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Complete genome sequence of an *Achromobacter xylosoxidans* strain H1_3_1 isolated from a hybrid biological-inorganic system reactor

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ABSTRACT We report the complete genome of *Achromobacter xylosoxidans* strain H1_3_1, which was isolated from a reactor of a hybrid biological-inorganic system. The complete genome comprised 7,071,873 bp, including 6,428 codings, 10 rRNA, and 70 tRNA, with 67.4% G + C content.

KEYWORDS *Achromobacter*, hydrogen-oxidizing bacteria, chemolithoautotrophy, hybrid biological-inorganic system

Achromobacter xylosoxidans is a common bacterium causing respiratory infection in cystic fibrosis patients (1). Members of the genus *Achromobacter* are aerobic Gram-negative bacteria, which can utilize a variety of organic acids and amino acids as carbon sources (2). *A. xylosoxidans* strain H1_3_1 was isolated from an enrichment of halotolerant hydrogen-oxidizing bacteria. A brackish water sample from Shiokawa (26.66 N, 127.99 E), a brackish river in Okinawa, Japan, was inoculated into a hybrid biological-inorganic system reactor with the minimum medium described in reference 3 containing 180-mM phosphate buffer. After three subculturing in the reactors, the medium of the third reactor was spread onto the same medium solidified with 1% (wt/vol) gellan gum and cultured under $H_2/CO_2/O_2$ (80:10:10) at 30°C. Colonies were further purified by streaking, resulting in the isolation of the strain H1_3_1. The strain H1_3_1 can grow chemolithoautotrophically under $H_2/O_2/CO_2$ atmospheres. To better understand the genetic features leading to chemolithoautotrophy, the complete genome of *A. xylosoxidans* strain H1_3_1 was determined.

The strain H1_3_1 was propagated in 20 mL of the minimal medium under $H_2/CO_2/O_2$ (80:10:10) at 30°C for 2 days and was harvested by centrifugation. Genomic DNA was extracted from the cell pellet using the Genomic-tip 20 /G Kit (Qiagen) with the Genomic DNA Buffer Set (Qiagen) according to the manufacturer's protocol and was qualitatively analyzed using a 5,200-fragment analyzer system with an Agilent high-sensitivity genomic DNA 50-kb kit (Agilent Technologies). The genomic DNA was then sheared into 10- to 20-kb fragments using a g-TUBE device (Covaris). The sequencing library was constructed using the SMRTbell Express template prep kit v.2.0 (PacBio) following the manufacturer's instructions and was sequenced using the PacBio Sequel IIe system. To generate high-fidelity (HiFi) reads, adapter trimming and computation of circular consensus sequencing were performed via SMRT Link v.11.0.0.146107. Consensus sequences with an average quality value of <20 were excluded, resulting in 17,329 HiFi reads with a mean size of 10,541 bp. After excluding HiFi reads shorter than 1,000 bp using Fitlong v.0.2.0 (https://github.com/rrwick/Filtlong), the remaining 15,064 reads were used for *de novo* assembly with Flye v.2.9 (4). Genomic circularity was confirmed by assessing the assembly graph using Bandage v.0.8.1 (https://github.com/rrwick/Bandage) (5). The assembled genomic data integrity was confirmed using CheckM

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v.1.2.0 (https://github.com/Ecogenomics/CheckM) (6), showing 99.5% completeness and 0.93% contamination. This resulted in a single 7,071,873-bp contig, specified as circular using Flye, with a coverage of 26× and an overall G + C content of 67.4%.

Functional annotation of the genome was performed using Prokka v.1.14.5 (https://github.com/tseemann/prokka) (7), predicted 6,510 genes, including 6,428 codings, 10 rRNA, and 70 tRNA. *In silico* DNA-DNA hybridization (DDH) value was calculated using the Genome-to-Genome Distance Calculator v.3.0 (https://ggdc.dsmz.de) (8), and average nucleotide identity (ANI) value was calculated using the ANI calculator (https://www.ezbiocloud.net/tools/ani) (9). The results showed a DDH value of 70.7% and an ANI value of 96.7% toward *A. xylosoxidans* LMG 1863 (assembly accession number GCA_000508285). Default parameters were used for all software unless otherwise specified.

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AUTHOR CONTRIBUTIONS

Xiang Feng, Investigation, Writing – original draft | Daichi Kazama, Investigation | Kozo Sato, Supervision.

DATA AVAILABILITY

The genome sequence of *Achromobacter* xylosoxidans strain H1_3_1 has been deposited at the DNA Data Bank of Japan (DDBJ) under the accession number AP028040. The raw reads have been deposited in the DDBJ Sequence Read Archive under accession number DRA016141. The BioSample and BioProject accession numbers are SAMD00597894 and PRJDB15726, respectively.

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