory cultures of microbial methanogens.

9:30 - 9:50 am

The Fate of Lipid Biosignatures in a Mars
Analogue Sulfur Stream

Jonathan Tan, Imperial College London

Past life on Mars will have generated organic remains that may be preserved in present day Mars rocks. The most recent period in the history of Mars that retained widespread surface waters was the late Noachian and early Hesperian and thus possessed the potential to sustain the most evolved and widely distributed martian life. Guidance for investigating late Noachian and early Hesperian rocks is provided by studies of analogous acidic and sulfur-rich environments on Earth. Here we report organic responses for an acid stream containing acidophilic organisms whose post-mortem remains are entombed in iron sulphates and iron oxides. Acid stream data indicate that the organic records of life, should they exist (or should life ever have arisen) on Mars will comprise microbial lipids. The data indicate that the organic records of Hesperian life on Mars could be present as microbial lipids. Lipids are a potential sizeable reservoir of fossil carbon on Mars, and can be used to distinguish between different biosynthetic pathways and domains of life. Concentrations of lipids, and particularly alkanolic or “fatty” acids, are highest in goethite layers that reflect high water-to-rock ratios and thus a greater potential for habitability. Goethite can dehydrate to hematite, which is widespread on Mars. Current and future Mars missions should seek to detect fatty acids or their diagenetic products in the iron oxide and iron oxide-hydroxide units associated with sulphur-rich environments.

9:50 - 10:10 am

A novel apatite-based oxygen paleobarometer
across the Neoproterozoic-Cambrian transition
*Amanda Garcia, University of California, Los
Angeles*

It has long been postulated that the Neoproterozoic-Cambrian transition was correlated with an increase in atmospheric oxygen, argued to be necessary for the evolution of oxygen-requiring complex metazoans through the ~541 Ma Cambrian explosion. Despite previous estimates, based largely on minimum physiological needs of metazoans, carbon isotopic excursions, and redox-sensitive element proxies, the oxygenation history during this geologically and biologically important time period is not yet adequately constrained. Globally-widespread phosphorite formations straddling this transition suggest a unique biogeochemical marine environment, intimately associated with increased availability of phosphorous, biological productivity, and carbon burial. Here we present fluorescence data of samarium-substituted apatite from two such deposits, the fossiliferous Neoproterozoic Doushantuo and Cambrian Chulaktau Formations, the spectral features of which are experimentally demonstrated to reflect oxygen levels during samarium emplacement. Association with well-preserved microfossils indicates an early-diagenetic history of apatite crystallization, before significant organic degradation and burial. These fluorescence signatures are thus interpreted to suggest primary oxygen levels in pore waters, offering a novel semi-quantitative and direct paleobarometer for the shallow-water depositional environments of these phosphorites. Such studies can aid in refining the growing body of evidence detailing the history of Neoproterozoic-Cambrian oxygenation, providing invaluable understanding of a significant environmental transition during the early stages of metazoan diversification, arguably among the most major events in the evolution of our planet.

Oral Session V
Wednesday, June 6th 2018, 10:30 - 11:50 am

10:30 - 10:50 am

Glycosylation of a Model Proto-RNA
Nucleobase with Non- Ribose Sugars:
Implications for the Origin of RNA

David Fialho, Georgia Institute of Technology

The emergence of nucleic acids is a central, but poorly understood, component of the origin of life. Although extant RNA features the sugar ribose exclusively, the known prebiotic routes to sugars are inherently nonselective, producing thousands of distinct monosaccharide products¹. We show that 2,4,6-triaminopyrimidine (TAP), a prebiotically plausible proto-nucleobase, is glycosylated in water by a variety of sugars in yields comparable to those found for the reaction of TAP with ribose. Furthermore, both ribosides and non-ribose glycosides of TAP show propensities for supramolecular self-assembly with a heterocyclic pairing partner in water, a process which may have facilitated the formation of the first genetic polymers². These results call into question the assumption that ribonucleotides, and hence, RNA, were produced selectively from prebiotic chemical processes, and suggest that the selection of, or refinement towards, ribose occurred at a later or higher-order stage in chemical evolution.

10:50 - 11:10 am

Dynamic Polymerization of Prebiotic
Depsipeptides Allows Selection of Stable
Structures

*Moran Frenkel-Pinter, Georgia Institute of
Technology*

A long-standing challenge of origins of life research is to find a plausible prebiotic route for the formation of peptides. Recently, a simplified route for prebiotic peptide formation has been reported, which involves subjecting a mixture of hydroxy acids and amino acids, to repetitive wet-cool/dry-hot cycles. It has been proposed that the resulting depsipeptides, containing both ester and amide linkages, might have constituted part of the primordial proto-peptides population.

We hypothesize that depsipeptides possess characteristics that would have facilitated their selection by chemical evolution, namely a propensity for self-assembly, a chemical stability sufficient for functionality, as well as a susceptibility to hydrolysis that allows regular recycling and exploration of sequence space. To demonstrate these properties, we have synthesized an OH-capped peptide library, ranging from dimers to octamers, which contain an N-terminal glycolic acid (the hydroxy acid analog of glycine) that, upon polymerization via ester bond formation, would produce depsipeptides with regularly spaced ester and amide linkages.

We have found that applying dry-hot conditions drives oligomerization of these OH-capped peptides and that a structural shift coincides with polymer growth. We have also found that shorter OH-capped peptides polymerize more readily than the longer OH-capped peptides. We will discuss investigations of depsipeptide stability and self-assembly propensity by a variety of spectroscopy- and microscopy-based methods. Additionally, we were able to find pronounced differences in the chemical stability of certain OH-capped peptides over others, and we have used these differences as a basis to show selection of certain OH-capped peptides in complex depsipeptide mixtures.

11:10 - 11:30 am

Prebiotic heterogeneity and its effect on nonenzymatic replication

Niraja Bapat, Indian Institute of Science Education & Research (IISER), Pune

Prebiotic soup would have been a heterogeneous solution containing a mixture of many different molecules. However, most of the prebiotically pertinent reactions are carried out in buffer solutions, ignoring the presence of any 'background' molecules. We recently analyzed the effect of pertinent co-solutes on nonenzymatic template-directed RNA copying reactions. In this first of its kind study, we found that lipid vesicles and polyethylene glycol, when present as co-solutes, adversely affects the fidelity of nonenzymatic copying reactions. More specifically, the rate of those reactions, in which a purine monomer was added against its cognate templating base, was reduced in the presence of co-solutes (Bapat and Rajamani, 2015).

Using relevant biophysical techniques like NMR and microscopy, we are working on dissecting the underlying mechanism behind the observed effects. Our preliminary results indicate that both, nucleotide stacking and RNA-lipid interactions seem to be enhanced in the presence of co-solutes. This might potentially be responsible for the reduction in the rate of copying, seen in our reactions. In conclusion, our results underline the importance of factoring in prebiotic heterogeneity while studying pertinent enzyme-free reactions, as our studies suggest direct implications for efficient replication of functional nucleic acid sequences in a complex prebiotic milieu.

11:30 - 11:50 am

No Laughing Matter: Nitrous Oxide Production by Chemodenitrification in the Ferruginous Proterozoic Ocean

Chloe Stanton, Penn State University

Dimmer solar luminosity required an enhanced greenhouse effect to sustain liquid water on early Earth's surface, but evidence for liquid water throughout Earth's history is incontrovertible. Solutions to this "Faint Young Sun Problem" are often attributed to CO₂ and CH₄ because more potent N₂O would have photodissociated during the anoxic Archean. N₂O may have become an important greenhouse constituent after the Great Oxidation Event at ~2.4 Ga. In this study, we tested the hypothesis that rapid reduction of NO by Fe²⁺ (chemodenitrification) could have resulted in higher N₂O fluxes from ferruginous Proterozoic seas. We measured N₂O production rates in anoxic seawater, varying NO and Fe²⁺ to empirically derive a rate law. The reaction orders for NO and Fe²⁺ were 1.0 and 0.3, respectively; the rate constant was 7.2 x 10⁻⁵ s⁻¹; and the resultant isotopic site preference was +16‰. We used this rate law to calculate that 25-100 pM NO would have been required to produce an N₂O flux of 130 x 10¹² g N yr⁻¹, assuming 0.1-10 mM Fe²⁺, modern N₂ fixation rates, and that all N₂ fixed was chemodenitrified to N₂O. The N₂O flux was fed into a 1-D photochemical model of steady-state atmospheric N₂O concentrations across variable surface-atmosphere fluxes and atmospheric O₂ (0.001-0.1 PAL). This model yielded 0.4-10 ppmv steady-state atmospheric N₂O, which could equate to up to 5°C greenhouse warming at near-modern CO₂ and CH₄. We conclude that coupled biotic-abiotic production of N₂O in ferruginous seawater could have contributed to Proterozoic habitability by amplifying greenhouse warming.

