Geophysical Research Abstracts
Vol. 12, EGU2010-937, 2010
EGU General Assembly 2010

Analysis of active microorganisms and their potential role in carbon dioxide turnover in the natural gas reservoirs Altmark and Schneeren (Germany)

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RECOBIO-2, part of the BMBF-funded *Geotechnologien* consortium, investigates the presence of active microorganisms and their potential role in CO_2 turnover in the formation waters of the Schneeren and Altmark gas fields, which are both operated by GDF SUEZ E&P Germany GmbH.

Located to the north west of Hannover the natural gas reservoir Schneeren is composed of compacted Westfal-C sandstones that have been naturally fractured into a subsalinar horst structure. This gas field is characterized by a depth of 2700 to 3500m, a bottom-hole temperature between 80 and 110˚C as well as a moderate salinity (30-60g/l) and high sulfate contents (∼1000mg/l). During RECOBIO-1 produced formation water collected at wells in Schneeren was already used to conduct long term laboratory experiments. These served to examine possible microbial processes of the autochthonous biocenosis induced by the injection of CO_2 (Ehinger et al. 2009 *submitted*). Microorganisms in particular sulfate-reducing bacteria and methanogens were able to grow in the presence of powdered rock material, CO_2 and H_2 without any other added nutrients. The observed development of DOC was now proven in another long term experiment using labelled $^{13}CO_2$.

In contrast to Schneeren, the almost depleted natural gas reservoir Altmark exhibits an average depth of 3300m, a higher bottom-hole temperature (111˚C to 120˚C), a higher salinity (275-350g/l) but sulfate is absent. This *Rotliegend* formation is located in the southern edge of the Northeast German Basin and is of special interest for CO_2 injection because of favourable geological properties.

Using molecular biological techniques two types of samples are analyzed: formation water collected at the well head (November 2008) and formation water sampled *in situ* from a depth of around 3000m (May 2009). Some of the wells are treated frequently with a foaming agent while others are chemically untreated.

Despite the extreme environmental conditions in the Altmark gas field, RNA of apparently active microorganisms was successfully extracted from all samples. Sequence analysis of 16S rRNA revealed mainly fermentative bacteria belonging to the phylogenetic group of *Actinobacteria* (e.g. *Propionibacterium* spp.) and α-*Proteobacteria* (e.g. *Hyphomicrobium* spp.) possibly involved in the nitrogen cycle. Cell numbers were determined using a PCR-independent molecular detection method (CARD-FISH) with universal 16S rRNA-specific probes (EUB338, ARCH915). The fraction of bacterial cells comprised up to 10^4 cells per milliliter, which corresponds to the cell numbers obtained with a generic DNA stain (DAPI). Archaeal cells could not be detected by CARD-FISH, though archaeal 16S rRNA gene fragments were amplified from DNA extracts using PCR.

So far differences have neither been observed between treated and untreated formation waters nor between well head and *in situ* sampled formation waters.

Further investigations are underway to elucidate whether particular metabolic pathways are present in the microbial assemblage of the Altmark gas field fluids. In addition, microbe-mineral interactions will be assessed using electron microscopic approaches.

Ehinger, S., Kassahun, A., Muschlle, T., Gniese, C., Schlömann, M., Hoth, N., Seifert, J. (2009 *submitted*) Sulfate reduction by novel *Thermoanaerobacteriaceae* in bioreactor inoculated with gas-field brine. *Environmental Microbiology*