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Draft Genome Sequence of *Paenisporosarcina* sp. Strain TG-20, a Psychrophilic Bacterium Isolated from the Basal Ice of Taylor Glacier

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We report the draft genome sequence of *Paenisporosarcina* sp. strain TG-20, which is 4.12 Mb in size and consists of 4,071 protein-coding genes and 76 RNA genes. The genome sequence of *Paenisporosarcina* sp. TG-20 may provide useful information about molecular adaptations that enhance survival in icy subsurface environments.

Paenisporosarcina sp. strain TG-20 was isolated from samples of debris-rich basal ice that were recovered via a tunnel excavated into the north margin of the Taylor Glacier, Antarctica. Recent studies have shown that glacial ice and subglacial environments contain viable and diverse psychrophilic microorganisms (8). Glacial ice presents a unique habitat, where entrapped microorganisms must possess various mechanisms to survive a variety of challenges, including constant subzero temperatures, high osmotic stress, damaging ice crystal formation, and extremely low pH (6). Since glacial microorganisms persist in a viable state under these conditions, they require cold-adapted proteins and may possess molecular adaptations that enhance their survival in ice (e.g., ice-binding proteins) (3, 4).

Individual bacterial colonies were isolated from agar-solidified medium (Difco Marine 2216) that was inoculated with meltwater samples from the basal ice of Taylor Glacier. In total, 36 isolates were recovered, 33 of which belonged to the genus *Paenisporosarcina*, highlighting the potential importance of this genus in basal ice environments. Therefore, we sequenced the genome of *Paenisporosarcina* sp. TG-20 to study if it possessed evidence for cold adaptation or was significantly different from cultured relatives given its presumed period of isolation beneath the East Antarctic Ice Sheet.

Paenisporosarcina sp. TG-20 is a Gram-positive and rod-and/or coccus-shaped bacterium (7). It is both psychrotrophic and halotolerant, as it grows at 4°C and maintains growth in media adjusted to 9.5% salinity. Genomic DNA isolated from *Paenisporosarcina* sp. TG-20 grown at 15°C for 5 days in Difco Marine 2216 medium was pyrosequenced using the Illumina HiSeq 2000 (San Diego, CA) (2) and assembled using the CLC Genomics Workbench v5.1 (CLC bio). The draft genome of *Paenisporosarcina* sp. TG-20 had 365 large contigs, with an average size of 11,275 bp and N_{50} contig size of 18,530 bp, the largest being 74,074 bp. Together, the libraries provided an estimated 2,109-fold coverage of the genome. The genome had an overall estimated G+C content of 36.6%. Potential coding sequences (CDSs) were predicted using Glimmer3 (5) and the rapid annotations using subsystems technology (RAST) annotation server (1). Approximately 77.8% of the nucleotides were predicted to be in protein-coding regions, and 2,521 (62.6%) of the protein-coding sequences were annotated with known proteins.

Comparison of entire genome sequences available from the RAST server showed that *Bacillus* sp. strain B-14905 (genome identifier, 101031.3; score, 537), *Lysinibacillus sphaericus* strain

C3-41 (genome identifier, 444177.5; score, 527), and *Bacillus* sp. strain B14905 (genome identifier, 388400.4; score, 526) were the closest neighbors of this strain. *Paenisporosarcina* sp. TG-20 possesses several genes for spore formation, including sporulation kinase, sporulation initiation phosphotransferase, spore coat protein, and spore germination protein. We also found genes for the low-temperature-requirement protein, cold shock DEAD box protein A, and cold shock protein (CspA), which are thought to be involved in cold adaptation. Further analysis of the *Paenisporosarcina* sp. TG-20 genome will be conducted to identify the genes linked to its specific evolutionary mechanisms for cold adaptation.

Nucleotide sequence accession number. This whole-genome shotgun sequence of *Paenisporosarcina* sp. TG-20 was deposited in GenBank under accession number [ALJG00000000](https://www.ncbi.nlm.nih.gov/nuclink/ALJG00000000).

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