Oral Session VI
Wednesday, June 6th 2018, 1:00 - 2:10 pm

1:00 - 1:10 pm
Warm Up Talk

Marcus Bray, Georgia Institute of Technology

problems and has express implications for construction of artificial biochemistries.

1:10 - 1:30 pm

Test of genetic code evolution hypotheses:
Reverse evolution of specific target proteins by
mRNA-display technique

*Valerio Guido Giaobelli, Charles University,
Department of Biochemistry*

Although extant proteins consist of 20 different amino acids, it has been proposed that primordial proteins consisted of a smaller set of “early” amino acids and that additional “modern” amino acids have gradually been recruited into the genetic code. This naturally leads to the questions: can structured and functional proteins be constructed using the “early” amino-acid alphabet? Can extant proteins be reverse-evolved while preserving their structure/function?

To test this, protein databases have been inspected to select model extant protein candidates with different structural folds. Our preliminary search contains proteins with both catalytic and binding/interaction functions.

The selected protein targets were “reverse-evolved” in vitro into variants where the “modern” amino acid were randomized by “early” ones. The libraries of randomized genes were incorporated into a genotype-phenotype linkage to be compatible with an appropriate library display (mRNA display) and selection method. The selection of successful candidates was based on conservation of structure and/or function and the most “successful” variants will be characterized.

This research will inform us of the essentiality of “modern” amino acids for building protein structure/function and thus will provide a direct test of the hypotheses about early proteins. In addition, proteins constructed from a limited amino acid alphabet are of importance in protein engineering and synthetic biology. Finally, this area touches upon the very basic link of protein sequence-structure-function that lies at the core of many biotechnological and biomedicine

1:30 - 1:50 pm

Microbial activity and adaptation at extreme elevations on Atacama volcanoes: the best Martian analogue on Earth?

Lara Vimercati, University of Colorado at Boulder

Soils at extremely high elevation on slopes of the high Andes represent some of the harshest ecosystems yet discovered on Earth. Microbial life in these environments has to cope with a complex interplay of parameters, such as a high UV flux, extreme diurnal freeze-thaw cycles, low atmosphere pressure and an extremely low nutrient content and water activity and are therefore considered as potential analogues for habitable zones on Mars and other planetary bodies. Only a very limited spectrum of bacterial and fungal lineages have overcome the harshness of this environment and may have evolved the ability to function in situ. Preliminary work on soil microcosms exposed to repeated extreme thermal fluctuations with water addition has revealed a significant shift in the total community composition with a few phylotypes becoming dominant. Among eukaryotic microorganisms, *Cryptococcus* dramatically increased in relative abundance when provided with water in simulated field thermal fluctuations and proved to be able to grow continuously in liquid culture subjected to extreme daily freeze-thaw cycles up to a high of 30 °C during the day and down to a low of -10 °C at night. My results provide evidence that *Cryptococcus* sp. has the capacity to grow during freeze-thaw cycles in the field, and that it may be able to mainly do that during periods of higher soil moisture. Genomic and transcriptomic analyses of *Cryptococcus* sp. will follow to shed light on strategies this organism uses to survive multiple challenges found in this life-limiting environment. Given its unique ability to survive under multiple environmental stressors, *Cryptococcus* sp. may be a model organism for exobiology and studies on stress resistance on Eukaryotes and its adaptive strategies could be crucial as predictive tools in investigating the limits of life.

1:50 - 2:10 pm

Comparison of *Bacillus subtilis* transcription profiles from separate missions to the ISS reveal common responses.

Michael Morrison, University of Florida

Exposure to the human spaceflight environment has been shown to have a variety of effects on microorganisms. Results from spaceflight experiments indicate that different bacteria exhibit altered growth kinetics, virulence, biofilm formation, and antibiotic susceptibility during spaceflight, but not in a consistent manner. Several transcriptome profiling studies have been performed utilizing a variety of micro-organisms and growth conditions to identify a molecular mechanism for the observed spaceflight changes, but these experiments have had limited success due to confounding factors such as different species, hardware, media used, and lack of experimental replication. To address this issue, the model organism *Bacillus subtilis* was flown on two separate Biological Research in Canisters (BRIC) missions, BRIC-21 and BRIC-23. Both BRIC missions utilized identical strain, media, hardware, and protocols to minimize these possible confounding factors. RNA-seq analysis was performed on BRIC-21 (n=3) and BRIC-23 (n=9) Flight (FL) and Ground Control (GC) samples using Illumina next-generation sequencing. Differential expression and gene set enrichment analyses of the RNA sequences were performed on BRIC-21 and BRIC-23 samples separately and compared to determine common genes and gene sets affected by exposure to spaceflight. Our analysis revealed a concordance of 32% and 35% in up- and down-regulated transcripts during both spaceflights. Among the consistently up-regulated transcripts were those involved in biofilm biosynthesis, providing the first molecular evidence for increased biofilm formation under microgravity conditions. Supported by NASA grants NNX14AT38G and NNX17AD51G.

Oral Session VII
Wednesday, June 6th 2018, 2:30 - 3:30 pm

2:30 - 2:50 pm

Unusual self-assembly properties of model
protocell membranes

*Anna Wang, Massachusetts General
Hospital/Harvard University*

Fatty acids, encountered commonly as soap, form micelles at pH values above their pKa and neat oil below their pKa. At a pH range about their pKa, however, they form bilayers much like the phospholipid membranes that comprise the cell membranes of life on Earth. Because fatty acids have been found on carbonaceous chondrites, it is likely that they were available on early Earth. Combined with prebiotic routes to synthesise these molecules, fatty acids hold great potential as components of the membranes of primitive, minimal cells.

We find that the ionic strength, pH, and presence of minerals can affect whether fatty acids self-assemble into well-separated membranes like the membranes we see in our cells (giant unilamellar vesicles or GUVs) or tightly-stacked onion-like multilayered structures (multilamellar vesicles MLVs). We look in particular at the effect of montmorillonite clay, which has been shown to catalyse RNA polymerisation of RNA [Ferris et al., *Nature* (1996)] and alter the the *creation* of vesicles from micelles [Hanczyc et al., *Science* (2003)], on vesicle morphology.

Surprisingly, we find that we can self-assemble giant, unilamellar vesicles under a range of conditions. To provide context, assembling such structures with phospholipids usually requires microfluidic devices. These results suggest that giant unilamellar vesicles may have formed in abundance in settings where sediment and porous substrates were likely present.

2:50 - 3:10 pm

Viruses can be antique, but not primitive
*Jose Alberto Campillo-Balderas, National
Autonomous University of Mexico*

The comparative genomics has allowed to trace the evolutionary history of all organisms and to infer the hypothetical existence of their last common ancestor (LCA). However, the origin and early evolution of viruses remains unclear. The recent availability of more biological, genomic, structural, and ecological data of viruses has provided the opportunity to analyze, in detail, their evolutionary relationships among them and their hosts. In a first approach to understand their origin, we compared and analyzed current biological and ecological data of several viral families. While some researchers sustain that viruses are the missing link between the RNA world and the first cells due to their morphological and genomic “simplicity”, our results revealed that the size distribution and the chemical nature of viral genomes do not show a correlation with the phylogeny of their corresponding hosts. We found that the supposedly “more complex” and longest viral genomes are found in double-stranded DNA viruses which infect only ancient domains (Bacteria and Archaea), e.g. phages, and ancient lineages of eukaryotes (protists), e.g. megaviruses. The most of the RNA viruses infect only the Eukarya domain. No RNA viruses have been found in Archaea yet. There are only two exceptional RNA viral families in prokaryotes, but we discovered that they infect animal-microbiota Proteobacteria. These preliminary results might suggest that DNA viruses could have a more antique origin that goes back to the LCA stage, while RNA viruses could hold a more recent origin in coevolution with eukaryotes.

3:10 - 3:30 pm

Agency-Steered Ecosystems on Planetary
Bodies

*Hikaru Furukawa, Arizona State University/
School of Earth and Space Exploration*

Humanity manages various ecosystems on Earth: some interventions result in catastrophic loss of species while others do not, in some cases even enriching biodiversity. Humanity has now set sights on creating closed, habitable ecosystems on Mars or the moon. There are thus growing interests in how technological species co-survive with their planetary environment, both on Earth and other planetary bodies. In this project we address the question, “What determines the robustness and self-sustainability of ecosystems universally, and how is this impacted by steering by agencies, such as that of a human civilization?”. Our aim is therefore to define sustainability from an astrobiological perspective. For studying the self- sustainability and robustness of ecosystems, we can gain insights from previously conducted physical simulations of closed ecosystems (e.g., Biosphere2, MELiSSA). Some successfully sustained a closed-loop while others resulted in unexpected problems, mainly due to the design of the systems. However, it still remains unclear what key factors of various types of ecosystems govern their total performance. We hypothesize general, predictive laws exist which dictate whether ecosystems can be self-sustaining and robust. For example, the behaviors of ecosystems can be influenced by the level of complexity of the system, and structure of the networks among species. We map various ecosystems depending on different levels of biodiversity and agent management, and tackle this question by network analysis of ecosystems. This research provides insights on how intelligent agents steer small-scale subsystems, which in turn affect planetary-scale processes.

