

PSEUDOMONAS PHAGE UANTARCTICA – A NOVEL LYTIC VIRUS ISOLATED FROM ANTARCTIC SOIL

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The Antarctic continent is considered the coldest and driest place on earth with simple ecosystems, devoid of higher plants. Biotopes in the ice-free regions of Antarctica are known to harbor a wide range of microorganisms from primary producers to grazers, yet their ecology and particularly the role of viruses is poorly understood.

In this study, we present biological characteristics and a complete genome analysis of *Pseudomonas* phage UAntarctica isolated from low-temperature terrestrial environments Antarctic samples collected in 2019 at the Ukrainian Antarctic Station 'Academician Vernadskiy', Argentina Islands.

Bacteriophage was isolated from soil and the dsDNA was extracted and sequenced using the MinION sequencing. Annotation of the UAntarctica genome was performed using the BLASTp, ExPASy and CD-search tools. The genome sequence of UAntarctica was deposited in GenBank under the accession number MZ605292.

TEM analysis revealed that phage UAntarctica has siphovirus morphology. Phage is characterized by an 48±2 nm isometric head and an apparently non-contractile flexible tail 156±5 nm in length. UAntarctica produces plaques surrounded by a constantly growing transparent zones on the *Pseudomonas fluorescens* FCKU 533 strain. After three days of incubation at 18°C, the plaques formed by UAntarctica are up to 1±0.1 mm in diameter, after five days - 0.15±0.05 in diameter. The phage plaques stop increasing in diameter after the fifth day of incubation. The 81.1 kbp genome of UAntarctica has a GC content of 58.4% and contains 119 putative protein encoding genes and 3 genes for tRNA^{Gln}, tRNA^{His} and tRNA^{Met}.

A comparative sequence analysis allowed for a putative functional annotation of 23 genes, including those coding for the proteins responsible for virion morphogenesis, phage-host interactions, and DNA metabolism. The closest relatives of UAntarctica are *Pseudomonas* phages PMBT3 (NC_047902) and Lana (NC_048166). The overall nucleotide sequence similarity calculated using VIRIDIC indicates low identity that ranges from 37.4% (UAntarctica vs PMBT3) to 35.8% (UAntarctica vs Lana). Their genomes share several regions of nucleotide similarity that cover the essential structural and virion morphogenesis protein-encoding genes, as well as genes related to DNA metabolism and modification. To determine the evolutionary relationship between UAntarctica and other bacterial viruses, the phylogenetic tree was constructed on the base of the alignment of the large terminase subunit proteins. The obtained dendrogram shows that UAntarctica represents a distinct branch and has no close relatives among studied phages.

In conclusion, our results indicate that UAntarctica is substantially different from the previously described phages and may be considered as a representative of a novel genus within the *Siphoviridae* family.

