Microbial metabolism in the deep subsurface in Olkiluoto, Finland

EMMA BELL[1], TIINA LAMMINMAKI[2], PETTERI PITKÄNEN[2], MANON FRUTSCHI[1], LOUISE BALMER[1], MAARIT YLI-KAILA[2], RAILA VIITALA[2], RIZLAN BERNIER-LATMANI[1*]

[1]Environmental Microbiology Laboratory, Ecole Polytechnique Federale de Lausanne (EPFL), Switzerland
*presenting author's e-mail: rizlan.bernier-latmani@epfl.ch
[2]Posiva Oy, Eurajoki, Finland

Olkiluoto Island is the site for the construction of the nuclear waste repository in Finland. It is important to construct an accurate model of the microbial metabolism in the subsurface of the island in order to evaluate its potential impact on the long-term safety of the repository. There are three types of groundwaters at this site and they vary in their bicarbonate, sulfate, methane, and chloride content. Evidence for sulfate reduction has been reported in some drillholes [1] where mixing between sulfate- and methane-rich groundwaters has occurred but the electron donor fueling the reduction is not well constrained. Possible compounds include hydrogen or methane gas, or organic carbon. We investigated three drillholes, each representing a different type of mixing case, and carried out detailed chemical, isotopic, metagenomic, metaproteomic, and single cell genomic characterization of the three groundwaters. We found that all three locations harbor sulfate reduction.

The most abundant microbial community is of limited diversity with the deeper waters harboring the least diversity based on 16S rRNA amplicon sequencing. This is in line with previous work that found most of the diversity to be confined to the low-abundance microorganisms [2].

Preliminary data suggest that, in the deepest groundwater, organic carbon compounds fuel sulfate reduction. In contrast, in another drillhole, sulfate reduction may be dependent on H_2 oxidation and possibly anaerobic methane oxidation. Additionally, there is evidence for a cryptic sulfur cycle and possibly cryptic iron and nitrogen cycles. Furthermore, this study has uncovered numerous candidate phyla with no cultivated representatives that will receive detailed scrutiny as to their metabolic potential using their genome sequence.

Altogether, this study sheds considerable insight into the complexity of biogeochemical cycling in the deep suburface in the Fennoscandian Shield bedrock and promises to provide information needed for improving the safety case of the repository in Finland.

[1] Wersin, P. (2014). *Posiva report # 2014-01*.
[2] Bomberg, M. et al. (2016) Biogeosciences, 13, 6031-6047.