

Expression of metabolic pathways in microbial communities from a tropical serpentinizing environment.K. I. Twing¹, M. Crespo-Medina², W. J. Brazelton³, R. Sanchez-Murillo⁴ and M. O. Schrenk⁵¹Dept. of Biology, University of Utah, Salt Lake City, Utah; katrina.twing@utah.edu²CECIA, Inter-American University of Puerto Rico, San Juan, Puerto Rico; melitzacm@inter.edu³Dept. of Biology, University of Utah, Salt Lake City, Utah; william.brazelton@utah.edu⁴School of Chemistry, National University of Costa Rica, Heredia, Costa Rica; ricardo.sanchez.murillo@una.cr⁵Dept. of Earth and Environ. Sciences, Michigan State University, East Lansing, Michigan; schrenkm@msu.edu**Introduction:**

Serpentinization is the hydrous alteration of mafic rocks in the ocean crust to form serpentine minerals. The set of reactions that constitutes serpentinization result in extremely high pH of surrounding fluids, an abundance of H₂, methane, abiotically generated organic molecules, and depletion of dissolved inorganic carbon. As a geochemical, abiotic source of organic molecules, serpentinization has astrobiological implications for the origin of life on Earth and possibly Mars, where serpentinization has likely occurred in the past and may occur in the present [1].

While serpentinization generally takes place within ocean crust, continental sites of serpentinization are found where the seafloor is obducted onto continental crust, making the process more accessible to study. Sites of continental serpentinization around the world have been the topic of recent studies [2,3,4] and have displayed consistently low microbial diversity and a surprising similarity in community composition among sites, namely a dominance of the classes Betaproteobacteria and Clostridia [2,3,4].

Recent studies have assessed the metabolic potential of continental serpentinization through analysis of shotgun metagenomic datasets, identifying genes involved in hydrogen [5,6], methane [7,8], and acetate [6] metabolisms as being key to biogeochemical cycling in these environments. However, to date, no published studies have directly assessed the activity of microbial communities in continental serpentinite environments through the use of metatranscriptomics.

The Santa Elena Ophiolite (SEO) is a site of continental serpentinization located in northwestern Costa Rica that experiences seasonal weather extremes of wet (May-Nov.) and dry (Dec.-April) seasons [9]. Sequences related to hydrogen and methane cycling organisms have been detected at SEO, as have genes involved in methanogenesis [8,9]. However, similar to other sites of serpentinization, microbial activity has not yet been assessed.

This study will identify what metabolic pathways are expressed in serpentinite fluids at SEO by analyzing metagenomic (metabolic potential) and metatranscriptomic (expression) data. These data will be analyzed in tandem with geophysical and environmen-

tal parameters to help define biogeochemical relationships within the serpentinite subsurface system. This study will help advance our understanding of microbial ecology and evolution in this astrobiologically relevant system.

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