Poster Session II
Wednesday, June 6th 2018, 3:30 - 5:30 pm

Poster 37

Effect of CO₂ Atmosphere in the Microbial
Diversity and Carbonate Precipitation of an
Hypersaline Mat

*Rodrigo Abans, Brazilian Synchrotron Light
Laboratory (LNLS)*

Based on evidence of salts, carbonates and fluvial erosion on Mars, it is possible that hypersaline environments were formed and a microbiote could have thrived on it, leaving inorganic biosignatures. Environmental samples were collected at Lagoa Vermelha (RJ, Brazil), a hypersaline lagoon with dolomite precipitation mediated by microbial activity. Coring was used to sample 20 cm deep sediment, which was contained in an adapted Winogradsky's Column. During two months, two treatments were carried out: one sealed with Earth's atmosphere and the other under a 1 atm CO₂ atmosphere, kept in flux. 16S rRNA gene was used as a marker for Bacteria and Archaea genetic diversity to compare both groups. To further characterize and assess the carbonate content, X-ray diffraction (XRD), X-ray fluorescence (XRF) and scanning electron microscope coupled to energy-dispersive X-ray spectroscopy (SEM/EDS) were used. XRD and XRF showed no apparent difference between carbonate and calcium content in both groups. SEM/EDS of the surface of the group kept under CO₂ showed an extensive presence of a carbonate layer, with a crystalline habit and Ca:Mg ration compatible with calcite, likely from abiotic origin and precipitated due to high CO₂ partial pressure. Whereas the other group only showed a surface covered by halite and biofilm. The 16S amplicon sequencing revealed no significant differences between both groups, which implies that the tested terrestrial hypersaline environment can be tested further in more complete Mars-like simulations as a good analogue. Furthermore, results imply that carbonates like calcite should be used with limitations as inorganic biosignatures.

Poster 38

Constraining Degradation of Biosignatures
Within a Fossilized Jurassic Redox Gradient in a
Mars Analogue Sediment from Painted Desert,
Arizona

Richard Archer, University of Colorado Boulder

Findings by Michalski and Noe Dobrea et al. (2010) suggest that Mawrth Vallis contains sedimentary deposits dating from the Noachian Epoch. Mawrth Vallis represents outflow fluvial and lacustrine deposits of phyllosilicate clays (ibid). Farrand et al. (2009) discovered a region of jarosite located within the Mawrth Vallis region with great potential for preservation of diverse biosignature preservation Noe Dobrea et al. (2010). Due to similarities in the interpreted hydrological environment and resulting mineralogy, the Painted Desert of Arizona serves as an analogue site. We identified a jarosite rind encasing ancient wood perimineralized by calcite and we speculated that this jarosite is anomalous in the context of a clay dominated environment and may be the result of sulfate reducing microbial activity. To test this, we separated the sample by depth and sent splits out for isotopic analysis while simultaneously characterizing the mineralogy by XRD and VNIR spectroscopy. Resulting visible microscopic gross morphology, together with, stable isotope - MS, XRD, VNIR, and geochemical modeling analysis are consistent with the preservation of a "fossilized" redox gradient describing Sulfate Reducing Bacteria (SRB) degradation of aquatic eukaryotic plant material decomposing in a cool, freshwater lacustrine environment. Two distinct mineralogical domains were found, partitioned by layer of pure gypsum. The first mineralogical domain was dominated by natrojarosite while the second domain was dominated by pyrite, graphite and diagenetic products of pyrite. Modeling results suggest differential sulfur oxidation as a function of oxygen fugacity and SRB activity. Sample horizon resolution of approximately 1.4mm $\delta^{34}\text{S}$ CDT samples are also consistent with SRB and conservative throughout. However, contrary SEM and Raman analysis at <50 μm scale fails to reveal, as of yet, preservation of

microbial morphologies, suggesting biomineral morphology diagenesis overprinting at microscopic scales. Although multiproxy lines of evidence regarding the depositional environment (MS, XRD, VNIR, $\delta^{34}\text{SCDT}$) are encouraging and macroscopically highly conservative, modeled redox potential across horizons is constrained with a suggested pH <2.5. This low depositional pH may degrade morphological biosignatures. Thus, while we conclude that jarosite may be an appropriate biogeochemical target sediment, but recovery of microbial morphologies from Martian jarosite seems unlikely.

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Poster 39

Hybridization as an Adaptive Force in Response to Extreme UV Conditions

Carla Bautista-Rodríguez, Institut de biologie intégrative et des systèmes (IBIS), Université Laval

The heterogeneous environment can end up presenting extreme conditions as high ultraviolet (UV) radiation. The presence of high UV radiation represents a particular challenge in terms of adaptability because it affects the viability of organisms by directly damaging the genome. However, the existence of extremophiles adapted to high UV radiation conditions has been reported. In this way, to discern the evolutionary mechanisms that underlie this extreme adaptation is a question remaining in evolutionary biology. It has recently been proposed that hybridization may be a useful process to colonize new ecological niches. In an interspecific hybridization event, alterations at the nucleotidic and chromosomal levels contribute to a high genome plasticity that could be key for adaptation in stressful environments. The present project aims to discover if hybridization promotes adaptive evolution under extreme conditions of UV radiation. The *Saccharomyces* interspecific hybrids are optimal model for the study of the adaptation of yeasts to stressful conditions by using the experimental evolution under UV conditions. Therefore, it will be possible to determine if after multiple generations there is a more marked increase in resistance to UV radiation in hybrids in comparison with the parental lines. In addition, following sequencing of the genome, it will be possible to elucidate what genomic changes occurred during evolution: mutations, copy number variations and chromosomal alterations. Altogether, this project will give us a general idea of the extent to which hybridization participates in adaptation to extreme conditions, contributing to important fields such as evolutionary biology and astrobiology.

Poster 40

The Disentangled Effects of Salt on Prebiotic
Lipid Monolayer Stability
Sandra Blair, University of Colorado Boulder

Enclosures are a necessary component of life. The most commonly used model system to study prebiotic enclosures is fatty acids as they were readily available on the early Earth and are the most prebiotically-plausible lipids. Fatty acid phase behavior is more complicated than modern phospholipids and vesicle formation requires relatively high concentrations. These fatty acid vesicles are permeable, but fragile as they are only stable over a narrow range of environmental conditions of pH, salt, and temperature. Currently, there are fundamental aspects of enclosure self-assembly that we do not understand, even for a simple single-tailed surfactant. There is considerable variance within the literature when efforts are made to characterize the stability of membrane structures under different environments. Intermolecular interactions of vesicle self-assembly are likely more complex than the commonly used concentration and pH model of micelle, vesicle, and oil droplet phase behavior. In this study the entangled effects of pH and salt environment on fatty acid membrane stability are separated by studying environments of differing salt concentration at their natural pH. Myristic acid is used in this study as a proxy for shorter-chained fatty acids that form vesicles. The surface behavior of monolayer films of myristic acid deposited on aqueous solutions of varying salinity is investigated using a Langmuir trough. Chloride salts are explored and include both monovalent cations (sodium and potassium) and divalent cations (magnesium and calcium). This work contributes to an understanding of the phase behavior of membranes in protocellular structures under different environmental conditions.

Poster 41

In situ Culturing with Isolation-Chip
Technology in Hydrogeothermal Springs
*Thomas Cantrell, Georgia Institute of
Technology*

An estimated 99% of the world's microbial species are traditionally uncultivable; however, when microbes can be cultured this yields valuable phenotypic, metabolic and extracellular information due to increased sample mass and purity [1,2]. Recent attempts to culture the uncultivable microbial "dark matter" have included co-culturing and culturing in situ [3,4]. An emerging microfluidic in situ culturing platform is the isolation chip (iChip) based on agarose gel trapping. Samples are taken, diluted and inoculated into the agarose matrix, followed by emplacement back in the site of origin, where nutrients are accessible from the environment. We tested these devices in hydrothermal fields in 2015 in Iceland, followed by additional field campaigns in Japan and Iceland in 2016. The Japan field campaign, described here, was conducted in the Negano prefecture, Japanese Alps. The site was monitored over ten days, during which temperature, conductivity and dissolved oxygen were recorded. Fluorescent confocal microscopy was used to visualize the morphologies. A majority of the growth occurred within 50 microns of the plug surface. Amplification and sequencing of the 16s rRNA region (V3-V4) indicated that of the samples selected, 2 were isolated extremophile monocultures. Two members of the genus *Anoxybacillus* were identified in a chip which had incubated in high levels of dissolved oxygen in the bulk fluid, which may indicate culturing selectivity. This work represents the novel application of an emerging microfluidic technology to provide pure monoclonal samples of extremophile organisms, potentially enabling study via molecular techniques that would otherwise be inaccessible.

