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Insights into microbial community composition and its response to the CO2 injection and storage in the saline aquifer, Ketzin, Germany

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CO2 capture and storage in saline aquifers is a promising method to dispose of CO2 that would be otherwise emitted into the atmosphere. Microbiological monitoring of these systems is essential when reservoirs are favourable to microbial life, as microbes can influence storage by lowering injectivity, or precipitating carbonate and/or other minerals. This study reports the development of efficient microbiological monitoring procedures at the CO2SINK project, located near Ketzin, west of Berlin, Germany. CO2SINK was a pilot project for testing and monitoring of CO2 storage in a saline aquifer. The target reservoir for CO2 storage is the Triassic Stuttgart Formation, consists of siltstones and sandstones interbedded by mudstones deposited in a fluvial environment. For the injection and monitoring of the CO2 in a natural saline aquifer, three 700 to 850 m deep holes were drilled by mud rotary drilling in 2007. The temperature and pressure of the formation fluid were approximately 35 °C and 62 bar, and the salinity was roughly 235 g l-1.

The potential influence of injection and long-term storage of CO2 in saline aquifers on the subsurface microbial communities is presently unexplored. Changes in microbial community composition and activity should result from the injection of CO2 into the reservoir. The decreased pH value and other geochemical change induced by CO2 injection has an influence on the metabolism of the both heterotrophic and lithoautotrophic microorganisms. Therefore, injection of the CO2 in the supercritical state (temperature above 31.1 °C, pressure above 72.9 atm) may induce metabolic shifts in the microbial communities. Furthermore, microbial populations and activity can be strongly influenced by changes in the pH value, pressure, temperature, salinity and other abiotic factors. Therefore, it is important to characterise the microbial community of the deep subsurface before and during the injection of CO2.

A description of microbial communities that originated from varied deep terrestrial settings has shown that those subsurface microbial communities could represent the greatest mass of living organisms on our planet. Furthermore, analyses of the composition of microbial communities will contribute to the understanding of biogeochemical processes in the deep subsurface and will enable better prediction of CO2 behaviour in saline aquifers. The interactions between microorganisms and the minerals of both the reservoir and the cap rock may cause major changes to the porosity and permeability of the reservoir. In addition, microbiologically enhanced precipitation and corrosion may occur around the well affecting the casing and the cement. Moreover, the growth of microorganisms on the metal surface (biofilms) can have a profound effect on metal deterioration, known as microbially-influenced corrosion (MIC).

By using Fluorescence in situ Hybridisation (FISH) and molecular fingerprinting such as Single-Strand-Conformation Polymorphism (PCR-SSCP) and Denaturing Gradient Gel Electrophoresis (PCR-DGGE), we have shown that the microbial community was strongly influenced by the CO2 injection. Before CO2 arrival, up to 6x106 cells ml-1 were detected by DAPI-staining at a depth of 647 m below the surface. The microbial community was dominated by the domain Bacteria, with Proteobacteria and Firmicutes as the most abundant phyla. Representatives of the sulphate-reducing bacteria, extremophilic and fermenting bacteria were identified. After CO2 injection, our study revealed temporal outcompetition of sulphate-reducing bacteria by methanogenic archaea. In addition, an enhanced activity of the microbial population after five months CO2 storage indicated that the bacterial community was able to adapt to the extreme conditions of the deep biosphere and to the extreme changes of these conditions. The completed analyses provide fundamental data on the predominant microbial processes and changes in those processes during the CO2 storage monitoring. Results of the microbiological analyses of the fluid samples taken from observation wells will be compared to those for samples taken from the sump of the injection well. For the results evaluation, a special focus will be placed on the chemical fluid composition and the well completion procedure.