

## Draft Genome Sequence of Paenisporosarcina sp. Strain TG-14, a Psychrophilic Bacterium Isolated from Sediment-Laden Stratified Basal Ice from Taylor Glacier, McMurdo Dry Valleys, Antarctica

Hye Yeon Koh, Sung Gu Lee, Jun Hyuck Lee, Shawn Doyle,  
Brent C. Christner and Hak Jun Kim  
*J. Bacteriol.* 2012, 194(23):6656. DOI: 10.1128/JB.01795-12.

---

Updated information and services can be found at:  
<http://jb.asm.org/content/194/23/6656>

---

### REFERENCES

*These include:*

This article cites 16 articles, 7 of which can be accessed free at:  
<http://jb.asm.org/content/194/23/6656#ref-list-1>

### CONTENT ALERTS

Receive: RSS Feeds, eTOCs, free email alerts (when new  
articles cite this article), [more»](#)

---

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>  
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

# Draft Genome Sequence of *Paenisporosarcina* sp. Strain TG-14, a Psychrophilic Bacterium Isolated from Sediment-Laden Stratified Basal Ice from Taylor Glacier, McMurdo Dry Valleys, Antarctica

Hye Yeon Koh,<sup>a,d</sup> Sung Gu Lee,<sup>a,b</sup> Jun Hyuck Lee,<sup>a,b</sup> Shawn Doyle,<sup>c</sup> Brent C. Christner,<sup>c</sup> and Hak Jun Kim<sup>a,b</sup>

Division of Polar Life Sciences, Korea Polar Research Institute, Incheon, South Korea<sup>a</sup>; Department of Polar Sciences, University of Science and Technology, Incheon, South Korea<sup>b</sup>; Department of Biological Sciences, Louisiana State University, Baton Rouge, Louisiana, USA<sup>c</sup>; and Department of Applied Marine Biotechnology and Engineering, Gangneung-Wonju National University, Gangneung, South Korea<sup>d</sup>

**The psychrophilic bacterium *Paenisporosarcina* sp. TG-14 was isolated from sediment-laden stratified basal ice from Taylor Glacier, McMurdo Dry Valleys, Antarctica. Here we report the draft genome sequence of this strain, which may provide useful information on the cold adaptation mechanism in extremely variable environments.**

*Paenisporosarcina* sp. TG-14 was isolated from sediment-laden stratified basal ice from Taylor Glacier, McMurdo Dry Valleys, Antarctica. The environments of Taylor Glacier in Antarctica include constant low temperatures, physical isolation, and permanent darkness (10). Glacial environments were thought to be virtually abiotic for many years (15). However, recent studies have shown that glaciers are one of the biotic environments containing many psychrophilic organisms (7, 13). Although various studies have been conducted to isolate microorganisms from glacial environments, there is little information on the survival mechanisms, such as cold adaptation, overcoming of low membrane fluidity, and activity of transcriptional/translational enzymes and protein folding (3, 4). We have sequenced the genome of *Paenisporosarcina* sp. TG-14 to study cold adaptation and mechanisms in an extreme environment.

Taylor Glacier ice was collected from Antarctica in November 2007. Individual bacterial colonies were isolated from agar-solidified medium (Difco R2A agar) that was directly inoculated with meltwater from sediment-laden stratified basal ice. *Paenisporosarcina* sp. TG-14 is a Gram-positive and rod-shaped bacterium. Based on its 16S rRNA sequencing, *Paenisporosarcina antarctica* N-05(EF154512) was the most closely related cultured representative in the EzTaxon database (<http://eztaxon-e.ezbiocloud.net/>). Similarity between the 16S rRNA gene of *Paenisporosarcina* sp. TG-14 and that of *Paenisporosarcina antarctica* N-05 was 99.71%. DNA was isolated from *Paenisporosarcina* sp. TG-14 using a genomic DNA (gDNA) extraction kit (Epicentre) and analyzed using the Illumina HiSeq 2000 (San Diego, CA) (2) with a 300-bp paired-end library (69,887,813 reads). The Illumina HiSeq 2000 sequencing achieved about 1,844-fold coverage. The reads generated by Illumina HiSeq 2000 were assembled using CLC Genomics Workbench v5.0 (CLC bio), and the resulting contigs were curated by CodonCode Aligner v3.7 (CodonCode Co.). Gene prediction and annotation were carried out using Glimmer3, tRNA-Scan, EzTaxon-e with hidden Markov model searching, NCBI Reference Sequences, and several open databases (5, 6, 9, 11, 12, 14, 16). The draft genome of *Paenisporosarcina* sp. TG-14 (about 3,826,160 bp) contains 135 contigs (the  $N_{50}$  contig size was approximately 60,912 kb). The G+C content was 37%. A total of 3,747 protein-encoding genes and 56 tRNA genes were annotated in the draft genome, and 5 rRNA operons were predicted based on the sequence coverage value. Approximately 82.4% of nucleotides