Poster 42

The Role of Paralogous Duplications in Early Protein Evolution

Alejandro Cisneros, Universidad Nacional Autónoma de México

Inventories of the gene content of the last common ancestor (LCA), i.e., the cenancestor, include sequences that may have undergone horizontal transfer events, as well as sequences that have originated in different pre-cenacestral epochs. However, the universal distribution of highly conserved genes involved in RNA metabolism provide insights into early stages of cell evolution during which RNA played a much more conspicuous biological role, and is consistent with the hypothesis that extant living systems were preceded by an RNA/protein world. Insights into the traits of primitive entities from which the LCA evolved may be derived from the analysis of paralogous gene families, including those formed by sequences that resulted from internal elongation events. Three major types of paralogous gene families can be recognized. The importance of this grouping for understanding the traits of early cells is discussed

Poster 43

Quantitative, Compositional Analysis of Trace Amino Acids in Europa Analogues with a Modular μ CE-LIF System

Zachary Duca, Georgia Institute of Technology

Europa's plume activity and evidence supporting a global subsurface ocean have made it a high-priority target for future NASA outer-planetary missions. In situ quantitative and compositional analysis of organic molecules in the plumes or subsurface ocean of Europa would provide relevant, detailed information on formation, habitability, and on-going planetary processes of these celestial bodies and could provide the first evidence of the potential for extant life beyond Earth. Microcapillary electrophoresis with laser-induced fluorescence (μ CE-LIF) enables highly-sensitive, automated, quantitative, and compositional analysis of organic molecule monomers and short polymers. Its potential for miniaturization and sub-parts-per-trillion (ppt) limit of detection (LOD) make it an enticing candidate for future planetary missions, like those to Europa. Mars Organic Analyzer (MOA) portable μ CE-LIF prototypes have been built and field tested in the Panoche Valley, CA, and in the Atacama Desert, Chile, and have conducted high resolution analyses of trace species in multiple relevant planetary analogue samples, including those from the Murchison meteorite, hydrothermal sites, the Saline Valley, and the Rio Tinto. Here, a benchtop μ CE-LIF detection system was constructed from commercially available components and tested by analyzing standard amino acid samples of alanine and glycine in 35 mM borate buffer, pH 9.5. Their LODs were found to be 2.11 nM and 2.91 nM, respectively, falling within the range of state-of-the-art μ CE-LIF instruments. Further experiments examine the LODs of an expanded amino acid standard solution, including serine, valine, glutamic acid, and aspartic acid, in Europa-like solutions containing sulfuric acid, carbonic acid, magnesium perchlorate, and magnesium sulfate.

Poster 44

Chiral Analysis of Exogenous Amino Acids
using Microcapillary Electrophoresis Mass
Spectrometry

*Dedra Eichstedt, Georgia Institute of
Technology*

The enantiomeric excess of chiral meteoritic amino acids delivers valuable information on the source of organic compounds in the solar system and provides insight into the origin of homochirality on the early Earth. Microcapillary electrophoresis mass spectrometry (uCE-MS) is a rapid, selective, and sensitive method to separate and quantitate the enantiomers of a variety of amino acids. The microcapillary electrophoresis system used, the ZipChip pioneered by 908 Devices, has delivered limits of detection as low as 10 nM for L-amino acids in this research. The peak efficiency for this assay is variable for each of the amino acids measured, with the average being about 180,000 theoretical plates, and the range being 350,000 to 50,000. A typical sample injection needs only approximately 110 picograms of sample in the 4 nL injection volume delivered to the separation channel. Chiral resolution is achieved by addition of alpha and beta cyclodextrins to the sample, which form complexes with L- and D-amino acids at different rates and strengths. Additionally, this assay can unambiguously obtain the identity and isotopic ratios of these amino acids, establishing whether detected enantiomeric excess is truly exogenous. This assay provides a method for investigation of meteoritic amino acid enantiomeric excess, aiding in the construction of a library of these values while minimizing the use of precious material.

Poster 45

Biology Meets Subduction: Subduction-Related
Geochemistry is a Driver of Microbial
Community Dynamics in Costa Rica

Katherine Fullerton, University of Tennessee

Along the Costa Rican convergent margin, the Cocos Plate actively subducts beneath the Caribbean Plate. Here, shallow dewatering processes and arc volcanism allow for fluids contained in subducted sediments and minerals to be released into the overriding plate, making chemical habitats that may be analogous to those on icy worlds where sufficient temperatures for life only exist in the subsurface. These fluids contain inorganic chemical species such as hydrogen, carbon dioxide, sulfide, and small hydrocarbons, providing the chemical conditions necessary to make this system a unique point of interest for studying biogeochemical cycling. Largely decoupled from photosynthetic primary production, deep subsurface microbial communities rely on these chemical species associated with geothermal fluxes for carbon and energy sources. Simultaneously in surface-associated transition zones, these deeply-sourced nutrients mix with terrestrial-derived materials to stimulate local microbial communities. Much of the Costa Rica arc system is subaerial, providing a unique opportunity to study an environment where the interface of biotic and abiotic biogeochemical cycling are intimately related, sometimes under conditions that approach the physical limits of life. In February 2017, 26 geochemically diverse sites in Costa Rica including hot springs, mud pots, and volcanic lakes were sampled for microbiological and geochemical analyses. This work aims to describe the spatial distribution and dynamics of microbial communities across this geothermally active subduction zone. Microbial diversity and abundance will be analyzed as a function of geochemical parameters using multivariable statistical analyses and network analysis to enhance our understanding of spatial microbial community dynamics across a volcanic arc.

Poster 46

Investigating the Network Topology of
Geobiochemical Systems
Dylan Gagler, Arizona State University

A variety of settings have been proposed as possible candidates for the origin of life, ranging from deep-sea hydrothermal vent systems to anoxic volcanic tide pools. What underlies these scenarios, and all other origin of life scenarios, is a complex interplay of energetics, geochemistry, and biochemistry, the dynamics of which are not well understood. Previous studies into the network structure of biochemical networks have found that biochemical networks are characteristically heterogeneous. Few, however, have looked into how these network topologies are altered when more realistic geochemical contexts and thermodynamic models are considered. Examining networks in such a manner also provides an opportunity to test the long-suggested idea that energetic and material fluxes have been critical to the emergence of life.

To explore the relationship between biochemical networks and geochemical systems, we plan to analyze the topological structure of metagenomes extracted from geothermal hot springs in Yellowstone National Park to determine how environmental parameters restructure metagenomic networks. Congruently, we will perform flux balance analysis (FBA) and energy balance analysis (EBA) on the networks in order to constrain steady state chemical availability when dynamics are considered. This merger of methodological tools, as well as the significant geochemical data that exist for hot springs at Yellowstone, will allow for the creation of biochemical networks that are embedded in a degree of geochemical and thermodynamic realism, thus offering insight into the structure of natural biochemical networks and allowing for progress towards an energetic conception of the origin of life

Poster 47

ATP-Hydrolyzing Peptide Coacervates
*Daniela Kroiss, The Graduate Center of the City
University of New York*

Adenosine triphosphate (ATP) is life's ubiquitous energy currency, with chemical energy released by its hydrolysis driving essential molecular processes to support the dynamic structures and functions of the cell. While the mechanism of ATP binding and hydrolysis in ATPases has been extensively studied, their evolutionary origin remains unclear and the molecular principles underlying these reactions are yet to be elucidated. Consequently, we were aiming to design a minimalistic system solely based on natural amino acids that allows for selective binding of ATP and its subsequent hydrolysis in absence of additional enzymes or cofactors.

We report on peptide/ATP ensembles where molecular recognition, self-assembly and catalytic activity are concurrently present and dependent on each other.

Using phage display, we identified the heptapeptide ADARYKS, that binds to ATP with millimolar affinity via electrostatic interactions, as shown by experimental and computational studies. Remarkably, ADARYKS and ATP undergo spontaneous phase separation after a 72-h lag phase to form coacervates, wherein ATP is hydrolyzed, first to adenosine diphosphate and subsequently to adenosine monophosphate and inorganic phosphate.

