

Complex organic matter degradation by secondary consumers in chemolithoautotrophy-based subsurface geothermal ecosystems

KAREN G LLOYD¹, RAEGAN PAUL^{2,3}, TIMOTHY ROGERS², KATHERINE FULLERTON², MATTEO SELCI⁴, MARTINA CASCONI⁴, ANGELINA CORDONE⁴, MURRAY STOKES², ANDREW STEEN², MAARTEN DE MOOR⁵, AGOSTINA CHIODI⁶, ANDRI STEFÁNSSON⁷, SAEMUNDUR A HALLDORSSON⁸, CARLOS RAMÍREZ-UMAÑA⁹, GERDARD JESSEN¹⁰, PETER H BARRY¹¹ AND DONATO GIOVANNELLI⁴

¹The University of Tennessee, Knoxville

²University of Tennessee

³Colorado State University

⁴University of Naples Federico II

⁵National University

⁶National University of Salta

⁷University of Iceland

⁸Nordic Volcanological Center, Institute of Earth Sciences, University of Iceland

⁹Servicio Geológico Ambiental de Costa Rica (SeGeoAm), San José, Costa Rica

¹⁰Austral University of Chile

¹¹Woods Hole Oceanographic Institution

Presenting Author: klloyd@utk.edu

Microbial communities in terrestrial geothermal systems often contain chemolithoautotrophs with well-characterized distributions and metabolic capabilities. However, the extent to which organic matter produced by these chemolithoautotrophs supports heterotrophs, remains largely unknown. Here we compare the abundance and activity of predicted extracellular peptidases and carbohydrate active enzymes (CAZymes) identified in metagenomic assemblies from 63 springs in three distinct geological provinces: the Central (Costa Rica and Panama) and South American convergent margins (Argentinian backarc of the Central Volcanic Zone), as well as the plume-influenced spreading center in Iceland. All assemblies contain two orders of magnitude more peptidases than CAZymes, suggesting that these microorganisms prefer proteins for their carbon and/or nitrogen acquisition instead of complex sugars. The CAZy families in highest abundance are GH23 and CBM50, and the most abundant peptidase families are M23 and C26, all four of which degrade peptidoglycan found in bacterial cells. This implies that the heterotrophic community relies on autochthonous dead cell biomass, rather than allochthonous plant matter, for organic material. Enzymes involved in the degradation of cyanobacterial- and algal-derived compounds are in lower abundance at every site, with volcanic sites having more enzymes degrading cyanobacterial compounds and non-volcanic sites having more enzymes degrading algal compounds. Activity

assays showed that many of these enzyme classes are active in these samples. High temperature sites (> 80°C) had similar extracellular carbon-degrading enzymes regardless of their province, suggesting a less well-developed population of secondary consumers at these sites, possibly connected with the limited extent of the subsurface biosphere in these high temperature sites. We conclude that in < 80°C springs, chemolithoautotrophic production supports heterotrophs capable of degrading a wide range of organic compounds that do not vary by geological province, despite the fact that the taxonomic and respiratory repertoire of chemolithoautotrophs and heterotrophs differ greatly across these regions.