were predicted as protein-coding regions, and 1,721 (45.2%) of the protein-coding sequences were annotated with known proteins. Comparison of genome sequences available from the rapid annotations using subsystems technology (RAST) server (1) shows that *Bacillus* sp. B-14905 (genome identification [ID], 101,031.3; score, 542) and *Lysinibacillus sphaericus* C3-41 (genome ID, 444,177.5; score, 529) are the closest neighbors of strain TG-14. *Paenisporosarcina* sp. TG-14 may possess antifreeze protein (AFP), which is involved in the cold adaptation mechanism. AFPs bind to ice crystals to suppress their growth so that freeze-tolerant organisms can survive at low temperatures (8). The genome sequence of *Paenisporosarcina* sp. TG-14 will provide significant genetic information to identify the genes linked to its specific evolutionary mechanisms for cold adaptation.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [AMGD00000000](https://doi.org/10.1093/nar/42/11/AMGD0000000). The version described in this paper is the first version, AMGD01000000.

## ACKNOWLEDGMENTS

The work was supported by a grant from the Korea Research Council of Fundamental Science and Technology (PG12010) and an NSF grant (ANT 0636828) to B.C.C.

## REFERENCES

1. Aziz RK, et al. 2008. The RAST server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
2. Bennett, S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438.
3. Christner BC. 2010. Bioprospecting for microbial products that affect ice crystal formation and growth. *Appl. Microbiol. Biotechnol.* 85:481–489.
4. D'Amico S, Collins T, Marx JC, Feller G, Gerday C. 2006. Psychrophilic microorganisms: challenges for life. *EMBO Rep.* 7:385–389.
5. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. *Bioinformatics* 23:673–679.
6. Eddy SR. 1998. Profile hidden Markov models. *Bioinformatics* 14:755–763.
7. Hodson A, et al. 2008. Glacial ecosystems. *Ecol. Monogr.* 78:41–67.

Received 20 September 2012 Accepted 25 September 2012

Address correspondence to Hak Jun Kim, [hjkim@kopri.re.kr](mailto:hjkim@kopri.re.kr).

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.01795-12

8. Jia Z, Davies PL. 2002. Antifreeze proteins: an unusual receptor-ligand interaction. *Trends Biochem. Sci.* 27:101–106.
9. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25:955–964.
10. Mikucki JA, Priscu JC. 2007. Bacterial diversity associated with Blood Falls, a subglacial outflow from the Taylor Glacier, Antarctica. *Appl. Environ. Microbiol.* 73:4029–4039.
11. Overbeek R, et al. 2005. The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Res.* 33:5691–5702.
12. Pruitt KD, Tatusova T, Klimke W, Maglott DR. 2009. NCBI Reference Sequences: current status, policy and new initiatives. *Nucleic Acids Res.* 37:D32–D36.
13. Simon C, Wiezer A, Strittmatter AW, Daniel R. 2009. Phylogenetic diversity and metabolic potential revealed in a glacier ice metagenome. *Appl. Environ. Microbiol.* 75:7519–7526.
14. Tatusov RL, Galperin MY, Natale DA, Koonin EV. 2000. The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Res.* 28:33–36.
15. Uetake J, Yoshimura Y, Nagatsuka N, Kanda H. 3 February 2012, posting date. Isolation of oligotrophic yeasts from supraglacial environments of different altitude on the Gulkana Glacier (Alaska). *FEMS Microbiol. Ecol.* doi:10.1111/j.1574-6941.2012.01323.x.
16. Yu C, Zavaljevski N, Desai V, Reifman J. 2009. Genome-wide enzyme annotation with precision control: catalytic families (CatFam) databases. *Proteins* 74:449–460.