

Genome Sequence of the Antarctic Psychrophile Bacterium *Planococcus antarcticus* DSM 14505

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***Planococcus antarcticus* DSM 14505 is a psychrophile bacterium that was isolated from cyanobacterial mat samples, originally collected from ponds in McMurdo, Antarctica. This orange-pigmented bacterium grows at 4°C and may possess interesting enzymatic activities at low temperatures. Here we report the first genomic sequence of *P. antarcticus* DSM 14505.**

Thirty-four million years ago, the Earth experienced severe decreases in the global temperature, and ice displaced the tropical vegetation in Antarctica. Around 23 million years ago, Antarctica separated completely from South America, and the continent stayed completely isolated. In addition, and since about 15 million years ago, Antarctica has been covered with a continental-scale ice sheet (2). *Planococcus antarcticus* DSM 14505 is an orange-pigmented, psychrophile bacterium which was isolated from a lake in the region of McMurdo, Antarctica (4). *P. antarcticus* DSM 14505 stayed isolated for 23 million years until its discovery in 2002, and it has been recently used by our research group as a microorganism which is not familiar to the human innate immune system (3).

We sequenced a total length of 2,443,440,884 bp and analyzed 24,192,484 paired-end reads by using the genome sequencer Illumina HiSeq2000 to highly oversample the genome (32× experimental coverage). We assembled all the reads using Velvet *de novo* sequence assembler 1.2.05 (5), and we optimized the contig N_{50} value with VelvetOptimiser 2.2.0, from the Victorian Bioinformatics Consortium of Monash University. All the computations were performed at the Cluster de Modelización Científica of the Oviedo University (<http://cms.uniovi.es>). Finally, we obtained a set of 234 unoriented contigs, with a total length of 3,788,630 bp. We analyzed the number of predicted genes included in the *P. antarcticus* DSM 14505 genome using the RAST server 4.0 (1). A total of 3,840 open reading frames (ORFs) were identified, and 43% of the ORFs were placed into the subsystems implemented in the RAST server. These subsystems are sets of functional roles that together implement a specific biological process or structural complex, and to date 1,525 completed subsystems are included in their databases. Seventy-two tRNAs were also identified, and the G+C content of our strain was 42.09%.

The RAST system was able to annotate 1,651 proteins in 401 subsystems. Among them, 111 stress response proteins were found, including proteins involved in resistance to cold/heat shock and osmotic stress. The presence of a complete ATP synthase, together with 39 proteins involved in the synthesis of electron accepting/donating proteins, suggests that *P. antarcticus* DSM 14505 might perform respiration. The presence of 52 proteins related to resistance to antibiotics and toxic compounds, including copper, cobalt, zinc, cadmium, mercury, arsenic, mercuric compounds, chromium compounds, tetracycline (ribosome protection type), fluoroquinolones, beta-lactamic compounds, and multidrug resistance efflux pumps, was noteworthy.

Surprisingly, the genome of *P. antarcticus* DSM 14505 contained three bile salt hydrolases, which are common in gut-associated bacteria of vertebrates. About 65 million years ago, Antarctica had a tropical/subtropical climate and a marsupial fauna and dinosaurs, all of which are believed to have disappeared with the Eocene-Oligocene extinction about 34 million years ago (2). Our analysis, including comparative genomics, will offer new insight into the evolution and history of some genes, including bile salt hydrolases and antibiotic determinants, thought to be restricted to the gastrointestinal environment or to be selected by human activity. Finally, this sequence will offer the possibility of studying several enzymatic activities working at low temperatures.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AJYB000000000](https://www.ncbi.nlm.nih.gov/nuccore/AJYB000000000). The version described in this paper is the first version, [AJYB010000000](https://www.ncbi.nlm.nih.gov/nuccore/AJYB010000000).

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