Investigating the catalytic activity of alanine-mutants of ADARYKS revealed that the aspartate-arginine salt bridge found in ADARYKS is essential to ATP hydrolysis, suggesting a similar catalytic mechanism as observed in F1-ATPases, where a conserved glutamate-arginine salt bridge activates water for nucleophilic attack of ATP.

Our results are of relevance to the proposal that liquid phase separated droplets may have acted as protocellular reactive environments, concurrently they suggest that short peptides could have served as precursors for more complex ATP-utilizing enzymes.

Poster 48

Viscosity-Mediated Replication of an RNA
Duplex containing a Ribozyme Motif
*Adriana Lozoya Colinas, Georgia Institute of
Technology*

The demonstration of an informational polymer (such as RNA) that can undergo sustained cycles of replication without the aid of protein enzymes remains a major goal in origins of life research. Existing studies of template-directed RNA synthesis have mainly focused on single-stranded templates and have rarely tackled the challenges associated with multiple rounds of information transfer, such as strand inhibition (i.e., the problem of accessing a template that is in the duplex state). We propose the use of viscous environment to enable the replication of a gene-length RNA duplex containing a ribozyme sequence. The environment provided by viscous solvents limits the diffusion and promotes the kinetic trapping of the template as single strands by favoring the rapid formation of intramolecular structures. Shorter nucleotide sequences can subsequently assemble on the kinetically trapped single stranded template and form a new copy of the template after being ligated. Additionally, the trapped single strands containing the ribozyme sequence are catalytically active in hydrated solvent conditions. Our results suggest that such viscous solvents, generated by water evaporation during day/night or seasonal cycles, could have provided a plausible environment that promoted the replication of highly folded nucleic acid structures such as ribozymes.

Poster 49

A Possible Path to Prebiotic Peptides involving
Minerals and Ester-Mediated Amide Bond
Formation
Aaron McKee, Georgia Institute of Technology

The presence of amino acids (AA) on extra-terrestrial bodies and in prebiotic environmental simulation experiments suggests the plausibility of their existence on early Earth, however, the poly-condensation of non-activated AA is thermodynamically unfavored in aqueous solution, though may proceed in the dry state at elevated temperature. Recent work has introduced β -hydroxy acids, a class of molecules found alongside AA in meteorites and prebiotic spark discharge experiments, into peptide forming systems. This has been shown as a robust route towards proto-polypeptides, producing long mixed-acid oligomers, referred to as depsipeptides, which contain both amide and ester backbone linkages. If depsipeptides are model proto-polypeptides, then increasing AA content, towards oligomers resembling extant peptides, would have been an important step in the chemical evolution that preceded life. Here we demonstrate that silica inclusion in alanine and glycine with lactic acid reactions effect the compositional distribution of oligomers for all chain lengths, in that the oligomers produced are AA enriched, relative to a mineral-absent control. For both AA, the dominant species produced in the presence of silica and lactic acid are rich with amide-bonding sequence motifs and largely ester deficient. Evidence of inter-facial ester formation suggests that the silica surface is directly involved in the oligomer growth process and AA enrichment. This observation departs from previous studies that found AA residues in a stabilized carboxylate form on metal oxides and demonstrates that depsipeptide systems are unique in this regard.

Poster 50

Carnobacterium Response to Pressure Extremes:
Growth, DNA Methylation, and Global Gene
Transcription

Kathleen Miller, University of Florida

Exploration of bacterial growth under simulated Martian atmospheric conditions has important implications both for astrobiology and planetary protection. The low pressure, low temperature, and CO₂-rich atmosphere on Mars is a significant barrier to growth of Earth microbes. To this end, our focus on pressure extremes in a prokaryotic genus, *Carnobacterium*, allows us to explore pressure as an understudied physical parameter influencing microbial responses. Members of this Gram-positive, facultatively anaerobic, and psychrotolerant genus have been isolated in ecological niches ranging from Siberian permafrost to deep-ocean trenches. Our previous work indicates that *Carnobacterium* spp. adapt to low pressure by altering their genetic and epigenetic responses. We propose that these microbes adapt to different pressure extremes via transcriptomic and methylomic modulation. While other prokaryotes generally live in rather narrow pressure ranges, *Carnobacterium* spp. are capable of growth over five orders of magnitude of pressure, from as low as 7×10^2 Pa up to 6×10^7 Pa. We are studying growth and molecular responses of 14 type strains of *Carnobacterium* spp. at a range of pressures. A wide range of growth rates were observed when strains were cultivated in CO₂ at 0°C and 10^3 Pa. Bioinformatic analyses of Methyl-Seq and RNA-Seq data generated from genomic DNA and total RNA from various *Carnobacterium* spp. cultured in different pressures ranging from 10^3 - 10^8 Pa is in progress. Supported by NASA Exobiology (NNH16ZDA001N-EXO) and DOE-JGI (CSP 502927).

Poster 51

A Major Primitive Evolutionary Transition:
Cooperation between Distinct RNA Replicators
Ryo Mizuuchi, Portland State University

In the RNA world or the RNA-protein world, it is believed that replicating RNAs expanded genetic information capacity through cooperation, linking distinct RNAs to form a large replication unit (e.g., hypercycle, Eigen & Schuster, 1977). A major challenge to this process is that such a cooperative replication is vulnerable to parasitic or selfish replicators, continuously generated by mutations (Maynard-Smith, 1979). The parasites do not cooperate but exploit cooperation to replicate faster, destroying the cooperative replication system. Although theoretically the cooperation can be sustained and developed in spatial structures such as compartments (Takeuchi & Hogeweg, 2012), experimental verification has remained a great challenge for decades, due to the lack of suitable systems. Here we constructed a novel cooperative RNA replication system encapsulated in micro-compartments, in which two RNAs, encoding replication or metabolic enzymes, cooperate for their replication. We performed long-term replication experiments via random fusion-division of the compartments and revealed that the cooperative relationship can be sustained in a broad range of RNA concentration, avoiding over-amplification of parasitic replicators and mis-encapsulation of the two RNAs in the same compartments. Moreover, we found that the two RNAs spontaneously reinforced their cooperation through Darwinian evolution; they coevolved toward a replication unit with higher replication activities. Our results provide the first experimental evidence of robust cooperation between evolving RNA replicators, suggesting that molecular cooperation may have been easier to develop than expected during the early evolution of life.

Poster 52

Exploration of Novel Subsurface Microbial
Communities within Seafloor Mantle Rocks
Sheri Motamedi, University of Utah

Ultramafic rocks in Earth's mantle represent a tremendous reservoir of carbon and reducing power. Mixing of these rocks with overlying seawater due to tectonic uplift causes an exothermic reaction known as 'serpentinization' that also releases hydrogen gas, methane, and small organic molecules.

The H₂ and CH₄-rich environments provided by serpentinization reactions are thought to be analogous to conditions found on the early Earth and perhaps other planets.

During October-December of 2015 the International Ocean Discovery Program Expedition 357 to the Atlantis Massif collected rocks from a subsurface site of active serpentinization for the first time. The main goals of this project are:

1) to characterize the diversity, genomic content, and metabolic potential of microbial communities that inhabit the serpentine rocks collected from the Atlantis Massif and,

2) to distinguish endemic microbial communities of serpentine subsurface rocks from seawater residents and other potential sources of contamination.

Initial analyses of the next-generation sequencing results from the environmental DNA of the subsurface rocks showed that the rock samples were inhabited by some intriguing bacterial taxa that could be endemic subsurface microbes and were not found in our control samples for contamination. These preliminary results indicate that our efforts have been at least partially successful in 1) avoiding overwhelming contamination of the rock core samples and 2) overcoming technical difficulties to extract, purify, and sequence DNA from the rock cores.

These results represent the first DNA sequencing study ever conducted on subsurface serpentine rocks.

Poster 53

Early Evolution of Methanogenic Routes
*Israel Muñoz, Universidad Nacional Autónoma
de México*

Acetate producing Bacteria (Homoacetogens) share with methane producing Archaea (Methanogens, specifically hydrogenotrophic methanogens) the autotrophic route of carbon fixation called Wood-Ljungdahl (WL) pathway, which of the six known autotrophic pathways is the only one shared by both domains, Archaea and Bacteria, for that reason has been proposed as one of the oldest metabolisms of autotrophic carbon fixation, may be present in the Last Common Ancestor (LCA); however only "western" (carbonyl) branch are the same in both domains while "eastern" (methyl) branch are different, in number of reactions and therefore in number of enzymes, which are not homologous. In this work we expose that some parts of methyl branch of archaeal Wood-Ljungdahl pathway (MBWL) are present in both, bacteria and non methanogenic archaeas, and we have the hypothesis that the entire MBWL could not be present in LCA, also we analyze the different variants of methanogenesis (hydrogenotrophic, acetoclastic and methylotrophic pathways) and we realize that every different pathway, even every independent enzyme or subunit (in the case of multimeric enzymes), has its own intricate evolutionary history.

