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Complete Genome Sequence of the Marine Cellulose- and Xylan-Degrading Bacterium *Glaciecola* sp. Strain 4H-3-7+YE-5▽

Barbara Klippel,[1] Adriane Lochner,[1,2] David C. Bruce,[3] Karen Walston Davenport,[3] Chris Detter,[3] Lynne A. Goodwin,[4] James Han,[4] Shunsheng Han,[3] Miriam L. Land,[2] Natalia Mikhailova,[4] Matt Nolan,[4] Len Pennacchio,[4] Sam Pitluck,[4] Roxanne Tapia,[3] Tanja Woyke,[4] Sigrid Wiebusch,[1] Alexander Basner,[1] Fumiyoshi Abe,[5] Koki Horikoshi,[5] Martin Keller,[2] and Garabed Antranikian[1]*

Institute of Technical Microbiology, Hamburg University of Technology, Hamburg, Germany[1]; Oak Ridge National Laboratory, Oak Ridge, Tennessee 37831[2]; Los Alamos National Laboratory, Los Alamos, New Mexico 87545[3]; DOE Joint Genome Institute, Walnut Creek, California 94598[4]; and Extremobiosphere Research Center (XBR), Japan Agency for Marine-Earth Science and Technology (JAMSTEC), Yokosuka, Japan[5]

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***Glaciecola* sp. strain 4H-3-7+YE-5 was isolated from subseafloor sediments at Suruga Bay in Japan and is capable of efficiently hydrolyzing cellulose and xylan. The complete genome sequence of *Glaciecola* sp. 4H-3-7+YE-5 revealed several genes encoding putatively novel glycoside hydrolases, offering a high potential for plant biomass degradation.**

Members of the genus *Glaciecola* are Gram-negative, aerobic, and halotolerant bacteria (3) that can be found in various marine habitats (1, 4, 11–15, 17, 18). *Glaciecola* sp. 4H-3-7+YE-5 was isolated from marine subseafloor sediments (31.4 m below the seafloor) collected at a water depth of 755 m at Suruga Bay (Japan) after enrichment on cellulose, xylan, and chitin as sole carbon sources. Until now, little was known about the cellulolytic and hemicellulolytic enzyme systems of *Glaciecola* spp., since only one endo-beta-1,4-xylanase from *G. mesophila* was characterized (8).

In order to gain insight into the complete gene repertoire of *Glaciecola* sp. 4H-3-7+YE-5, the genome was sequenced at the DOE Joint genome Institute (JGI) using a combination of Illumina (2) and 454 technologies (10). To this end, we constructed and sequenced an Illumina GAii shotgun library which generated 50,060,436 reads totaling 3,804 Mb, as well as a 454 Titanium standard library which generated 233,681 reads and three paired-end 454 libraries with average insert sizes of 10.0 kb, 5.4 kb, and 5.9 kb which generated 272,557 reads, totaling 164.4 Mb of 454 data. All general aspects of library construction and sequencing can be found at http://www.jgi.doe.gov/. The initial draft assembly contained 55 contigs in 2 scaffolds. The 454 Titanium standard data and the 454 paired-end data were assembled with Newbler, version 2.3, while the Illumina sequencing data were assembled with VELVET, version 0.7.63 (16). The Newbler and Illumina VELVET consensus data, as well as read pairs in the 454 paired-end library, were integrated using parallel phrap, SPS version 4.24 (High Performance Software, LLC). Consed software (5–7) was used in the following finishing process. Illumina data were used to increase consensus quality using the software Polisher (A. Lapidus, unpublished). Misassemblies were corrected using gapResolution (C. Han, unpublished) or Dupfinisher (9) or by sequencing cloned bridging PCR fragments. Gaps between contigs were closed by editing in Consed, by PCR, and by bubble PCR (J.-F. Cheng, unpublished) primer walks. A total of 209 additional reactions were necessary to close gaps and to raise the quality of the finished sequence. The total size of the genome is 5,393,591 bp, and the final assembly is based on 137.8 Mb of 454 draft data which provides 25.6× average genome coverage and 1,774 Mb of Illumina draft data which provides 329× average genome coverage.

The genome of *Glaciecola* sp. 4H-3-7+YE-5 is contained within one large chromosome (5,052,309 bp) and one plasmid (pGLAAG01, 341,282 bp). The complete genome has a total G+C content of 45% and comprises 4,548 predicted protein-encoding ORFs.

This is the first complete genome sequence for a member of the genus *Glaciecola*. In-depth analysis revealed the presence of numerous ORFs encoding carbohydrate-active enzymes, including glycoside hydrolases, glycosyl transferases, and carbohydrate esterases, making the organism a promising source of biocatalysts needed for polysaccharide degradation.

Nucleotide sequence accession numbers. The complete chromosome and plasmid sequences of *Glaciecola* sp. 4H-3-7+YE-5 have been deposited in GenBank under accession numbers CP002526 and CP002527.

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* Corresponding author. Mailing address: Institute of Technical Microbiology, Hamburg University of Technology, Kasernenstr. 12, D-21073 Hamburg, Germany. Phone: 49 40 42878 3117. Fax: 49 40 42878 2582. E-mail: antranikian@tuhh.de.

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