Goldschmidt 2024 Abstract
https://doi.org/10.46427/gold2024.24641

Cultivation of chemosynthetic life from the subseafloor crustal aquifer of the Juan de Fuca Ridge flank

ILEANA PEREZ-RODRIGUEZ[1], JESSICA K CHOI[1,2], KALIOPI BOUSSES[1], ABHIJIT MANNA[1], CHARLOTTE DE VAULX[1], NATALIA APONTE BORGES[1], LEAH VAN DYKE[1,3], GABRIEL GONSALVES-BERTHO[1,4], MAYA KREGER[1], JACOB COTE[1], JOHN CARR[1], OLIVIA NIGRO[5], STEPHANIE CARR[6], ARKADIY GARBER[7] AND MICHAEL RAPPE[8]

[1]University of Pennsylvania
[2]University of Michigan
[3]University of California, Santa Cruz
[4]Yale University
[5]Hawai'i Pacific University
[6]Hartwick College
[7]Arizona State University
[8]University of Hawai'i at Manoa

Presenting Author: ileperez@sas.upenn.edu

The sediment-covered subseafloor crustal aquifer of the Juan de Fuca Ridge (JdFR) flank contains hot, anoxic H_2-rich crustal fluids that support microbial life [1]. Here, we used 65 °C anoxic crustal fluid collected from borehole U1362B (during R/V Atlantis cruise AT42-11 in May 2019) to enrich for chemosynthetic primary producers of the crustal subseafloor. Microbial enrichments, established at temperatures between 60 °C and 80 °C, selected for autotrophic microbial growth via the oxidation of H_2 coupled to the reduction of NO_3^-, SO_4^{2-}, Fe(III), AsO_4^{3-}, or CO_2. Through these efforts, we generated 11 putative isolates representing all of the anaerobic respiration processes we enriched for, after five to six consecutive dilution-to-extinction series. These cultures grow much slower, and many display significantly different morphologies, than members of the same metabolic functional groups from deep-sea vent systems at mid ocean ridges (MOR). Illumina short-read sequencing approaches to date have revealed one pure culture (enriched under AsO_4^{3-} reducing conditions) closely related to *Thermaerobacter marianensis* (isolated from sediment of the Challenger Deep in the Mariana Trench; [2]). Near complete genomes related to the genome of *Thermus scotoductus* (isolated from hot tap water in Iceland; [3]) were obtained from cultures enriched under both NO_3^-- and SO_4^{2-}-reducing conditions. Other 16S rRNA gene sequences in co-culture with our *Thermus* spp. suggest that we may still have mixed cultures within some of our putative isolates, as well as potential contaminants contained in our sequences. Results to date reveal notable differences associated with the cultivation and phylogenetic identification of H_2-oxidizing chemolithoautotrophs from the subseafloor crustal aquifer of the JdFR flank, in comparison to that of deep-sea vent microorganisms performing the same metabolisms at MORs.

[1] Nigro O. D. et al. (2017), *mBio* 8(2), e02129-16; [2] Takai K. et al. (1999) *IJSEM* 49(2), 619-628; [3] Kristjansson J.K. et al. (1994), *Syst. Appl. Microbiol.* 17(1), 44-50.