Poster 54

Ontology, Astrobiology, and the Periodic Table
of Life

Angeera Naser, NASA Glenn Research Center

Bionics and biomimetics have been humankind's first choices for solving a vast spectrum of technical problems for thousands of years – so much so, in fact, that they are fundamentally inextricable from the core of any engineering workflow. Despite this, bio-inspiration as a specialized science is still considered relatively nascent, and there fails to be an aggregate resource for the purpose of helping engineers through the systematic process of finding biomimetic inspiration for their work. To fill this void, V.I.N.E. (Virtual Interchange for Nature-inspired Exploration) at NASA Glenn Research Center is currently developing PeTaL (the Periodic Table of Life) – a design tool to assist in the development of solutions to human challenges via data analytics for model construction. Astrobiology plays a significant role within PeTaL; said models heavily incorporate paleomimesis (the mimicking of Earth's evolutionary past) and physio-teleology (studies concerning the purposes of life) in an effort to observe deep time evolutionary trends. From an astrobiological standpoint, PeTaL has been used to store and model data concerning the abilities of various extremophiles (such as xerophiles, methanogens, and psychrophiles) to thrive in harsh environments. Our specific approach to data aggregation is tailored to work most effectively with PeTaL's biomimetic engineering ontology system. The ontology labels and classifies data based on the three approaches to biomimetics an engineer may employ: form, function, and environment. When employed alongside PeTaL's statistical modeling and text classification capabilities, it allows the system to more thoroughly identify the complex relationships between qualitative and quantitative data facilitating biomimetic inspiration.

Poster 55

The Use of Environmental Cycles to Lend
Insight into Viscosity Mediated Replication
*Chiamaka Obianyor, Georgia Institute of
Technology*

RNA is often considered a major precursor to cellular life, however years of research has yet to produce a prebiotic mechanism that allows for multiple rounds of replication. This is partly due to the strand inhibition problem, which prevents the binding of nucleotide substrates on separated duplex strands in an aqueous environment. Recent work has shown that strand inhibition can be overcome with the use of viscous solvents. These solvents decrease the rate of the duplex reformation by kinetic trapping of separated duplex strands, thus enabling copying of separated gene-length strands. Our research is focused on investigating the robustness of this viscosity mediated process, as it presently offers the simplest path nature could have taken to enzyme free nucleic acid replication. The goal of this work is to demonstrate that the environmental cycling of earth's day-night temperature and relative humidity can lead towards selection of catalytic active gene-length templates. Preliminary results show that a viscous solvent can be generated by evaporation of water from a potentially prebiotic pool, while simultaneously allow denaturing of the strands. We also demonstrate that the varying humidity of the environment can lead to selection of a kinetically trapped template or a newly copied template. These findings suggest that a prebiotic plausible path that allows for a dynamic viscosity mediated approach to solve the strand inhibition problem can be established.

Poster 56

Awaruite and CO₂ Reduction in Early
Biochemical Evolution

Martina Preiner, Heinrich-Heine-University

When it comes to life's origin, one thing we can say for sure: For chemical reactions to take place that could ultimately lead to complex molecules and metabolism, energy release is required. The H₂/CO₂ redox couple in hydrothermal vents is especially interesting as a source of early energy: hydrogen is an ancient source of electrons while CO₂ is an ancient source of carbon. Prebiotic CO₂ reduction (carbon fixation) has been an issue for the vent hypothesis – the midpoint potential of H₂ is not conducive to direct reduction to complex carbon compounds. Modern anaerobes employ flavin dependent electron bifurcation involving iron-sulfur proteins to reduce CO₂ with H₂. Although FeS is a candidate to for abiotic CO₂ reduction, in known biological systems this is always a two-electron reaction which makes FeS an unlikely reductant of CO₂. Was there a step before FeS? Some acetogens and methanogens use native iron, Fe⁰, as their sole electron donor, so native metals might solve the question about early CO₂ reduction. We are investigating the intermetallic compound awaruite, which occurs naturally in hydrothermal vents and contains native nickel (Ni⁰) and Fe⁰. To this day, several enzymes involved in carbon fixation utilize both metals in their active centers. We can show that combinations of awaruite, CO₂, H₂ and water react to more complex carbon compounds like acetate, pyruvate and other molecules that strikingly resemble carbon metabolism in primitive autotrophs.

Poster 57

Building Complexity via the Aqueous
Photochemistry of Simple Lipids

Rebecca Rapf, Lawrence Berkeley National Lab

Sunlight can provide the energy needed to drive organic photochemical reactions, which, in aqueous environments, generate complex molecular structures required for life. As a class of molecules, α -keto acids, undergo aqueous photochemistry characterized by the formation of covalently-bonded dimers and trimers from the recombination of photochemically-generated radical species, even in very dilute solutions. This mechanism is general for α -keto acids of varying alkyl tail lengths, but the branching ratios are quite sensitive to reaction conditions, including oxygen and the pH of the solution. In addition, α -keto acids also act as photo-initiators, driving reactions of non-photoactive species. The oligomers formed from photolysis of alkyl α -keto acids are amphiphiles, many of which have two or three alkyl chains. The photoproducts generated from alkyl α -keto acids are surface-active and spontaneously self-assemble into monodisperse, spherical aggregates over the course of photolysis, which has important environmental implications for the early Earth. The formation of such multi-tailed lipids and aggregates on the early Earth may help answer questions about how the first protocells evolved.

Poster 58

The Condensation of a Model Proto-RNA Nucleobase with Ribulose: A Prebiotic Pathway to RNA

Tyler Roche, Georgia Institute of Technology

The origin and early evolution of life is thought to have been dependent on the emergence of RNA as primarily a genetic and perhaps secondarily as a catalytic polymer. However, it is hypothesized that the canonical form of RNA found in life was not the original informational polymer associated with life. Multiple challenges for the prebiotic formation of the canonical nucleosides exist, including evidence that the canonical nucleobases do not react with ribose to form ribonucleosides, as well as the lack of a selective prebiotically plausible pathway for the formation of ribose. While the prebiotic plausibility of the ribose sugar necessary for RNA is low, the keto-sugar ribulose, which can interconvert to both ribose and arabinose, has a plausible formation pathway under prebiotic conditions. Here we show the reaction of 2,4,6-triaminopyrimidine (TAP) with ribulose under varying conditions to form TAP-ribosides and TAP-arabinosides, thereby providing a prebiotically plausible pathway for the formation of proto-ribonucleosides.

Poster 59

Rapid Crustal Growth and Recycling in the Early Earth: Implications for Hadean and Archean Geodynamics

Juan Rosas Bonilla, Yale University

The geodynamic regime of the early Earth remains elusive, with so far proposed hypotheses ranging from stagnant lid convection to rapid plate tectonics. Available geological data are severely limited for the first two billion years of the Earth history, and this scarcity of relevant data is often compounded by the nonuniqueness of interpretation. Here we show that the samarium-neodymium isotope evolution, which has been suggested to be consistent with stagnant lid convection in the early Earth, is better understood as the result of rapid crustal growth and extensive crustal recycling. We quantify the most likely scenario of crustal evolution through geochemical box modeling with an exhaustive exploration of the model parameter space, and our results suggest that the net crustal growth was complete by the end of the Hadean and that the rate of crustal recycling could have been as high as 4×10^{22} kg Gyr⁻¹ in the Hadean and has gradually decreased since then. Such crustal evolution yields a specific prediction for the present-day distribution of crustal formation ages, which is shown to be in remarkable agreement with a recent estimate based on the global compilation of zircon age data. The mode of subsolidus mantle convection after the putative magma ocean is probably plate tectonics, but its style could have been very different from that of contemporary plate tectonics, characterized by more affluent magmatism and more destructive subduction.

Poster 60

Simple Sequences in Early Evolution of Life
*Alma Carolina Sanchez Rocha, Universidad
Nacional Autónoma de México*

Simple sequences are segments of proteins and nucleic acids, which are biased in residue composition and frequently contain repeat motifs. The conservation of simple sequences in ancient proteins, suggest their presence in the last common ancestor (LCA). It is likely that primitive polymerases, as the current ones, had slipped-strand mispairing (slippage) as an unavoidable characteristic, generating simple sequences in early evolution of life and possibly contributing to the origin of genes, promoting the formation of raw material, the increase of genome size and genetic variability; nevertheless the evidence is limited because the preservation of the characteristic compositional bias of simple sequences is due to functional or structural reasons. With the aim of inquire about the possible roles of simple sequences in early evolution of life, proteins possibly present in the LCA were analyzed and different predictors were employed in their search. Amino acid composition of each type of simple sequences, their localization in protein functional domains or in carboxy- and amino- terminal regions of proteins, suggests that they were already present in the LCA and some of them may have played a significant role during the RNA/protein world stage.

