Sulfur biogeochemistry in a cold, hypersaline arctic spring

C.R. COUSINS[1], M. FOX-POWELL[1], A. MORERAS-MARTI[1], M. C. MACEY[2], K. OLSSON-FRANCIS[2], G.R. OSINSKI[3], L. PURKAMO[1]

[1]School of Earth and Environmental Sciences, University of St Andrews, St Andrews, UK. KY16 9AL
[2]Faculty of Science, Technology, Engineering and Mathematics, The Open University, Milton Keynes, UK. MK7 6AA
[3]Centre for Planetary Science and Exploration, University of Western Ontario, London, Ontario, Canada

Axel Heiberg Island in the Canadian Arctic hosts unique hypersaline (>10 wt. %) and perennially low temperature (-5 to 8 °C) springs that precipitate sodium sulfate and chloride salts [1, 2]. Of these, Lost Hammer Spring has been studied as an analogue system to past and present hypersaline environments on Mars and Europa respectively [2,3], and provides an opportunity to investigate the microbiology of extreme low-temperature, hypersaline habitats. Previous metagenomic surveys have shown that sulfur cycling plays an important role here [4]. Lost Hammer Spring (79.076856, -90.210472) emerges as a single outlet from a valley floor. A salt dome surrounds the vent, flanked by salt aprons and an outflow stream. Brine and sediment were taken from the vent, and at two downstream locations to a final distance of 15 m from the vent. At the time of sampling, the vent contained brine to a depth of ~50 cm with salt crystals dominating the bottom sediment. Vent and outflow brines ranged from pH 5.7 - 6, while temperatures increased from -3.6 °C (vent) to 1.8 °C (furthest outflow), becoming more oxic downstream (~0 to 7.7 mg/l DO) with a concurrent decrease in dissolved sulfide (~10 to 0 ppm). We investigated the microbiology and $\delta^{34}S$ values recorded along this spring system to explore sulfur biogeochemical cycling in these environments. DNA was extracted from sediments, and bacterial and archaeal communities characterised by 16S rRNA long read sequence assays. The role of microorganisms within the S-cycle was invesitgated using functional genes and metagenomic analysis. These data are combined with sulfate and sulfide $\delta^{34}S$ values from brine and sediment to investigate sulfur-based metabolisms, biogeochemical cycling, and stable isotope biosignatures.

[1] Ward, M. K. & Pollard, W. H. (2018) EPSL, 504, 126-138. [2] Fox-Powell, M. G. et al. (In Revision) GRL. [3] Battler, M. M. et al. (2013) Icarus, 224, 364-381. [4] Lay, C. –Y. et al. (2013) AEM, 79, 3637–3648.