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Microbial Life in an Underground Gas Storage Reservoir

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While underground gas storage is technically well established for decades, the presence and activity of microorganisms in underground gas reservoirs have still hardly been explored today. Microbial life in underground gas reservoirs is controlled by moderate to high temperatures, elevated pressures, the availability of essential inorganic nutrients, and the availability of appropriate chemical energy sources. Microbial activity may affect the geochemical conditions and the gas composition in an underground reservoir by selective removal of anorganic and organic components from the stored gas and the formation water as well as by generation of metabolic products. From an economic point of view, microbial activities can lead to a loss of stored gas accompanied by a pressure decline in the reservoir, damage of technical equipment by biocorrosion, clogging processes through precipitates and biomass accumulation, and reservoir souring due to a deterioration of the gas quality.

We present here results from molecular and cultivation-based methods to characterize microbial communities inhabiting a porous rock gas storage reservoir located in Southern Germany. Four reservoir water samples were obtained from three different geological horizons characterized by an ambient reservoir temperature of about 45 °C and an ambient reservoir pressure of about 92 bar at the time of sampling. A complementary water sample was taken at a water production well completed in a respective horizon but located outside the gas storage reservoir.

Microbial community analysis by Illumina Sequencing of bacterial and archaeal 16S rRNA genes indicated the presence of phylogenetically diverse microbial communities of high compositional heterogeneity. In three out of four samples originating from the reservoir, the majority of bacterial sequences affiliated with members of the genera Eubacterium, Acetobacterium and Sporobacterium within Clostridiales, known for their fermenting capabilities. In contrast, bacteria belonging to Enterobacteriaceae were the most frequently encountered species in the sample from the water production well. Furthermore, bacterial sequences belonging to thermophiles within the family Thermotogaceae were found in all samples investigated. Archaeal community analysis revealed the dominance of methanogens clustering with members of Methanosarcinaceae, Methanomicrobiaceae and Methanobacteriaceae in three reservoir samples and the sample from the water production well. Cultivations of water samples under an atmosphere of storage gas blended by hydrogen as electron source at in situ-like conditions (45°C, 92 bar, $p(H2) = 6$ bar) revealed that hydrogen was quickly consumed in all laboratory microcosms with reservoir samples. Quantitative PCR analysis of the gene encoding for methyl-coenzyme M reductase (mcrA) along with reaction educt and product analyses suggested that methanogenesis was primarily responsible for hydrogen consumption during the experiments. While it is currently in question whether or not the laboratory data can be upscaled to actual reservoir conditions, they may allude to fermenting and thermophilic bacteria playing an important role for the investigated reservoir microbiology and also indicate potential stimulation of hydrogenotrophic methanogens if hydrogen would be introduced into the reservoir.