

GLOBAL METABOLOMICS AS A MEANS OF LINKING MICROBIAL ACTIVITIES AND THEIR BIOGEOCHEMICAL CONSEQUENCES IN SERPENTINIZING SYSTEMS. L. Seyler^{*1,2}, T. Hoehler³, T. McCollom⁴, M. Kubo³, M. Sabuda¹, L. Williams¹, and M. Schrenk¹, ¹Department of Earth and Environmental Sciences, Michigan State University, USA, ²Blue Marble Space Institute of Science, USA, ³NASA Ames Research Center, USA, ⁴Laboratory for Atmospheric and Space Sciences, University of Colorado, USA, ^{*}Presenting author (lmseyler@gmail.com).

Introduction: The first biochemical pathways likely evolved by mirroring geochemical reactions favored in hydrothermal environments, where hot circulating fluids chemically react with mafic and ultramafic rock. Of these reactions, serpentinization produces copious abiogenic organic compounds and has been speculated to play a central role in several origin of life scenarios [1,2]. The ubiquity of water-rock reactions in our solar system raises the question of whether this could happen elsewhere- providing a mechanism for life on Mars, or icy worlds such as Europa and Enceladus [3,4,5]. On modern Earth, these reactions provide energy and materials that may be harnessed by chemosynthetic microbial communities. Serpentinites are known to support microbial communities that feed off of the products of serpentinization, while adapted to harsh environmental conditions such as high pH and low DIC availability [6,7,8,9,10]. However, the biochemistry of microbial populations that inhabit these environments are understudied and are complicated by overlapping biotic and abiotic processes.

Environmental metabolomics is an emerging approach used to study ecosystem properties. Through bioinformatic comparisons to metagenomic data sets, metabolomics can be used to study microbial adaptations and responses to varying environmental conditions. Since the techniques are highly parallel to organic geochemistry approaches, metabolomics can also provide insight into biogeochemical processes. These analyses are a reflection of metabolic potential and intersection with other organisms and environmental components. Here, we use an untargeted metabolomics approach to characterize both intracellular and aqueous metabolites from environmental biomass samples obtained from an actively serpentinizing habitat, in order to characterize the flow of metabolites and describe overlapping biogenic and abiogenic processes (including acetogenesis and methanotrophy) impacting carbon cycling in serpentinizing rocks. The aim of this study is to deconvolute the ongoing biotic and abiotic processes of these environments on Earth and to identify potential biomarkers to aid in the search for life in similar habitats on other worlds.

Methods: We applied untargeted metabolomics techniques to environmental biomass samples taken from the Coast Range Ophiolite Microbial Observatory

(CROMO), a subsurface observatory consisting of a series of eight wells drilled into an actively serpentinizing ophiolite in the California Coast Range. Sample splits were analyzed via quadrupole time-of-flight liquid chromatography tandem mass spectrometry (QToF-LC/MS/MS), and NMR and FT-ICR-MS were utilized through an ongoing collaboration with the Environmental Molecular Sciences Laboratory (EMSL) for analysis of continental serpentinites. Metabolomes and previously obtained metagenomes were imported into Progenesis QI software for statistical analysis and correlation, and metabolic networks constructed using the Genome-Linked Application for Metabolic Maps (GLAMM), a web interface tool. Further multivariate statistical analyses and quality control was performed using EZinfo.

Results: Metagenomic data from the CROMO wells suggests that the metabolism of methane and small organic acids (e.g. formate, acetate) play an important role in carbon cycling in these microbial communities. Identification of several intermediate metabolites involved in these processes supports this hypothesis. Additionally, we found evidence of fermentation of large organic molecules in both the metagenome and the metabolome, which may reflect surface water influence in the wells. Our results are promising regarding the future use of metabolomics techniques in this and other serpentinizing environments, for the identification of biomarkers and metabolic pathways.

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