

**LIFE AND BIOGEOCHEMICAL CYCLING IN DEEP SUBSURFACE BRINES.** S.J. Payler<sup>1</sup>, C.S. Cockell<sup>1</sup>, S. Paling<sup>2</sup>, J. Biddle<sup>3</sup>, B. Sherwood Lollar<sup>4</sup>, U. Trivedi<sup>5</sup>, J. Telling<sup>6</sup>, K. Hudson-Edwards<sup>7</sup>, D. McLuckie<sup>8</sup>, T. Edwards<sup>8</sup>, J. Genis<sup>8</sup>. <sup>1</sup>UK Centre for Astrobiology, School of Physics and Astronomy, Kings Buildings, University of Edinburgh, UK, EH9 3JZ, S.J.Payler@ed.ac.uk, <sup>2</sup>STFC Boulby Underground Science Facility, Cleveland, UK, <sup>3</sup>College of Earth, Ocean, and Environment, University of Delaware, USA, <sup>4</sup>Department of Earth Sciences, University of Toronto, Canada, <sup>5</sup>Edinburgh Genomics, University of Edinburgh, UK, <sup>6</sup>School of Geographical Sciences, University of Bristol, UK, <sup>7</sup>Department of Earth and Planetary Sciences, Birkbeck University of London, UK, <sup>8</sup>Cleveland Potash Ltd, UK.

**Introduction:** Interest in the deep subsurface biosphere has grown in recent years due to its influence on a variety of research areas including climate change, deep subsurface repositories and the oil industry. Of these deep subsurface environments, evaporite deposits are an important terrestrial analogue for deep subsurface environments on Mars [1]. Despite the interest in these saline environments, little is known about how the microbial communities within them gain carbon and energy. We examined two spatially separated brine pools present in a 1.1km deep British salt mine to advance our understanding of life in deep hypersaline environments.

**Methodology:** Samples were collected from two brine pools in sterile Falcon tubes and anaerobic serum bottles. A suite of geochemical analyses was performed on both brines, including ion chromatography, ICP-MS and colorimetric assays. Solid halite (NaCl) and sylvite (KCl) samples were taken from the surrounding area at both brine pools and analysed for trapped gases using a gas chromatograph. Metagenomic and amplicon sequencing techniques were used to investigate the communities within the pools. This involved examining the functional and phylogenetic profile of the community to determine the presence specific genes and pathways related to carbon utilisation and energy production. Organisms were also enriched on a variety of carbon sources under both aerobic and anaerobic conditions to validate the metagenomic observations and test directly for the presence of organisms capable of using energy sources available in the brines.

**Results:** The sequencing results indicate that the brine pools are dominated by Archeal communities from the family Halobacteriaceae. Community structure closely resembles those found in saturated hypersaline environments at the surface (Figure 1). The organisms present are dominated by chemoorganotrophs, suggesting fixed organic carbon is one dominant energy source to the community, in spite of the generally carbon limited conditions. Functional genes and enrichment of microorganisms reveal the community is able to utilise a variety of carbon sources for growth,

from simple sugars such as glucose, to complex long chain polysaccharides such as xylan and cellulose. The lack of a detectable autotrophic community indicates that these communities may be dependent on ancient buried carbon. This buried carbon could be in the form of cellulose [2] or other recalcitrant sources trapped in the Permian salt. Trapped gas analysis revealed a number of gases present, including methane, which could also act as a carbon source for the community. Ongoing work aims identify this carbon source, whilst also examining how the microbial community is shaped by the Permian ocean chemistry which deposited the evaporite.

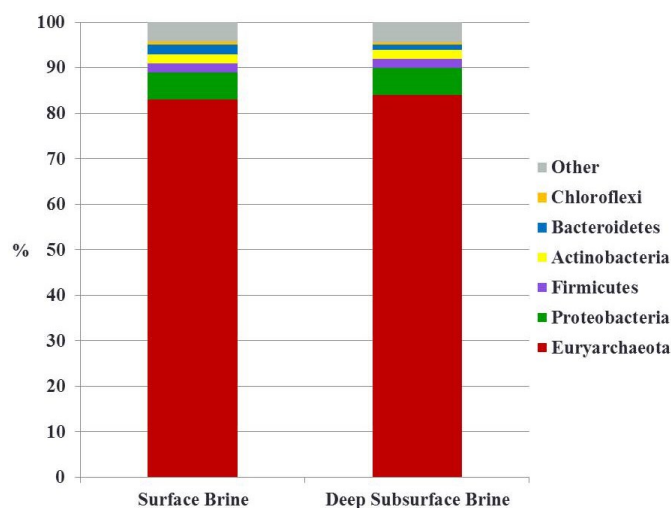


Figure 1: Top 6 phyla present in the brine pools compared to a saturated hypersaline surface brine [3].

#### References:

- [1] Cockell C. S., Payler S., Paling S. and McLuckie, D. (2013) *A&G*, 54, 2.25-2.27.
- [2] Griffith J.D., Willcox S., Powers D.W., Nelson R. and Baxter B.K. (2008) *Astrobiology*, 8, 2.
- [3] Rodriguez-Valera F. <http://metagenomics.anl.gov/linkin.cgi?project=34>.

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