

Communities of potentially corrosive microorganisms of the littoral zone of Kislaya Guba (Barents Sea)

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ABSTRACT. The destruction of different materials in natural environments takes place because of combination of different external factors: biological, physical and chemical. The biocorrosion represents up to 50% of all corrosive losses. Our research objective is to observe the microbially induced corrosion processes of various materials in the Barents Sea inshore ecosystems. The complete phylogenetic composition of microbial communities in water column and bottom sediments in the littoral zone of Kislaya Guba (Murmansk Oblast) was investigated, using new generation sequencing of 16S rRNA fragments. For the first time, all potentially corrosive groups of microorganisms were identified in the coastal zone of the Barents Sea – such as sulfate-reducing, sulfur-, hydrogen-, iron- and manganese-oxidizing, nitrifying, ammonifying and phototrophic microorganisms. In the samples from bottom sediments, about 13% of all microorganisms were sulfate-reducing bacteria, which are one of the most active microorganisms in terms of corrosion. In the water samples, up to 20% of all microorganisms are bacteria of the genus *Pseudomonas*, which are known to possess a very labile metabolism and the ability to form corrosive biofilms. The obtained data will contribute into scientific knowledge of physiology and ecology of potentially corrosive microorganisms as well as of possible effects of mixed microbial populations on structural and physicochemical properties of materials used in modern hydrotechnical constructions under extreme Arctic conditions.

Keywords: The Barents Sea, bottom sediments, microbially induced corrosion (MIC), sulfate-reducing bacteria, sulfur-oxidizing bacteria, iron-oxidizing bacteria.

1. Introduction

Almost all materials are subject to biodegradation. The economic losses from corrosion amount to billions of dollars. Corrosion is a complex physicochemical and multifactorial process in which microorganisms play a significant role, the part of biocorrosion in total corrosion is estimated to be about 50%. Complex microbial communities involve into microbially induced corrosion (MIC) and include various physiological and phylogenetic groups of microorganisms. The MIC can occur due to the direct impact of the metabolic products of microorganisms on materials or due to the biochemical reactions involved chemical compounds from materials (Aviam et al., 2004; Grengg et al., 2018). The composition of microbiota is highly dependent on the state of the environment, the availability of carbon and energy sources, pH and Eh, humidity, temperature, etc. Biofilms are formed on the surface of materials, in which the cells of microorganisms are immersed in a polymeric matrix of microbial origin (Warscheid and Braams, 2000). For this reason, it is necessary to determine the relationships between the

environmental conditions, the properties of materials and the development of biodeterioration processes. These processes are especially interesting in marine ecosystems, where the rate of MIC can be extremely high.

The objective of our research is to study the phylogenetic composition of potentially corrosive microorganisms and their influence on various structural materials in natural conditions of the coastal ecosystems of the Barents Sea.

2. Material and methods

Sampling was carried out in the littoral zone of Kislaya Guba (Murmansk Oblast) in August 2018. Water samples were filtered through a large-pore glass fiber filter GF/C and then through Millipore nitrocellulose membrane filter (pore diameter 0.22 µm). Bottom sediment samples were taken into sterile, hermetically sealed, 10 ml glass bottles. Total DNA was isolated from the samples, and fragments of 16S rRNA genes were amplified and sequenced in the MiSeq

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system (Illumina, USA) using a reagent kit providing a reading length of 300 nucleotides from each end of the amplicon. The sequences were grouped in OTU with the similarity level of 97%, using the Silva reference base of 16S rRNA.

3. Results

In the samples of bottom muddy sediments from the littoral zone of Kislaya Guba, sulfate-reducing bacteria (SRB) belonging to the *Deltaproteobacteria* class, *Desulfobacterales* order (13% of all bacteria in the sample) were detected by 16S rRNA gene sequencing. These SRB belonged to *Desulfobulbaceae* (57% of all *Desulfobacterales*) and *Desulfobacteraceae* (43% of all *Desulfobacterales*) families. In the same bottom sediments, purple sulfur bacteria (*Gammaproteobacteria* class, *Chromatiales* order) were also detected in the amount of 0.5% of all bacteria in the sample. These were representatives of *Granulosicoccaceae* (65% of all *Chromatiales*) and *Ectothiorhodospiraceae* (24% of all *Chromatiales*) families mainly. Among groups of bacteria capable to microlithotrophy using reduced sulfur compounds or able to oxidize sulfur compounds without using them as an energy source, the *Pseudomonas* (19.68% of all bacteria in the sample) and *Alcaligenes* (6.25%) genera were detected in water samples. Also, nitrifying bacteria of the *Nitrospirae* phylum, *Nitrospira* class were found in the bottom sediments and water samples (0.4% and 0.03% of all bacteria in the sample, correspondingly). Iron bacteria of the *Acidithiobacillus* genus (*Gammaproteobacteria* class, *Acidithiobacillales* order), that can obtain energy through the oxidation of ferrous iron, accounted for 0.06% of all bacteria in the bottom samples. In addition, 16S rRNA gene fragments of *Actinobacteria* (2% of all bacteria in the sample) and *Acidobacteria* (0.09%) phyla, many representatives of which are considered as iron-oxidizing bacteria, were detected in the samples from the bottom sediments.

4. Discussion and conclusions

Sulfate-reducing bacteria (which produce deleterious H₂S, and cause in addition cathodal depolarizing and stress corrosion of metals) together with sulfur-oxidizing and nitrifying bacteria (which produce acids) represent the most important and widespread corrosive microorganisms (Herrison et al., 2013). The obtained data on phylogenetic structures of complex microbial communities will contribute into scientific knowledge of physiology and ecology of potentially corrosive microorganisms as well as of strong effects of microorganisms on structural and physicochemical properties of materials used in modern hydrotechnical constructions under extreme conditions of Arctic seas.

Acknowledgements

The reported study was funded by RFBR, project number 18-29-05031.

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