



Geochemical and microbial monitoring during CO₂ storage in deep subsurface saline aquifers in Ketzin pilot site, Germany

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The development of strategies for sustainable and secure technologies to reduce substantially emission of greenhouse gases to the atmosphere is one of the major challenges of the next decades. Geological CO₂ storage is a promising technology to reduce effectively anthropogenic greenhouse gas emissions to the atmosphere. In the frames of the EU Project CO₂SINK a field laboratory was established to develop efficient monitoring procedures for assessing the processes that are triggered by CO₂ injection into a saline aquifer (Würdemann *et al.* 2010).

Our studies aim at monitoring of microbiological and geochemical processes and their impact on the technical effectiveness of CO₂ storage technique. Investigation on subsurface saline aquifers has shown an active biosphere composed of diverse groups of microorganisms in the subsurface. Since microorganisms represent very effective geochemical catalysts, they may influence the process of CO₂ storage significantly. The interactions between microorganisms, the fluids and the minerals of both the reservoir and the cap rock may cause changes to the structure and chemical composition of the rock formations, which may influence the reservoir permeability locally. In addition, precipitation and corrosion may be induced around the well affecting the casing and the casing cement. Therefore, 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.

This study comprises an interpretation of changes in the fluid chemistry and the microbiology of laboratory experiments and downhole samples after CO₂ exposure. Although the saline aquifer could be characterised as an extreme habitat for microorganisms due to reduced conditions, high pressure (62 to 78 bar) and salinity (235 g/l), a high number of diverse groups of microorganisms were detected with downhole sampling in the injection and observation wells at a depth of about 650m depth.

By using Fluorescence *in situ* Hybridisation (FISH) and molecular fingerprinting such as Single-Strand-Conformation Polymorphism (SSCP) and Denaturing Gradient Gel Electrophoresis (DGGE), we have shown that the microbial community was influenced by the CO₂ injection. Before CO₂ arrival, up to 10⁶ cells ml⁻¹ were detected by DAPI-staining of downhole samples. 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 (Morozova *et al.* 2010a) and increasing numbers of microorganisms after one year of CO₂ exposure (Morozova *et al.* 2010b).

In order to investigate processes in the rock substrate long term CO₂ exposure experiments on freshly drilled, pristine Ketzin reservoir core samples were accomplished for about three years months using sterile synthetic brine (181 g/l) under in situ pressure and temperature conditions. The composition of the microbial community was dominated by chemoorganotrophic bacteria and hydrogen oxidizing bacteria. The mineralogical changes (dissolution of plagioclase, K-Feldspar and anhydrite, see Fischer *et al.*, EGU 2011) are consistent with changes in fluid composition during the course of the experiments that indicate notably increased K⁺, Ca²⁺, Mg²⁺, and SO₄²⁻ concentrations. K⁺, Ca²⁺, Mg²⁺ concentrations exceeded the reservoir brine composition significantly and can be attributed to the CO₂ exposure (Wandrey *et al.*, 2011). The increase of SO₄²⁻ concentration can already be explained by equilibrium reactions between rock and synthetic brine.

Fischer, S. *et al.* Mineralogical and petrophysical results of long-term CO₂-exposure experiments on reservoir sandstone from the Ketzin pilot site, Germany EGU General Assembly 2011 ERE2.1

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