Genome Sequence of Sulfide-Dependent Denitrification Bacterium Thermomonas sp. Strain XSG, Isolated from Marine Sediment

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ABSTRACT  We report the draft genome sequence of Thermomonas sp. strain XSG, isolated from a marine sediment. The genome is 3,047,478 bp long with a GC content of 68.5%. Strain XSG was found to be closely related to strain NBRC 101115 of Thermomonas koreensis.

The genus Thermomonas, belonging to the family Xanthomonadaceae branch within the Gammaproteobacteria, was first proposed by Busse et al. in 2002 (1). Currently, the genus Thermomonas includes 7 species with validly published names (https://lpsn.dsmz.de/genus/thermomonas) (2). Members of the genus Thermomonas have been isolated from a wide diversity of habitats, such as kaolin slurry (1), a hot spring (3), a denitrification reactor (4), a ginseng field (5), the soil of a coal mine (6), and an industrial wastewater treatment plant (7). The genus Thermomonas is considered to be part of an abundant group of denitrification bacteria in ecosystems. The DNA G+C content of strains of species of the genus Thermomonas ranges from 64.7 to 68.7% (1, 3–7).

In the present study, we report the whole-genome sequence of Thermomonas sp. strain XSG, isolated from a marine sediment at Xiangshan Harbor, Ningbo, Zhejiang, People's Republic of China. The sample was collected at a depth of 14 m in January 2018. We attempted to isolate Thermomonas sp. XSG using the enrichment method (8). Genomic DNA was extracted using the Mag-MK bacterial genomic DNA extraction kit (Songon Biotech, People's Republic of China), and extracted DNA was used for both Nanopore and Illumina sequencing. The long reads for Thermomonas sp. XSG were generated with PromethION sequencing (Oxford Nanopore Technologies). The genomic DNA was sheared to generate fragments for long-insert library preparation. The BluePippin system (Sage Science, Beverly, MA) was used to size select DNA fragments. The sequencing library was prepared using a ligation sequencing kit (SQK-LSK109) and was run in an R9.4.1 flow cell. Base calling and demultiplexing were performed using Guppy v3.2.6. For the Illumina sequencing, the library constructed using the NEBNext Ultra DNA library prep kit for Illumina was sequenced using the Illumina NovaSeq platform (150-bp paired-end reads). A total of 106,844 and 72,265,892 reads were obtained for the Nanopore and Illumina sequencing, respectively. Fastp v0.20.0 (9) was used to filter the raw Illumina reads and remove adapters. The Nanopore reads were adapter trimmed and quality controlled using the MinKNOW software package, which contains Albacore v1.1.2 and Guppy v3.2.6, and were corrected using Canu v1.8.0 (10). The

Citation Wu X-T, He Y-Q, Li G-X, Xiao H, Dai X-Y, Yang M-R, Bao P. 2021. Genome sequence of sulfide-dependent denitrification bacterium Thermomonas sp. strain XSG, isolated from marine sediment. Microbiol Resour Announc 10:e00057-21. https://doi.org/10.1128/MRA.00057-21.

Editor Frank J. Stewart, Georgia Institute of Technology

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Received 29 January 2021
Accepted 25 March 2021
Published 15 April 2021
genome sequence was obtained by de novo hybrid assembly using SPAdes v3.14.1 (11). The final assembly was polished using Pilon v1.23 (12). Default parameters were used for all software unless otherwise noted.

The assembly resulted in one circular chromosome with a total length of 3,047,478 bp and a G+C content of 68.5%. The average sequence depths were 275.6× (Nanopore) and 3,238.18× (Illumina). Annotation was performed using the Prokaryotic Genome Annotation Pipeline (PGAP) (13). From a total of 2,861 predicted sequences, 2,786 and 56 were protein and RNA coding sequences, respectively. To assess similarity, 16S rRNA gene sequences were searched using BLAST against the NCBI sequence database. Strain XSG exhibited 16S rRNA gene sequence similarity of 99.86% to the strain NBRC 101115 of Thermomonas koreensis. Our data suggest that the strain XSG is a member of the genus Thermomonas. The strain was temporarily classified as T. koreensis.

Data availability. This whole-genome project has been deposited in GenBank under the accession number CP061497.1. The raw sequencing data have been deposited in the SRA under BioProject accession number PRJNA661730.

ACKNOWLEDGMENTS
This work was supported by the National Natural Science Foundation of China (General Program number 42077287) and Ningbo Public Welfare project number 202002N3101.

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