

Draft Genome Sequence of *Winogradskyella psychrotolerans* RS-3^T, Isolated from the Marine Transect of Kongsfjorden, Ny-Ålesund, Svalbard, Arctic Ocean

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The 4.3-Mb genome of *Winogradskyella psychrotolerans* strain RS-3^T, isolated from a sediment sample of a marine transect of Kongsfjorden, Ny-Ålesund, Svalbard, Arctic Ocean, is reported.

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Winogradskyella psychrotolerans strain RS-3^T is a Gram-negative, nonmotile, rod-coccus shaped bacterium. It was isolated from a marine transect sample from Kongsfjorden, Ny-Ålesund, Svalbard, Arctic Ocean. *Winogradskyella pacifica* and *Winogradskyella thalassocola* were reported to be the most closely related species by the 16S rRNA gene sequence analysis, with sequence similarities to the type strains of these species of 98.5 and 97.7%, respectively (1).

The Roche 454 (FLX Titanium) pyrosequencing platform was used to sequence the genome of *W. psychrotolerans* strain RS-3^T. The sequencing yielded 121,341,791 bases in 288,329 reads, which is 28× coverage of the genome. The GS *de novo* assembler (v2.8) was used for the assembly of the raw sequencing data, which yielded a genome of 4,342,100 bp in 219 contigs, with a G+C% mol of 37.70%. The genome annotation was performed using the Rapid Annotations using Subsystems Technology (RAST) server (2), tRNAs were predicted by tRNAscan-SE (v1.23) (3), and rRNA genes were predicted by RNAmmer (v1.2) (4).

The annotation has a total of 4,068 genes, including 44 RNA genes. The annotation has 54 genes providing resistance against different antibiotics and toxic compounds. There are 107 genes for membrane transport, including 5 ABC transporters and 5 cation transporters. The genome also has 67 genes for different stress responses, including 33 genes for oxidative stress, 14 heat shock response genes, and 5 cold shock response genes.

A functional comparison of the genome was performed using the SEED framework (4) which revealed the closest neighbors of *W. psychrotolerans* RS-3^T to be *Flavobacteriales* bacterium ALC-1, *Croceibacter atlanticus* HTCC2559, *Cellulophaga* sp. MED134, *Dokdonia donghaensis* MED134, and *Zunongwangia profunda*

SM-A87, with similarity score values of 513, 391, 358, 344, and 343, respectively.

Whole-genome sequencing of this bacterium will help in understanding the metabolism and evolution of bacteria under extreme weather conditions, like the Arctic Ocean.

Nucleotide sequence accession numbers. The draft genome sequence of *W. psychrotolerans* RS-3^T has been deposited in DDBJ/EMBL/GenBank under the accession no. [ATMR000000000](https://www.ncbi.nlm.nih.gov/nuccore/ATMR000000000). The version described in this paper is the first version, ATMR01000000.

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