Ancient organic matter in black shales as a carbon source for deep subsurface life

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Abstract

The fluids at black schist-rich bedrock in the Fennoscandian shield have been shown to carry extensive methane (Kietäväinen and Purkamo 2015, Kietäväinen et al. 2017). The sources of methane, abiotic, microbial, thermogenic, or their mixtures, are not well understood (Etiope and Sherwood Lollar 2013, Douglas et al. 2017). While previous field and laboratory studies have concentrated on oxic degradation of relatively low metamorphic grade black shales (e.g., Matlakowska et al. 2012, Petsch et al. 2005), our goal was to explore the genetic potential of microbial communities in naturally anoxic, oligotrophic and moderately saline bedrock fluids in contact with high-metamorphic grade organic carbon containing black schist.

We tested if the microbial metabolisms could explain the extensive methane detected from the fluids at black schist -rich bedrock in the Fennoscandian shield. We aimed to determine the difference between abiotic and biotic methane formation in Palaeoproteorozoic bedrock using novel methane isotopologue measurements and evaluate the ability of natural microbial communities to use black schists as a carbon source in enrichment cultures and compare these to the previously reported cultures.

Two study sites, namely the Outokumpu Deep Scientific Drill Hole at depth of 1470 m and Juuka/Miihkali116 overflowing deep drill hole in Finland, were selected for comprehensive geochemical and microbiological sampling. The sampling campaign involved collecting samples for methane isotopologues, intrinsic microbial community, and fluid for inoculation of laboratory microcosms. Ground and sterilized black shists of two different maturities obtained from Finnish bedrock, ^{13}C-labeled graphite, cellulose, acetate and CO_2 were used as different carbon sources for intrinsic deep subsurface fluids, and these microcosms were incubated for 8-20 months. Subsequently, the gas phase of the microcosms was analyzed for CH_4, CO_2, N_2O, O_2, and N_2 concentrations, as well as isotopic ratios of carbon in CH_4 and CO_2. Bacterial, archaeal and fungal communities were characterized using phylogenetic marker gene amplicon sequencing from both the intrinsic deep subsurface fluids and the microcosms after the incubation period.

The results of this study indicate that methane in these sites is likely formed abiotically, as evidenced by the isotopologue data and the absence of methanogenic archaea in the microbial communities. Moreover, the gas data and isotope ratios obtained from the microcosms suggest that graphitic carbon is predominantly transformed into carbon dioxide rather than methane, further supporting the isotopologue data. Throughout the incubation period, the microbial communities within the microcosms exhibited dynamic changes. Specific microbial groups known for their capacity to utilize complex or recalcitrant organic matter and xenobiotics were observed, indicative of the challenging, oligotrophic and nutrient-deficient subsurface environments. Moreover, microbes regarded as keystone species in the deep terrestrial biosphere were observed.

This study sheds light on the processes driving methane formation and the associated microbial communities in ancient black shales. The findings suggest a predominantly abiotic origin for methane in these Finnish Palaeoproterozoic bedrock formations, highlighting the potential for alternative mechanisms of microbial carbon assimilation and the importance of microbial communities in carbon cycling in subsurface ecosystems.

Keywords

deep terrestrial biosphere, carbon cycling, methane, clumped isotopes, microcosm experiment, bacteria, fungi

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