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Theme

- -Theme 5: Arctic Observations in the context of Global Observing initiatives

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Poster title (brief) WHOLE-GENOME SEQUENCING – A USEFUL TOOL FOR AN ASSESSMENT OF THE PATHOGENIC POTENTIAL OF ARCTIC MICROBIAL COMMUNITIES

Abstract - text box

Arctic permafrost is a natural reservoir of ancient prokaryotic mobile genetic elements (MGE) that can carry virulence and antimicrobial resistance (AMR) determinants. It has been shown that ancient MGE has an ability of integration and effective expression in the genomes of modern bacteria. Horizontal transfer of virulence and antibiotic resistance genes between ancient and modern bacteria could lead to the formation of new bacterial genotypes with high epidemic potential. Thus, the release of paleomicroorganisms or their DNA from degrading permafrost and melting glaciers due to the global climate changes is associated with the risk of emergence of new pathogens or reactivation of ancient ones. Several bacterial genomes isolated from Pleistocene mammoth fauna were annotated as a result of our team investigations. The presence of the markers specific for modern epidemic clones in the genomes of Arctic paleobacteria was found. Therefore, we suppose that effective monitoring of the pathogenic potential of the polar microbiota should be implemented. Based on this data we believe that the formation of epidemic clones of opportunistic bacteria is more likely determined by the natural selection of strains carrying genetic determinants of pathogenicity or drug resistance in the environment than by their formation in human society de novo.