Geophysical Research Abstracts
Vol. 15, EGU2013-9874, 2013
EGU General Assembly 2013

Characterization of the indigenous microorganisms in Exter Formation sandstone rock cores obtained during deep drilling and evaluation of contamination by drill mud using fluorescein.

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Microorganisms are very effective catalysts and have an important function in mineral and elemental distribution within geological formations. CO_2 injection may influence the microbial activities by affecting the composition of the rock-fluid system. Reactions like mineral dissolution and precipitation, related to biological processes may influence aquifer injectivity or permeability of faults.

In subsurface reservoirs, a baseline characterization of pristine rock cores is required to monitor changes in the indigenous microbial communities and to study interactions with geotechnical installations. However, drilling procedures and technical fluids, particularly drill mud, are sources of core contamination. To measure the penetration of drill mud into the cores the tracer fluorescein was tested under laboratory as well as under field conditions. The actual penetration depths seem to be related to differences in geology, such as structural heterogeneities or microfractures. The application of fluorescein was successfully applied during a deep drilling campaign at the CO_2 storage pilot site in Ketzin, Germany, in August 2011. During inner coring, crowns of 17.5 mm were removed from the outside. Fluorescein analysis showed that after an inner coring 45% (five samples out of eleven) were not influenced by drill mud. The results highlight that the use of tracers is indispensable to ensuring the quality of core samples for microbiological and biogeochemical analysis.

Core samples of the Exter Formation (sandstone above the caprock, 400-440 m depth) were retrieved in order to investigate the indigenous microbial community and to investigate the interaction between CO_2, fluid formation, rock substrate and microorganisms in long term experiments with geochemical and molecularbiological techniques. The microbial baseline characterization for rock cores of Exter Formation before CO_2 exposure revealed a similar bacterial community composition in all samples. First results of sequence analyses indicated the presence of bacteria related to Acinetobacter sp., Comamonadaceae and Sphingobium sp. which can be found in various deep subsurface or soil habitats (e.g. Ochrobactrum sp.).