Geophysical Research Abstracts
Vol. 18, EGU2016-17951-1, 2016
EGU General Assembly 2016

Biogeochemical and microbiological characteristic of the pockmark sediments, the Gdansk Deep, The Baltic Sea

Nikolay Pimenov (1), Timur Kanapatskiy (1), Vadim Sivkov (2,3), Stepan Toshchakov (2), Aleksei Korzhenkov (2), Marina Ulyanova (2,3)

(1) FRC Fundamentals of Biotechnology, Winogradsky Institute of Microbiology RAS, Moscow, Russian Federation, (2) Immanuel Kant Baltic Federal University, Kaliningrad, Russian Federation, (3) Atlantic branch of Shirshov Institute of Oceanology RAS, Kaliningrad, Russian Federation

Comparison of the biogeochemical and microbial features was done for the gas-bearing and background sediments as well as near-bottom water of the Gdansk Deep, The Baltic Sea. Data were received in October, 2015 during 64th cruise of the R/V Akademik Mstislav Keldysh. Gas-bearing sediments were sampled within the known pockmark (Gas-Point, depth 94 m). Background sediments area (BG-Point, depth 86 m) was located several km off the pockmark area.

The sulphate concentration in the pore water of the surface sediment layer (0-5 cm) of Gas-Point was 9,7 mmol/l, and sharply decreased with depth (did not exceed 1 mmol/l deeper than 50 cm). The sulphate concentration decrease at BG-Point also took place but was not so considerable. Sulphate concentration decrease is typical for the organic rich sediments of the high productive areas, both as for the methane seep areas. Fast sulphate depletion occurs due to active processes of its microbial reduction by consortium of the sulphate-reduction bacteria, which may use low-molecular organic compounds or hydrogen, formed at the different stages of the organic matter destruction; as well as within the process of the anaerobic methane oxidation by consortium of the methane-trophic archaea and sulphate-reduction bacteria.

Together with sulphate concentration decrease the methane content increase, typical for the marine sediments, occurred. At the Gas-Point the methane concentration varied within 10 μmol/dm3 in the surface layer till its maximum at sediment horizon of 65 cm (5 mmol/dm3), and decreased to 1.5 mmol/dm3 at depth of 300 cm. The BG-Point maximum values were defined at sediment horizon 6 cm (2,6 μmol/dm3).

Methane sulfate transition zone at the Gas-Point sediments was at 25-35 cm depth; whereas it was not defined at the BG-Point mud.

High methane concentration in the gas-bearing sediments results in the formation of the methane seep from the sediments to the near-bottom water. So the Gas-Point near-bottom waters were characterized by high methane concentration (0.36-0.50 μmol/l) even in the water 2-5 m above the bottom (0.08-0.28 μmol/l), whereas at the BG-Point sediments methane concentration in the near-bottom water was 0.06-0.08 μmol/l.

In order to get insights into the structure of microbial community responsible for realization of these redox processes we performed microbial community profiling using high-throughput 16S amplicon sequencing. DNA was extracted from sediments and water column in pockmark and background zones. NGS libraries were prepared with fusion primers for V4 variable region (Caporaso et al., 2012) and sequenced on the MiSeq system. Results well correlated with new data obtained from the analysis of the intensity of microbial processes.

The study was financed by the Russian Scientific Fund (grant 14-37-00047).

Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Huntley J, Fierer N, Owens SM, Betley J, Fraser L, Bauer M, Gormley N, Gilbert JA, Smith G, Knight R. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME J. 2012 Aug;6(8):1621-4