

Effects of hydrogeochemistry on the microbial ecology of terrestrial hot springs

CARLA BARBOSA^{1,2}, JAVIER TAMAYO-LEIVA^{3,4,5},
JAIME ALCORTA³, OSCAR SALGADO^{3,6}, BEATRIZ
DIEZ^{3,4,5} AND DIEGO MORATA^{1,2}

¹Departament of Geology, Facultad de Ciencias Físicas y Matemáticas, Universidad de Chile

²Centro de Excelencia en Geotermia de los Andes (CEGA), FCFM, Universidad de Chile

³Department of Molecular Genetics and Microbiology, Pontifical Catholic University of Chile

⁴Center for Climate and Resilience Research (CR)², University of Chile

⁵Center of Genome Regulation (CGR), University of Chile

⁶Laboratorio de Bioinformática, Facultad de Educación, Universidad Adventista de Chile

Presenting Author: carla.barbosa@ug.uchile.cl

Terrestrial hot springs are natural ecosystems that host an enormous diversity of microorganisms that survive in extreme conditions. The water chemistry of these systems is also diverse and plays a critical role in shaping microbial communities. However, the interactions of biotic and abiotic factors at this terrestrial-aquatic interface are still not well understood on a global scale, and the question of how underground events influence microbial communities remains open. To answer this, 16S rRNA amplicon sequencing (V4 region) from 11 new samples in El Tatio geothermal field (Chile) and 191 samples from previous publications in 13 geothermal fields spread between the Taupo Volcanic Zone (New Zealand) [1], the Yellowstone Plateau Volcanic Field (United States of America) [2], and the Eastern Tibetan Plateau (China) [3], were analyzed together with their temperature, pH, electrical conductivity, and major ion concentrations.

Microbial diversity was lower in acid-sulfate waters than in chloride and bicarbonate waters, and no significant correlations with temperature were found. The highest correlations between taxa and chemical parameters, although moderate, were found between pH, SO_4^- , and abundances of members of the families Thermaceae, Hydrogenobaculaceae, Acidithiobacillaceae, and Desulfurellaceae. The hydrochemical gradients of pH and SO_4^- were explained by phase separation, condensation, and thermal fluids dilution, which were identified as key processes shaping these communities. Ordination and PERMANOVA analyzes showed that the hydrochemistry of major elements explains only 25% of microbial community structure. Thus, most of the variance in the thermophilic community remained unexplained, suggesting that other environmental or biotic factors are also involved and highlighting the environmental complexity of the ecosystem. It will be now necessary to include more hydrochemical variables and other metagenomic tools to better understand the role of hydrochemical gradients and water origin in the metabolism of hot springs microbial communities.

[1] Power et al. (2018), *Nature Communications* 9(1), 1-12. doi: 10.1038/s41467-018-05020-y.

[2] Hamilton et al. (2019), *mSystems* 4(6), 1–25. doi: 10.1128/msystems.00498-19.

[3] Guo et al. (2020), *Science of the Total Environment* 720, 137574. doi:10.1016/j.scitotenv.2020.137574.