

Biogeochemical Cycling in Globally Distributed Hypersaline Environments

Michael C. Macey – Postdoc and presenting author, AstrobiologyOU, The Open University

Ermias Balcha – Addis Ababa Science and Technology University

Susanne P. Schwenzer – AstrobiologyOU, The Open University

Hagos Miruts – Mekelle University

Felipe Gomez – Centro De Astrobiologia

Barbara Cavalazzi – Department of Biological, Geological, and Environmental Sciences, University of Bologna

Karen Olsson-Francis – AstrobiologyOU, The Open University

Studying extremophiles allows the characterisation of the boundaries of life on Earth and the identification of metabolic processes that fuel biogeochemical cycling under extreme conditions. Here we present an analysis of the microbiomes of globally distributed hypersaline environments.

We screened published metagenomes produced from a range of hypersaline environments (Marine salterns in Spain, hypersaline lakes in Chile and Antarctica, and soda lakes in Egypt and Mongolia [1–5]) for the presence, diversity, and abundance of shared functional genes that encode for the enzymes relevant to biogeochemical cycling. The study was expanded by generating metagenomes from DNA extracted from the salt and water of an Ethiopian hypersaline lake in the Dallol Depression. Analysis was performed to compare the functional gene profiles between the hypersaline environments.

The microbial community within the Ethiopian Lake was comprised of Cyanobacteria, Candidate Phyla, and halophilic bacteria and archaea. Screening of the metagenomes identified that phototrophs in hypersaline environments typically possessed the majority of the genes relating to carbon dioxide and nitrogen fixation, indicating that they play a major role in driving both the carbon and nitrogen cycles [6-7]. High abundances of genes involved in denitrification, methylamine utilisation, and carbon monoxide oxidation classified as Halobacterial were also identified in all the metagenomes, indicating that these taxa are also key players in biogeochemical cycling in hypersaline environments [8-9]. Cultivation efforts are required to further define the interactions between the distinct functional clades identified in the hypersaline environments.

References:

1. Zhao D, Zhang S, Xue Q, Chen J, Zhou J, Cheng F, et al. *Front Microbiol.* 2020;11(July):1–17.
2. Hagagy N, Hamedo H, Elshafi N, Selim S. Shotgun Metagenomic Sequencing of Extremophilic Community from Soda Lake, Ga'ar Lake, in Wadi Al-Natrun, Egypt. *Egypt. J. Exp. Biol. (Bot.)*. 2021;1.
3. Fernandez AB, Ghai R, Martin-Cuadrado AB, Sanchez-Porro C, Rodriguez-Valera F, Ventosa A. *Genome Announc.* 2013;1(6).
4. Yau S, Lauro FM, Williams TJ, Demaere MZ, Brown M v., Rich J, et al. *ISME Journal.* 2013;7(10):1944–61.
5. Kurth D, Elias D, Rasuk MC, Contreras M, Farias ME. *PLoS One.* 2021;16:1–21.
6. Lay CY, Mykytczuk NCS, Yergeau É, Lamarche-Gagnon G, Greer CW, et al. *Appl Environ Microbiol* 2013;79:3637–3648.

7. Mehda S, Ángeles Muñoz-Martín M, Oustani M, Hamdi-Aïssa B, Perona E, et al. *Microorganisms* 2021;9:1–27.
8. Sorokin DY, Merkel AY, Messina E, Tugui C, Pabst M, et al. *ISME J* 2022;1–13.
9. King GM. *Proc Natl Acad Sci* 2003;51:278–291.

Acknowledgements to the Europlanet Society, Science and Technology Facilities Council and the Research England Expanding Excellence in England (E3) fund for funding the research.