



Draft Genome Sequence of the Alkaliphilic, Lithoautotrophic Homoacetogen *Fuchsiella alkaliacetigena* Z-7100^T

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ABSTRACT *Fuchsiella alkaliacetigena* is a spore-forming, alkaliphilic hydrogenotrophic homoacetogen that was isolated from the soda lake Lake Tanatar III in Russia. The genome of the type strain Z-7100 (= DSM 24880) is 2.9 Mb, with a G+C content of 36.2%.

Fuchsiella alkaliacetigena Z-7100^T was an obligate and extreme natronophile belonging to the family *Halobacteroidaceae* of the order *Halanaerobiales* (1). It was an alkaliphilic acetogen that could grow lithotrophically with H₂ plus CO₂, which was similar to the family members *Fuchsiella ferrireducens* and *Acetohalobium arabaticum* but different from *Natroniella acetigena* (1–4). The strain Z-7100^T could utilize only limited substrates, i.e., ethanol, lactate, and pyruvate, with acetate and CO₂ as the only metabolic products (1). Nitrate, selenate, anthraquinone-2,6-disulfonate (AQDS), and trace thiosulfate could be used as electron acceptors (1).

F. alkaliacetigena Z-7100^T was anaerobically cultivated at 40°C using DSMZ medium 1352. The genomic DNA was extracted from an exponentially growing culture using the MasterPure Gram-positive DNA purification kit (Epicentre) following the manufacturer's instruction. The extracted DNA was used to construct Illumina shotgun paired-end sequencing libraries using the TruSeq DNA PCR-free library preparation kit (Illumina) and then was sequenced with the Illumina HiSeq 2000 platform (100-bp paired-end reads). A total of 22,931,582 read pairs (a total of 45,863,164 reads or 4.59 Gbp) were obtained. Quality trimming was performed using fastp v0.20.1 (-detect_adapter_for_pe -W 6 -M 20 -r -l 78) (5). *De novo* assembly with SPAdes v3.14.1 (-isolate -k 21, 33, 41, 65, 77) (6) generated 116 contigs (>1,000 bp) with a total of 2.9 Mb. The assembly was estimated to have a completeness of 99.14% by CheckM v1.0.18 (7) using KBase (8). The G+C content of the draft genome was 36.2%. Gene prediction with Prokka v1.14.0 (default parameters) (9) yielded 2,747 genes, comprising 2,700 protein-encoding genes and 46 RNA genes, including 3 rRNA genes, 43 tRNA genes, and 1 transfer-messenger RNA. The genome contains genes encoding the enzymes of the Wood-Ljungdahl pathway, which is responsible for carbon fixation. Genes encoding F-type ATPase, the electron transport complex Rnf, and several hydrogenases associated with energy conservation were also present. In addition, genes encoding enzymes for pyruvate oxidation to acetyl-coenzyme A (CoA) were present in the genome. The availability of this draft genome will aid in research on the metabolism mechanism and adaptation strategies of haloalkaliphilic acetogens for the extreme environment.

Data availability. This draft genome and the raw sequence data have been deposited in NCBI GenBank and Sequence Read Archive (SRA) under the accession numbers [JALKBZ000000000](#), and [SRR19261504](#), respectively.

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