Poster 61

Spatial Model for an RNA World
Vismay Shah, McMaster University

In the RNA world, RNA strands are thought to have been replicated by general RNA polymerases. The issue with general polymerases in the RNA world is that functional strands are not favoured over any other 'parasitic' strands. These RNA polymerases must find their complements and replicate while dealing with the pressure from the parasites. Parasitic strands can be of any length and consist of any non-functional sequence, so they dominate the sequence space and replicate faster than longer functional strands. Without selection for functional strands, parasitic strands can take over a system and drain the resources until death. Such selection can be permitted by localization and arrangement or by means of protocells. I introduce and characterize a spatial model different from the lattice models and protocell models currently used to simulate RNA world scenarios. I compare the resulting error thresholds from the spatial simulations to those of existing models to determine whether a protocell like structure is necessary for the survival of the RNA world. I also discuss preliminary results analyzing the viability for an RNA polymerase to be formed by means of temporary hydrogen bonds between two subunits, as opposed to the usual structure held together by permanent covalent bonds. Such RNA polymerases may be able to accelerate the rate at which they are replicated by existing as separate subunits when acting as a template, decreasing the time taken to replicate.

Poster 62

Characterization of Shifts in Microbial
Community Structure between Snow-Covered
and Exposed Sediments

*Anna Simpson, University of Washington,
Seattle*

The planets and moons most likely to harbor life in our solar system are all considerably colder than Earth. Alpine and polar ecosystems on Earth can be studied as potential analogues for these extraterrestrial environments. Shifts in microbial community structure from exposed, non-frozen environments to frozen, ice-covered environments gives us information on where and how microbial life could exist in our solar system. In particular, more information is needed on microbial community shifts in snow-covered volcanic sediments, which may prove the closest analog to the most 'habitable' non-terrestrial environments for Earth microorganisms. We sampled in volcanic sediment along gradients of elevation and snowmelt at two high-elevation permanent snowfields in the Cascade Range of the United States: Muir Snowfield and Sahale Glacier. 16S metagenomic sequencing of DNA from sediment under snowpack and dry sediment on the edge of snowpack revealed significant differences in microbial communities between the two sites and between snow vs. non-snow samples. Samples taken from exposed sediments had greater species richness and diversity compared to under-snow samples. We found that bacteria from the genus *Geobacter*, obligate anaerobes which are known to reduce a number of metal oxides, were more abundant under snowpack. Contrary to our expectations that photosynthetic bacteria would characterize exposed sediment, abundance of the non-photosynthetic, deeply-rooted cyanobacteria from the putative class ML635J-21 was the largest predictor of melt. Site and availability of dissolved organic carbon were the factors most strongly associated with differences in the microbial community, and significantly overshadowed changes caused by snowmelt or elevation.

Poster 63

Time, Heat, and Geochemistry: Foundations for
Modeling an Ocean World

*Elizabeth Spiers, Georgia Institute of
Technology*

Europa, an icy-shelled moon, likely contains an ocean interior, which poses novel and exciting questions regarding astrobiology and its habitability. However, a liquid-water ocean is not the only component required for support of life. A complex system involving internal energy inputs and feedbacks, from thermal and/or chemical sources, such as those operating on Earth, may provide a viable environment. Understanding the coupled thermal and geochemical fluxes within Europa's interior over time is, therefore, a crucial concern in the discussions of habitability and life on this Jovian satellite. Despite the varied range of geochemical models already available, these are only loosely constrained by thermal inputs over time, and no model exists that fully couples the interdependent geochemical and thermodynamic evolution of Europa, which will be the focus of my work. I aim to create a first order, one-dimensional coupled systems model of Europa's shell and interior. Due to the many complexities of planetary evolution, a number of simplifying assumptions will be utilized, including integrating the best available constraints from other models. This will be achieved through a box model system constructed in MATLAB. The utility of such a model is that it divides the system into simpler elements with realistically-solvable, dynamic equations and thereby enables a focus on fundamental, long-term interactions. The interior will consist of five boxes: upper ice shell, lower ice shell, ocean, silicate interior, and iron core. The model will calculate thermal and chemical fluxes between each box with temperature and pressure as controlling factors.

Poster 64

Field Exploration and Life Detection Sampling via Planetary Analogue Research (FELDSPAR): Microbial Trends Observed at an Alluvial Plain
Scot Sutton, Georgia Institute of Technology

In preparation for missions to Mars, Earth analogues can provide insight into key signatures of habitability. The extreme temperatures, limited nutrient availability, and desiccation of Arctic volcanic regions provide a unique opportunity to study environments with multiple similarities to extraterrestrial systems. In July 2016, FELDSPAR conducted a field campaign to Dynjúsundur, Iceland, an alluvial plain of nutrient-poor volcanic basaltic tephra with spectroscopic similarities to analogous geological features observed on Mars. Sampling collection was conducted as developed in prior campaigns in 2013 and 2015. Triangular grids of samples beginning at the 10cm scale and increasing to the 1km scale were returned to the Georgia Institute of Technology for home lab analysis. In addition, an ASD spectrometer was brought to the field for in situ analysis of samples during collection. Biological analyses involved overall DNA quantification by Qubit, and bacterial and archaeal DNA quantification by qPCR. Mineralogical assays included grain size and moisture content measurements. Initial measures across all samples suggest total DNA concentrations ranging from 0.05-0.3ng/uL, and bacterial DNA concentrations of 5.0×10^{-8} - 5.0×10^{-7} ng/uL. There appear to be variations in DNA concentration at different spatial scales. Continued analysis of the Dynjúsundur samples will educate our sampling on future expeditions, and act as a starting point for temporal analysis at this location.

Poster 65

Metaproteomics Reveals a Novel Betaproteobacterium with Roles in Metal and Nitrogen Cycling in the Deep Subsurface
Nadia Szeinbaum, Georgia Institute of Technology

The advent of metaproteomics has enabled detection of novel genes from microbes that resist cultivation attempts. We evaluated the metaproteomic profile of a Mn-reducing sediment microbial community. Deep sediments from ancient ocean analogue Lake Matano, Indonesia were inoculated into under anoxic conditions with soluble Mn^{3+} -pyrophosphate as sole electron acceptor and methane as sole electron donor. Changes in community taxonomic composition were monitored by 16S rRNA gene amplicon sequencing. Metaproteomic sequencing was carried out on a high accuracy tandem mass spectrometer. Relative quantification of shotgun metaproteomic data on a corresponding metagenomic dataset revealed that cultures were dominated by a new species of Dechloromonas (Betaproteobacteria), for which we propose the name “Candidatus Dechloromonas occultata”. “Ca. D. occultata” expressed an uncharacterized cytochrome-c-rich operon containing NHL-repeat proteins and an extracellular undecaheme protein also present in other Betaproteobacteria from metal-rich ecosystems. Paradoxically, the enzymatic machinery for denitrification were among the most expressed proteins despite the lack of nitrogen oxides in the media. The metabolic potential recovered from metaproteomes implicates “Ca. D. occultata” and by extension possibly other Betaproteobacteria like deep subsurface Gallionellales and Rhodocyclales, in metal and nitrogen metabolisms.

Poster 66

Differences in Bacterial Diversity by Spatial Distance in Homogenous Icelandic Mars Analog Environments

George Tan, Georgia Institute of Technology

Utilizing Earth analog environments to estimate multi-scale spatial and temporal variation in key biosignatures will help mission architects design future sampling strategies. Icelandic lava fields are often studied as Mars analog sites due to similarity in environmental conditions. Previous work found statistically different ATP concentrations and qPCR counts of microbial abundance among sites evaluated at four spatial scales (1 m, 10 m, 100 m, and >1km) despite apparent homogeneity of these sites at 'remote imaging' resolution (Amador, et al., 2015, Gentry, et al., 2017). Here, we performed the first characterization of soil communities in Fimmvörðuháls. This lava field formed from a basaltic effusive eruption associated with the 2010 Eyjafjallajökull eruption. A triangular grid of sample locations spaced at four spatial intervals was established and triplicate sample set at 10 cm spacing was taken at each grid point. High-throughput sequencing of PCR amplicons spanning the V3 and V4 hypervariable regions of 16S rRNA gene to assess the microbiome taxonomic composition. Sequencing was performed on an Illumina MiSeq using a 500 cycle kit and analyzed using the QIIME pipeline and R. Proteobacteria and Actinobacteria were the dominant microbial phyla representing over 50% of total sequences in all samples, but a large number of other phyla (22) were also detected. Although microbial richness did not vary significantly among samples (Chao1 index; $p > 0.05$), the phylogenetic composition (weighted Unifrac metric) of the soil microbiome differed significantly among apparent homogenous site separated by >1 km ($p < 0.05$), suggesting distinct microbial signatures despite apparent homogeneity.

