MICROBES AND THE MOLECULAR SIGNATURES THEY LEAVE: SIGNS OF LIFE FROM OUR

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Introduction: One of the driving priorities of outer solar system exploration is the search for signs of life. Several planets and moons of the outer solar system harbor liquid water and salts, in addition to hydrocarbons and nitrogenous compounds in some cases [1]. Likewise, the case for thermal or abiotic energy sources and potential for redox compounds which could potentially fuel metabolism have been made. These are the basic ingredients for habitability and missions to access some of these outer Ocean Worlds (e.g. Europa, Enceladus, and Titan) are in the planning stages.

One of the key requirements for missions that set out to detect signs of life is the ability to discern life and biogenic byproducts apart from abiotic particles and chemistries. Molecular complexity generated by abiotic processes is remarkable [2], and in and of itself is not a biosignature. However, different habitats on Earth carry distinct signatures of amino acid composition, demonstrating that patterns of complexity carry evidence of life [3]. However, the resounding impact of photosynthesis in driving many of Earth's ecosystems is pervasive, thus it's not only important to study systems void of light-driven processes, but as those where abiotic processes predominate. It's the relationship between microbes and molecular compositional and structural patterns that form the basis for detecting signs of life. Given the priority of outer solar system life detection mission planning, it is prudent to step back and look at Earth as an Ocean World unto itself.

Here we take a astrobiological perspective to oceanographic data sets with the intent of generating a base of information that can be used when developing benchmarks for Ocean World biosignature detection. Studies from the Southern Ocean, Central North Pacific, and Sargasso Sea will be considered with a fresh look into connections between microbes and dominant energetic pathways, and between organic carbon, amino acid composition, and patterns of chirality.

Findings: We report on a recent data set collected from a winter study in the Southern Ocean where carbon-limited oligotrophic seas harbor low levels of biological biomass, yet tracers of biological production are still evident upon amino acid analysis [4]. Here, periodic hot spots of biological activity are being paired with microbial compositional data to link patterns of production and primary microbial energetic pathways. We also consider the patterns of oceanderived dissolved amino acids as biosignatures in comparison to data collected from meteorites to investigate discerning power of composition across data sets. One of the findings suggests that often, the most abundant amino acids detected, are not only proteinogenic, but are used by Bacteria in ancillary structural and potentially functional roles. Finally, we examine the enantiomeric excesses found in natural ocean waters in three ocean systems spanning surface waters to the abyss where patterns reveal not only relative differences between the D:L representations on a peramino acid basis, but that there is a broad range in excesses of L-enantiomers found span between 11-88% [4, 5]. Further we consider the differences between data available in which the dissolved fraction is compared to the whole water fraction (inclusive of microbial cells) to identify relative contributions of living biomass to the biosignature.

In conclusion: This suite of ocean data provides a base to establish benchmark sites for astrobiological study. Life on Earth undoubtedly will present different patterns than what may occur on an inhabited ocean world of the outer solar system. However, through considering the patterns that life and associated molecular tracers in relevant Earth ocean and icy habitats with "astrobiological lens", we will more accurately set realistic expectations for data interpretation in systems where data acquisition will undoubtedly be far more challenging. An important outcome of this effort identifies the need for data sets where complimentary information is considered in an integrated fashion to understand the connections between microbes and their molecular byproducts.

References: [1] Waite, J. H. et al. (2009), *Nature*, 460:487-490. [2] Schmitt-Kopplin, P. et al. (2010), *PNAS*, 107:2763-2768. [3] Moura, A. et al. (2013), *PLoS ONE* 8:e77319. [4] Shen, Y. et al. (2016), *JGR-Oceans (in press)*: 10.1002/2016JC01230. [5] Kaiser and Benner (2008), *Limnol. Oceanogr.* 53:99-112.