



## **Chemical, mineralogical and molecular biological characterization of the rocks and fluids from a natural gas storage deep reservoir as a baseline for the effects of geological hydrogen storage**

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Planned transition to renewable energy production from nuclear and CO<sub>2</sub>-emitting power generation brings the necessity for large scale energy storage capacities. One possibility to store excessive energy produced is to transfer it to chemical forms like hydrogen which can be subsequently injected and stored in subsurface porous rock formations like depleted gas reservoirs and presently used gas storage sites. In order to investigate the feasibility of the hydrogen storage in the subsurface, the collaborative project H2STORE ("hydrogen to store") was initiated. In the scope of this project, potential reactions between microorganism, fluids and rocks induced by hydrogen injection are studied. For the long-term experiments, fluids of natural gas storage are incubated together with rock cores in the high pressure vessels under 40 bar pressure and 40°C temperature with an atmosphere containing 5.8% He as a tracer gas, 3.9% H<sub>2</sub> and 90.3% N<sub>2</sub>. The reservoir is located at a depth of about 2 000 m, and is characterized by a salinity of 88.9 g l<sup>-1</sup> NaCl and a temperature of 80°C and therefore represents an extreme environment for microbial life. First geochemical analyses showed a relatively high TOC content of the fluids (about 120 mg l<sup>-1</sup>) that were also rich in sodium, potassium, calcium, magnesium and iron. Remarkable amounts of heavy metals like zinc and strontium were also detected. XRD analyses of the reservoir sandstones revealed the major components: quartz, plagioclase, K-feldspar, anhydrite and analcime. The sandstones were intercalated by mudstones, consisting of quartz, plagioclase, K-feldspar, analcime, chlorite, mica and carbonates. Genetic profiling of amplified 16S rRNA genes was applied to characterize the microbial community composition by PCR-SSCP (PCR–Single-Strand-Conformation Polymorphism) and DGGE (Denaturing Gradient Gel Electrophoresis). First results indicate the presence of microorganisms belonging to the phylotypes alfa-, beta- and gamma-*Proteobacteria* and *Actinobacteria*. Sequences of these organisms have been found in subsurface environments before, e.g. in saline, hot, anoxic, and deep milieus. Due to the saline and hyperthermophilic reservoir conditions, the quantification of those microorganisms by DAPI staining revealed very low cell numbers of about 10<sup>2</sup> cells ml<sup>-1</sup>.

Investigations of the microbial community composition, mineralogy and fluid chemistry after 6 months of incubation are in progress to determine to what extent hydrogen injection may contribute to a shift in the microbial community structure and abundance, microbial-mineral interactions and hydrogen-based methanogenesis.