Poster 67

Characterization of Light-Harvesting Complexes From a New Purple Sulfur Bacterium Isolated From Yellowstone

Jennifer Thweatt, Pennsylvania State University

Purple sulfur bacteria (PSB) are anoxygenic phototrophs that typically live in anoxic or microoxic environments containing sulfide. They are often found in stratified environments growing beneath oxygenic phototrophs like cyanobacteria. In order to survive in this specialized niche PSB must be able to harvest the wavelengths of light unused by overlaying phototrophs. Their special light-harvesting complexes allow them to do just that by extending their absorption from visible wavelengths to beyond 900nm. Studying the light-harvesting of purple photosynthetic bacteria has extended our knowledge of the wavelengths of light capable of supporting phototrophic growth, which is of particular interest as more habitable zone exoplanets are being discovered regularly.

In this study we look at light-harvesting complexes from a newly isolated PSB from the genus *Thiohalocapsa*. This organism was isolated from Mushroom Spring in Yellowstone National Park and is one of only a few thermophilic PSB that have been studied. Initial characterization of the light-harvesting complexes shows that three complexes are present. Typical PSB contain two light-harvesting complexes denoted LH1 and LH2. However, some PSB have been shown to express two variations of LH2 in response to differing light conditions. Here we will describe the light-harvesting complexes present and their expression based on varying growth conditions. Understanding the regulation and function of these different light harvesting complexes will help us understand how these organisms acclimate to their specialized light niche.

Poster 68

Exploring the Unevolved Protein Space
Vyacheslav Tretyachenko, Charles University

The protein sequences found in nature represent a tiny fraction of the potential sequences that could be constructed from the 20-amino-acid alphabet. To help define the properties that shaped proteins to stand out from the space of possible alternatives, we conducted a systematic computational and experimental exploration of random (unevolved) sequences in comparison with biological proteins. In our study, combinations of secondary structure, disorder, and aggregation predictions are accompanied by experimental characterization of selected proteins. We found that the overall secondary structure and physicochemical properties of random and biological sequences are very similar. Moreover, random sequences can be well-tolerated by living cells. Contrary to early hypotheses about the toxicity of random and disordered proteins, we found that random sequences with high disorder have low aggregation propensity (unlike random sequences with high structural content) and were particularly well-tolerated. This direct structure content/aggregation propensity dependence differentiates random and biological proteins. Our study indicates that while random sequences can be both structured and disordered, the properties of the latter make them better suited as progenitors (in both in vivo and in vitro settings) for further evolution of complex, soluble, three-dimensional scaffolds that can perform specific biochemical tasks.

Poster 69

The Importance of the Imidazole Group in the Evolution of Biological Catalysis
Alberto Velázquez Salazar, Universidad Nacional Autónoma de México

The five-membered heterocyclic imidazole group, which is an essential component of purines, histidine and many cofactors, has been abiotically synthesized in different model experiments that attempt to simulate the prebiotic environment. The evolutionary significance of imidazoles is highlighted by experimental reports of its ability to restore the catalytic activity of ribozymes and, of course, by its presence in histidine, the amino acid most frequently found in the catalytic site of enzymes. It has been shown that simple histidine-containing di-peptides have catalytic properties. Histidyl-histidine (His-His) catalyzes the dephosphorylation of deoxyribonucleoside monophosphate, the hydrolysis of oligo (A)₁₂, and the oligomerization of 2',3'-cAMP under cyclic wet-dry reaction conditions. However, as of today there are no reports of histidine in carbonaceous chondrites, and although the abiotic synthesis of His reported by Shen et al. proceeds via an Amadori rearrangement, like in the biosynthesis of histidine, neither the reactants nor the conditions are truly prebiotic. Nevertheless, imidazole derivatives are formed in the prebiotic syntheses of purines and other molecules, which in addition to the manifold roles that imidazole molecules play in extant metabolism, strongly suggest a case of evolutionary continuity between prebiotic chemistry and the emergence of the biosphere, and raises the question on the role of this chemical group during the origin and early evolution of life, specially in the evolution of biological catalysis.

Poster 70

Repurposing Artificial Ecosystem Selection to Study the Chemical Origins of Life

Lena Vincent, Wisconsin Institute for Discovery

The capacity to evolve adaptively is a defining feature of life. However, it is often assumed that the onset of evolution required the existence of a self-replicating entity (a protocell or RNA molecule), the spontaneous appearance of which is highly improbable. As an alternative, some theorists have suggested that adaptive evolution may have initiated in a much simpler state when autocatalytic chemical ensembles became spatially localized on a mineral surface. Such systems would tend to become better at collective propagation and colonizing new mineral surfaces by “neighborhood selection,” a process similar to group selection but acting in the absence of bounded units. Under this model, life-like chemical systems that can propagate and evolve adaptively might arise quite easily. Motivated by this theory, we have developed an experimental paradigm analogous to artificial ecosystem selection, “chemical ecosystem selection” (CES), to find new life-like systems based on their capacity to respond to selection. This approach involves incubating complex mixtures of organic compounds with populations of mineral grains. Serial transfers are then performed to select for surface-associated systems that are better at being transmitted from grain to grain. We are using the CES framework to evaluate conditions representative of different origins of life scenarios (hydrothermal vents and volcanic pools) for their potential to yield life-like entities. Even if we are not successful in finding such systems, the proposed framework will advance our understanding of how evolvable chemical systems networks emerged on prebiotic Earth and how readily they might arise elsewhere in the Universe.

Poster 71

Life and its Preservation through Millennia in Antarctica’s Lake Untersee

Nicole Wagner, Georgetown University

Lake Untersee, located in Queen Maud Land, East Antarctica, is a little-studied perennially frozen lake that resides in an extremely arid climate, making it a good terrestrial analog for the extreme conditions on Mars and icy moons of Jupiter and Saturn. The similarity of Lake Untersee with these alien environments provides us with a unique opportunity to study the potential for preservation of biosignatures in such unforgiving landscapes. Samples from the modern basin of Lake Untersee as well as its relict shorelines and nearby paleomats date back decades to hundreds of years, and samples collected from a nearby cirque are as old as 10,000 years. This roughly continuous spectrum allows us to study the process of biosignature preservation during the early stages of diagenesis, where the vast majority of deterioration occurs. To ascertain the preservation and degradation of cells as well as information-rich biosignatures, we are using metagenomics and metatranscriptomics to track changes in community diversity, structure, and metabolic activity, as well as free-floating nucleic acids. The taphonomy of these biosignatures—along with other important biomolecules, including proteins and lipids—may have implications the search for life on Mars and icy moons.

Poster 72

Atmospheric Parameters and Ages of M Dwarfs
in the Solar Neighborhood

*Ellen De Almeida, Universidade Federal do Rio
de Janeiro*

M dwarfs are the most numerous stars in the Galaxy, accounting for about $\sim 70\%$ of its baryonic mass. They are prime candidates to shelter habitable earthlike planets, as stressed by the recent discoveries of terrestrial exoplanets inside the habitable zones of the nearby M dwarfs Proxima Centauri and Ross 128. Both the transit and radial velocity techniques for detecting exoplanets are much more sensitive to the presence of earth-size planets around M dwarfs than in solar-type dwarfs. Thus the first habitable exoplanet will probably be detected and characterized in a M dwarf environment, making these stars extremely relevant to both astrobiology and planetary science. Even though they are hotspots for the detection of habitable earthlike planets, our knowledge of their properties and even their accurate census stills lags behind with respect to more massive stars. We aim to improve our knowledge of the $T_{\text{eff}}/[\text{Fe}/\text{H}]$ of nearby, still poorly studied M dwarfs, by means of moderate resolution, high S/N NIR spectra, obtained at the coude spectrograph of the Brazilian 1.6m telescope. We derived a competitive PCA spectral line index calibration able to derive $T_{\text{eff}}/[\text{Fe}/\text{H}]$ with internal errors $<100\text{K}$ and <0.1 dex respectively, calibrated against stars with interferometric T_{eff} and $[\text{Fe}/\text{H}]$ from solar-type binary companions. We present preliminary results for 180 stars, about half of which has no previous $T_{\text{eff}}/[\text{Fe}/\text{H}]$ determination.

We also plan to estimate stellar ages by measuring chromospheric fluxes of the Ca II triplet lines, plus an activity-age calibration specifically tailored to M dwarfs derived by our own group.