INVESTIGATION OF MICROBES IN THE STRATOSPHERE

[1]MATEUSZ GRZYBOWSKI, [2]AGNIESZKA KURDYN, [3]PAULINA PODPIRKO, [4]DAWID REKOWSKI, [5]BEATA KRAWCZYK

[1,2,3,4,5]Faculty of Chemistry, Gdańsk University of Technology, Poland
E-mail: [1]grzybek_mg@o2.pl, [2]agnieszka.kurdyn123@gmail.com, [3]paulinass1996@gmail.com, [4]dawrex@tlen.pl, [5]beata.krawczyk@pg.edu.pl

The stratospheric microbiota has been investigated many times using the methods of classical microbiology. In this research a few modern methods, including NGS sequencing and multiple displacement amplification of DNA, were in use. The analysis of metagenome helped to determine the content of various species of bacteria in the sample collected in the stratosphere by a hydrogen-filled balloon holding a gondola with specialistic apparatus. Also the comparison of DNA amounts in specimens collected in the stratosphere and in a ventilated room within a building has been done,which has shown that the stratospheric air is not poor in bacteria, unlike the previous notions suggested. By running experiments with a vacuum chamber, the possibility of destruction of bacterial cells due to a pressure shock during the fall of the gondola with the samples was disproven. Collected cells were unable to be cultivated on agar media in any temperature. The results of the metagenomic 16S rRNA coding gene sequencing revealed that a great amount of the collected DNA came from undescribed species. The most dominant genes among the known bacteria wereEnterococcus, Staphylococcusand Bacillus.

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