



Complete Genome Sequence of *Glutamicibacter mysorens* NBNZ-009, Isolated from Jin Lake Sediment

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ABSTRACT Members of the genus *Glutamicibacter* have been reported from soil samples or some industrial pollution environments. Here, we present the genome of strain *Glutamicibacter mysorens* NBNZ-009, which was isolated from sediment from Jin Lake (Wuhan, China). The genome consists of a 3.68-Mbp circular chromosome and possesses 3,372 coding sequences.

Recently, some species of the genus *Arthrobacter* were reclassified into a novel genus, *Glutamicibacter* gen. nov. (1). Members of *Glutamicibacter* have been isolated from soil samples or some industrial pollution environments (2). This study aimed to isolate ammonia-degrading bacteria from sediments. *Glutamicibacter mysorens* strain NBNZ-009 was isolated from samples that had been collected at a depth of 0 to 20 cm below the shallow sedimentary layer of Jin Lake (Wuhan, China [114.1917°N, 30.6516°E]) in 2021. A total of 25 distributed samples were collected (1 to 2 kg each). One-gram sediment samples were serially diluted with sterile water and were spread on lysogeny broth (LB) plates. After incubation for 2 days at 30°C, a single colony was purified by repeated streaking on LB plates. To characterize the strain, the 16S rRNA gene sequence was obtained by PCR amplification with the universal primers 27F and 1492R (3). Phylogenetic analysis was performed using the EZBioCloud database (4). NBNZ-009 showed the greatest similarity to the *G. mysorens* type strain LMG 16219 (GenBank accession number [AJ639831.1](#)) (99.52% identity).

Purified colonies were inoculated into LB medium and cultivated to the mid-logarithmic growth stage at 30°C. Genomic DNA for both long- and short-read sequencing was prepared using the blood and cell culture DNA kit (Qiagen, Germany) according to the manufacturer's instructions. DNA concentrations were determined with a NanoDrop One UV-visible spectrophotometer (Thermo Fisher Scientific, USA) and a Qubit 4.0 fluorometer (Invitrogen, USA). Sample integrity and purity were determined by 0.75% agarose gel electrophoresis. For long-read sequencing, size selection was performed using the PippinHT system (Sage Science, USA). The DNA library was prepared using a ligation sequencing kit (SQK-LSK-109; Oxford Nanopore Technologies [ONT], Oxford, UK) without DNA shearing and was sequenced with a Nanopore PromethION sequencer (ONT) on an R9.4.1 flow cell (FLO-MIN106). Base calling, barcode segmentation, and removal of adapter sequences for the raw sequences were performed using Guppy v.4.4.2 (5). In this study, default parameters were used for all software. A total of 128,263 reads (3,014 Mb), with an average length of 23,504 bp, were generated; the N_{50} value was 30,457 bp. For short-read sequencing, genomic DNA was randomly fragmented with an LE220 focused ultrasonicator (Covaris, USA), and the DNA fragments were selected with AMPure XP magnetic beads (Beckman, Germany) to an average size of 200 to 400 bp. A paired-end DNA library was prepared following the MGIEasy FS PCR-free DNA library preparation set (catalog number 1000013455; MGI Tech Co., Ltd.). Sequencing was performed on an DNBSEQ-T7 instrument (MGI Tech Co.), using 150-nucleotide-long reads. Raw data were processed using the FASTQ preprocessing program fastp v.0.23.2 (6) for the purpose of trimming adapters and low-quality data, which yielded 7,986,830 short reads, with a total length of 1,197,917,560 bp.

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The high-quality long- and short-read sequences were assembled into a complete and circularized chromosome using Unicycler v.0.4.8 (7). The average coverage is 1,144×. The chromosome of *G. mysorens* strain NBNZ-009 is 3,681,770 bp in length, with a GC content of 61.7%, and contains 3,372 coding sequences, 65 tRNA genes, 19 rRNA genes, and a CRISPR array, as determined by NCBI PGAP v.5.3 (8).

Data availability. The 16S rRNA gene has been deposited in GenBank under the accession number [OP020885.1](https://doi.org/10.26434/chemrxiv-2022-09-01). The whole-genome shotgun project has been deposited in GenBank under the accession number [CP099453.1](https://doi.org/10.26434/chemrxiv-2022-09-01). The raw sequencing data have been deposited in the Sequence Read Archive (SRA) under accession numbers [SRR19970076](https://doi.org/10.26434/chemrxiv-2022-09-01) (MGI Tech Co.) and [SRR19974005](https://doi.org/10.26434/chemrxiv-2022-09-01) (ONT).

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