



Microbial community response to the CO₂ injection and storage in the saline aquifer, Ketzin, Germany

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The concept of CO₂ capture and storage in the deep underground is currently receiving great attention as a consequence of the effects of global warming due to the accumulation of carbon dioxide gas in the atmosphere. The EU funded CO₂SINK project is aimed as a pilot storage of CO₂ in a saline aquifer located near Ketzin, Germany. One of the main aims of the project is to develop efficient monitoring procedures for assessing the processes that are triggered in the reservoir by CO₂ injection. This study reveals analyses of the composition and activity of the microbial community of a saline CO₂ storage aquifer and its response to CO₂ injection.

The availability of CO₂ has an influence on the metabolism of both heterotrophic microorganisms, which are involved in carbon cycle, and lithoautotrophic microorganisms, which are able to use CO₂ as the sole carbon source and electron acceptor. Injection of CO₂ in the supercritical state (temperature above 31.1 °C, pressure above 72.9 atm) may induce metabolic shifts in the microbial communities. Furthermore, bacterial population and activity can be strongly influenced by changes in pH value, pressure, temperature, salinity and other abiotic factors, which will be all influenced by CO₂ injection into the deep subsurface. Analyses of the composition of microbial communities and its changes should contribute to an evaluation of the effectiveness and reliability of the long-term CO₂ storage technique. The interactions between microorganisms and the minerals of both the reservoir and the cap rock may cause major changes to the structure and chemical composition of the rock formations, which would influence the permeability within the reservoir. In addition, precipitation and corrosion may occur around the well affecting the casing and the casing cement.

By using Fluorescence in situ Hybridisation (FISH) and molecular fingerprinting such as Polymerase-Chain-Reaction Single-Strand-Conformation Polymorphism (PCR-SSCP) and Denaturing Gradient Gel Electrophoresis (PCR-DGGE), we have shown that the microbial community was strongly influenced by 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.

In order to draw broader conclusions about the microbial community in the deep biosphere, more intensive sampling and methodologies are necessary. The limiting factors such as high expenses of the downhole sampling and time-consuming analyses should be taken into consideration. This study can thus provide only an early insight into the community structure and its changes due to the CO₂ injection. Further studies on the activity, quantity and physiology of these microbial communities using molecular cloning and real-time PCR are in progress.