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Microbial characterization of seabed sediments overlaying the proposed CO2 storage site Johansen formation

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Deep marine aquifers, as the Johansen formation in the North Sea, have a great potential as future storage sites for CO2. The aquifer is located at 3000 mbsf and 500-600 m below the oil and gas containing sand layers of the Troll field. In the lifetime of a storage site diffuse migration of CO2 from the reservoir to the overburden and subseafloor may occur. Generally microbes are sensitive and may respond quickly to changes in environmental conditions. Therefore the microbial consortium has been proposed to be the first part of the biota to be affected. Deviation from baseline conditions due to CO2 induced environmental changes has been suggested as a measure for early detection.

In this pilot project we have used metagenomic analysis of DNA and geochemical analysis with the aim to increase our understanding of the baseline characteristics prior to the possible future CO2 injection at the Johansen formation. The sediments investigated (sample 4-T) were collected at the center of a pockmark located 9.5 m below the surrounding seabed level at water depths of 315 m.

The sediments were characterized as silty clay with hydrocarbon concentrations (C10-C36) of 2.8 mg kg-1and TOC of 0.64%. DNA was extracted from the sediments and sequenced by GS-FLX titanium (454-Roch). The filtered dataset generated containing 1 227131 sequences with average sequence length of 346 base pairs, was uploaded to MG-RAST, Metagenomics SEED Viewer 2.0 for analysis. The phylogenetic profile was computed based on 576 348 hits against the SEED protein non-redundant database and on 528 hits against the 16S RNA database Greengenes. Of the 518982 classified sequences 90% were assigned to Bacteria and 8% to Archaea.

The phylogenetic profile of Bacteria was diverse with seventeen phyla represented. In Archaea the respresentation of Crenarchaeota (20989) and Euryarchaeota (20111) was almost equal. The dataset gave hits to 1018 strains but a few strains were highly abundant. This profile indicates a diverse and complex consortium with great variation in the population size of the various species. The high abundant strains observed with about 6000 sequences assigned were: Nitrosopumilus maritimus SCM1 (17645), Solibacter usitatus Ellin6076 (14093), Blastopirellula marina DSM 3645 (12767), Sorangium cellulosum So ce 56 (10302), Desulfococcus oleovorans Hxd3 (8734), Pirellula sp. 1 (8538), Syntrophobacter fumaroxidans MPOB (8308), Desulfuromonas acetoxidans (7763), gamma proteobacterium KT 71 (7195), Acidobacteria bacterium Ellin345 (6623), Nitrosococcus oceani ATCC 19707 (6110), Geobacter uraniumreducens Rf4 (5985). Of these N. maritimus, N. oceani and G. uraniumreducens are chemoautotrophs assimilating CO2 with ammonia, iron or manganese as electron donors. These high abundant species are possible candidates to be affected by increased CO2 content in the sediments.

There are several pathways for CO2 fixation in prokaryotes but in sample 4-T most sequences (966) were assigned to genes involved in CO2 uptake by carboxysomes. The chemoautotrophs are possible candidates for monitoring of CO2 migration in marine sediments. This preliminary study indicates that metagenomic analysis is a useful approach to increase our knowledge of the complex microbial consortia in seabed sediments.