Nickel and methanogens

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Methanogens require Ni for their growth and as a consequence the microbial fractionation of Ni isotopes can be used as a biomarker for activity of methanogenic communities [1]. Anaerobic laboratory experiments was performed using methanogens to investigate methanogenic growth in a modified nutrient media [2] with olivine Fo91 (5g/l) added as an additional mineral nutrient source and as the only H_2 provider. One of the investigated methanogens showed an increased growth in the experiments with added olivine. There were also a close relationship between the mobilized Ni and the growth of the methanogen. This is the first experimental evidence of a close methanogen-mineral interaction. Ni is an element that previously has been neglected in the study of fossilized microorganisms and their interaction with mineral substrates and, thus, there are no records or published data of Ni in association with microfossils. However, we have detected enrichments of Ni in fossilized microorganisms and ichnofossils, respectively, from three separate locations. Ni is not present in the host rock in none of the samples, thus, it is more probable that the Ni content is primary, a remnant of the live microorganisms. More extensive analysis is required to understand the uptake, preservation and fractionation of Ni by methanogens as well as the preservation and magnitude of Ni in microfossils.

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Characterization of microbial diversity of a geothermal plant after long-term shutdown periods

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The geothermal plant in Soultz-sous-Forêts, located at the western part of the Upper Rhine Graben, is running as an EGS, including four wells ranging to a depth of 5 km. By long-term circulation of deep brines in the reservoir geothermal fluids with a total dissolved solid content of 97 g/L, a temperature around 160°C and a pH around 4.5 are produced. In order to characterize the microbial diversity and its potential involvement in scaling and corrosion processes after long-term shutdown periods, a series of fluid samples from the production well GPK2, taken during two plant restarts, were analyzed. Characterization of the microbial community was done by genetic fingerprinting (PCR DGGE) and qPCR.

Results indicate a diverse microbial community in the fluid of the production well after shutdown periods. In both sampling campaigns a clear shift in the Bacteria community composition was visible after the restart, which could be explained by the increasing temperature and the increasing amount of reservoir fluid. The diversity of the Archaea was not affected.

Sulfate reducing Bacteria (SRB), as indicated by the presence of their 16S rRNA gene and dsr genes, were found only until a produced fluid volume of 260 m^3 (Two borehole volumes) during the first sampling campaign. This indicates the growth of these microorganisms and biofilm formation on the well casing during the shutdown period and their removal after restart of the fluid production. Preliminary quantification results underline this assumption: highest levels of DNA, 16S rRNA gene copies and dsr gene copies were found in the first samples after the restart, while in later samples values were lower or below the detection limit.

The results, as well as further analyzes like the creation of clone libraries or the detection of cell numbers will contribute to characterize the potential involvement of the found microorganisms in corrosion processes and enhance the understanding of the microbial community associated with geothermal plants.

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