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GENOME SEQUENCES

Draft Genome Sequence of the Extremely Haloalkaliphilic and Homoacetic Bacterium *Natroniella acetigena* Z-7937^T

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ABSTRACT *Natroniella acetigena* Z-7937^T (= DSM 9952^T) is a heterotrophic homoacetogenic natronophile. The draft genome sequence is 2.6 Mb in 116 contigs, with a G+C content of 34.1%.

Acetogens are found in nature worldwide, and over 100 species have been discovered (1). Given their ability to fix carbon, acetogens play vital roles in the biogeochemical carbon cycle. *Natroniella acetigena* Z-7937^T is a mesophilic, haloalkaliphilic acetogen growing at high salinity of up to 26% and pH of up to 10.7 and requiring sodium carbonate and chloride ions (2). The haloalkaliphile was isolated from the bottom mud of soda-depositing Lake Magadi and is capable of using lactate, ethanol, pyruvate, glutamate, and propanol, with acetate as the primary end product (2). However, unlike its halophilic counterparts *Acetohalobium arabaticum* and *Fuchsiella alkaliacetigena* of the order *Haloanaerobiales*, *N. acetigena* Z-7937^T was not able to grow chemolithoautotrophically with H_2/CO_2, although findings were positive for the original isolate (2–6). Despite its uniqueness as a functional member in soda lake ecology (7), little is known about *N. acetigena* Z-7937^T with respect to metabolism mechanism, physiological function, and ecological niche. Here, we present the draft genome of *N. acetigena* Z-7937^T.

Strain Z-7937^T was obtained from the culture collection DSMZ and cultivated anaerobically in DSMZ medium 784. Genomic DNA was extracted from cells at log phase by using the MasterPure Gram-positive DNA purification kit (Epicentre) according to the manufacturer's instructions. Draft genome sequencing was performed by using the Illumina HiSeq 2000 platform (100-bp paired-end reads) at Hokkaido System Science (Hokkaido, Japan). The paired-end library was constructed by using the TruSeq DNA PCR-free library preparation kit (Illumina). A total of 4.53 Gb of paired-end raw reads was generated and trimmed by fastp v0.20.1 (–detect_adapter_for_pe –W 6 –M 20 –r –l 78) (8). The clean data were sequentially assembled by using SPAdes v3.14.1 (–isolate –k 21, 33, 41, 65, 77) (9). The assembly resulted in a 2.6-Mb draft genome containing 116 contigs (>1,000 bp). The genome coverage was 350×. The G+C content was 34.1% as calculated by BBmap v38.18 (default parameters) (https://sourceforge.net/projects/bbmap). Genome annotation was conducted by the automated NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.1 (10). This genome contains 2,558 genes, including 2,499 protein-coding genes, 5 rRNA genes (5S, 16S, and 23S), 50 tRNA genes, and 4 noncoding RNA genes. The genome annotation was double-checked by NCBI CD-Search (11). The annotation suggested that the genome contained all genes encoding enzymes of the Wood-Ljungdahl pathway. Genes encoding hydrogenases and the Rnf complex were also present, supporting the hypothesis that *N. acetigena* conserves energy via electron transfer phosphorylation based on an ATPase-involving chemiosmotic mechanism (12). Further comparative genomic analyses will provide a better understanding of the metabolism and adaptation strategies of haloalkaliphilic acetogenic bacteria in high salinity and pH.

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Data availability. This draft genome and the raw sequence data have been deposited in NCBI GenBank and the Sequence Read Archive (SRA) under the accession numbers JALKBX000000000 and SRR19259016, respectively.

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