



## **Characterisation of the microbial community of the CO<sub>2</sub> reservoir in saline aquifer in Ketzin, Germany**

M. Wandrey, S. Lerm, **D. Morozova** and H. Würdemann

GeoForschungsZentrum Potsdam

Telegrafenberg, 14473 Potsdam, Germany

(dariam@gfz-potsdam.de / Phone +49 (0) 3312881579)

The investigations on the possibilities to reduce the CO<sub>2</sub> emissions are receiving a great attention as driven by the global warming effects of the carbon dioxide gas, accumulated in the atmosphere. One possibility to reduce the volume of CO<sub>2</sub> emitted into the atmosphere is the CO<sub>2</sub> capture and geological storage in the deep underground.

In the frames of the international “Greenhouse-gas Removal Apprenticeship and Student Program (GRASP)”, sponsored by the European Commission, our working group aims to investigate the baseline for the storage technique by injecting CO<sub>2</sub> into saline aquifer near Ketzin, west of Berlin, Germany. The main emphasis is placed on the characterisation of the underground processes, including physico-chemical reactions as well as microbial reactions between the gas (either dissolved in water or in the supercritical state), fluid and the mineral content of both the reservoir rock and the cap rock. From the biological point of view, due to reduced conditions, high pressure and salinity the saline aquifer could be characterized as extreme habitat.

In order to understand processes of the deep biosphere that will occur after CO<sub>2</sub> injection three 700-850 m deep holes were drilled by mud rotary drilling in March/April 2007 within the scope of the CO<sub>2</sub>SINK project. The rock cores and fluid samples were collected from the reservoir rock of the CO<sub>2</sub> storage side in Ketzin. The microbial community of the samples was investigated using DNA analyses with PCR SSCP method (PCR–Single–Strand–Conformation Polymorphism–Based Genetic Profiles of

Small-Subunit rRNA Genes). The contamination control for the determination of the drill mud influence on rock and fluid samples was done using Uranine as a tracer.

The first results of the fluid samples analyses revealed high diversity of the saline aquifer inhabitants. The deep biosphere community was dominated by the haloalkaliphilic fermentative bacteria (*Orenia*, *Halomonas*, *Halolactibacillus*, *Halobacteroides* and others). Representatives of the extremophilic organisms (like *Deinococcus*) were also found. First investigations revealed that the penetration of the drill mud into the core was minimal with an overage of 2 cm. No Uranine was detectible after pumping of 70 m<sup>3</sup> mud. Further investigation of the drilling core microbial community are in progress.