

Submission: T-2020-186-69

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Theme

- -Theme 1: Design, Optimization and Implementation of the Observing System

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Poster title (brief) Pathogenic potential of the microbial communities associated with Western Svalbard glaciers.

Abstract - text box

Introduction: The melting of permafrost and ice due to global warming in the polar regions of the Earth can lead to the activation of ancient pathogens and the introduction of their genetic material into modern ecosystems. This process increases the risk of epidemic outbreaks in the polar regions of the planet. Microbiological studies in areas of active melting of Arctic glaciers are strongly needed.

Purpose: The aim of the study was to assess the taxonomic composition of bacteria found in aquatic ecosystems associated with actively melting glaciers in Svalbard.

Material and methods

We use membrane filtration method for the aquatic microbiome investigation in water samples from glacial meltwater streams and lakes at Nordensheld Land, West Spitsbergen. The taxa of the isolated bacteria was studied by using of MALDI-TOF and 16s rRNA gene sequencing.

Results: Opportunistic bacteria, attributed to the Enterococcus, Pseudomonas, Yersinia, Stenotrophomonas; Escherichia, Acinetobacter genera were isolated among psychroactive microboita. The study described a strain of Acinetobacter calcoaceticus, which has a serious pathogenic potential : received 90 contigs (N50 = 93140). The genome size was 3,882,273 nucleotide pairs (n.p.). GC - 38.8%. This strain (denoted by us as 105-3) shows the highest degree of phylogenetic affinity for the 16S rDNA gene and the housekeeping gene with strains of the species Acinetobacter calcoaceticus. A 40862 bp plasmid was identified in the genome; there are two prophages and a number of IS elements. A number of pathogenicity factors have been identified, including genes for hemolysins and type IV and VI secretion systems, sequences of enterobactin operon genes and two PgaABCD biofilm operons, which show a significant similarity with the corresponding sequences, those present in the Acinetobacter oleivorans DR1 genome (GenBank Acc. No. CP002080.1).Conclusion

The study confirms the importance of microbiological monitoring of glacial ecosystems as an element of assessment and prediction of biological risks associated with global climate warming.