Geophysical Research Abstracts
Vol. 16, EGU2014-12286, 2014
EGU General Assembly 2014

Geomicrobial characterization of a 60 m long permafrost core from Svalbard

Siren Fromreide (1), Pål Tore Mørkved (1,2), Graham Lewis Gilbert (3,4), Hanne H Christiansen (3,5), and Laila Reigstad (1)

(1) Centre for Geobiology (CGB), Department of Earth Science, University of Bergen, Bergen, Norway, (2) Institute for Energy Technology, Kjeller, Norway , (3) The University Centre in Svalbard, Longyearbyen, Norway , (4) The University of Oslo, Oslo, Norway, (5) Center for Permafrost, University of Copenhagen, Copenhagen, Denmark

In connection with a planned CO_2 storage pilot project in the Arctic, a 60 m long permafrost core was drilled in Adventdalen, Svalbard. The on-shore drilling was performed through mainly marine and deltafront sediments, ending at the bedrock. The core has undergone detailed analyses of sedimentary stratigraphy, age, as well as the permafrost ice and carbon content at The University Centre in Svalbard (UNIS), and at the Center for Permafrost (CENPERM), Copenhagen.

The main aim of the study presented here is to link the geochemical properties of the permafrost to the microbial community structure and its potential functions. As little is known about microbial life in permafrost at such depths this study will contribute to the understanding of these inaccessible ecosystems.

A baseline geomicrobial description of 7 different depths in the 3 – 60 m interval of the permafrost core was done by culture independent methods such as 16S rRNA amplicon 454 pyrosequencing and functional and ribosomal gene quantifications. Additionally, geochemical analyses of the extracted pore water have been performed, as well as measurements of carbon content and major elements.

The enumeration of the total prokaryotic community indicated similar numbers of bacteria and archaea down to approximately 50 m depth, while below this depth there was a dominance of archaeal cells. The bacterial 16S rRNA copy numbers ranged between 10^8 copies per gram sediment at 3 m depth to 10^4 copies per gram at the bedrock. Concerning the archaeal cells, the 16S rRNA copy numbers per gram sediment were in the range of 10^7 at the top of the core, ending at 10^5in the top of the bedrock.

Detection and quantification of selected functional marker genes indicated high numbers of sulphate reducing bacteria at certain sediment depths, and a significant potential for microbial methanogenic activity throughout the core. Correlations studies between geochemical data and microbial community composition are currently ongoing.