



Baseline characterization of the deep microbial life for the Enhanced Gas Recovery in the Altmark natural gas reservoir

Daria Morozova (1), Mashal Alawi (1), Dagmar Kock (2), Martin Krüger (2), and Hilke Würdemann (1)

(1) Helmholtz Centre GeoForschungsZentrum Potsdam, Centre for CO₂ storage, Potsdam, Germany (daria.morozova@gfz-potsdam.de), (2) Department of Geomicrobiology, Federal Institute of Geoscience and Natural Resources (BGR), Hannover, Germany.

The storage of CO₂ in deep geological formations is a promising technology to reduce greenhouse gas emissions into the atmosphere. Potential geological reservoirs for CO₂ (e.g. saline aquifers, hydrocarbon reservoirs) contain complex biogeochemical systems, including a broad diversity of minerals, brines and largely uncharacterized microbial ecosystems. Many important processes in geological systems are partly or even completely catalyzed by microorganisms. The injection of large volumes of CO₂ perturbs the environmental conditions especially pH, temperature and pressure. These changes in reservoir conditions can stimulate microbial activity, which might influence the long-term safety of CO₂ storage in the subsurface. For example, stimulation of the microbial activity by CO₂ injection might enhance the dissolution of certain minerals, thus increasing the permeability and storage capacity. Conversely, the precipitation of mineral or biological compounds may lead to reduced permeability and loss of injectivity in the reservoir. Furthermore, reactions between supercritical CO₂ and rock materials might produce fluids with increased concentrations of dissolved organic compounds, which can supply the autochthonous microorganisms with energy.

Within the CO₂ Largescale EGR in the Altmark Natural-gas field (CLEAN) project, the microbial community of the natural gas reservoir was investigated. The reservoir is nearly gas-depleted and thus a suitable site for testing enhanced gas recovery processes. The reservoir located at the depth of approximately 3500 m, is characterised by high salinity (up to 420 g/l), high pressure and temperatures between 120° and 130°C. Detailed characterisation of the reservoir and near-reservoir layers is a crucial component of the project. Mineralogy, structure and geochemistry of the reservoir rock and the cap rock as well as interaction with reservoir fluids affect the microbial community composition and its activity. This study represents the results of the comparative molecular biological analysis of the fluid samples from altogether 3 different wells, which differ in their temperature profiles and operative history. Special aseptic downhole sampling technologies were developed in order to avoid contamination. The microbial community of a 3.5 km deep depleted gas reservoir in Altmark, Germany was analyzed by molecular genetic techniques. In order to investigate processes in the deep biosphere that will occur between injected CO₂, or traces of oxygen, nitrous and sulphur oxides, the rock substrate and the microorganisms, the PCR SSCP method (PCR–Single-Strand-Conformation Polymorphism-Based Genetic Profiles of Small-Subunit rRNA Genes) and DGGE (Denaturing Gradient Gel Electrophoresis) are used. These studies aim at localising and identifying microbes within mineralized environments, unravelling the origin and fate of dissolved organic matter (potential substrates and metabolites of microorganisms), and characterising microbial life in extreme habitats and its influence on creation and dissolution of minerals.

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