

Draft Genome Sequence of Acid-Tolerant *Clostridium drakei* SL1^T, a Potential Chemical Producer through Syngas Fermentation

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***Clostridium drakei* SL1^T is a strictly anaerobic, H₂-utilizing, and acid-tolerant acetogen isolated from an acidic sediment that is a potential platform for commodity chemical production from syngas fermentation. The draft genome sequence of this strain will enable determination of the acid resistance and autotrophic pathway of the acetogen.**

Received 8 April 2014 Accepted 25 April 2014 Published 15 May 2014

Citation Jeong Y, Song Y, Shin HS, Cho B-K. 2014. Draft genome sequence of acid-tolerant *Clostridium drakei* SL1^T, a potential chemical producer through syngas fermentation. *Genome Announc.* 2(3):e00387-14. doi:10.1128/genomeA.00387-14.

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Acetogenic bacteria produce over 10¹² kg of acetic acid annually, which comprises 10% of the global acetate production (1). In this process, acetogens autotrophically reduce CO₂ to acetate with H₂ as the sole electron donor through the reductive acetyl coenzyme A (acetyl-CoA) pathway, also known as the Wood–Ljungdahl pathway (2). In addition, CO, one of the most abundant syngases, can be utilized for autotrophic growth as the sole electron donor. Because of these metabolic capabilities, acetogens are an attractive platform for the production of useful multi-carbon compounds by syngas fermentation. Among acetogenic clostridial species, *Clostridium drakei* SL1^T is a unique acetogen isolated from the sediment of an acidic coal mine pond (3). Moreover, to date, most of the acetogens have been isolated from a habitat with neutral pH, which suggests that an acidic environment is unfavorable for acetogens (4). Further, *C. drakei* utilizes a wide range of substrates such as glucose, fructose, arabinose, and xylose to produce acetate as the main reduced end product (3). To understand the unique physiological properties, including acid resistance, and metabolic capabilities of syngas utilization of *C. drakei*, we obtained its genome sequence information.

The *C. drakei* genome was sequenced using Illumina MiSeq with a 2×150-cycle paired-end platform (Illumina, San Diego, CA). The sequencing library was constructed using a TruSeq DNA sample prep kit (Illumina). Before sequence assembly, phiX sequences were removed and the reads were trimmed by their qualities (low-quality sequence, 0.05 limit, and ambiguous nucleotides, maximum of 2 nucleotides allowed) using CLC Genomics Workbench (CLC Bio, Aarhus, Denmark). We obtained a total of 4,441,384,356 bases in 30,418,087 reads, which were then assembled using CLC Genomics Workbench (minimum contig length, 302; automatic bubble size, yes; word size, 61; perform scaffolding, yes). The assembly resulted in 140 contigs, the largest of which is 1,132,561 bases. The draft genome sequence was annotated using the RAST server (5).

The resulting draft genome sequence of *C. drakei* comprises 5,635,531 bases, with a 35% G+C content and 5,763 predicted protein-coding sequences (CDSs). Eleven rRNAs and 100 tRNAs

were predicted using the RNAmmer 1.2 server (6) and tRNAscan-SE 1.23 (7), respectively. The genome of *C. drakei* is larger than those of other acetogenic clostridial species such as *C. ljungdahlii* (4.6 Mbp) (8) and *Moorella thermoacetica* (2.6 Mbp) (2) but smaller than those of *C. ultunense* Esp (6.2 Mbp) (9) and *C. methoxybenzovorans* (7.0 Mbp) (accession number ATXD000000000). *C. drakei* possesses the metabolic pathway required to produce butanol from acetyl-CoA, which is mediated by the NADH-dependent butanol dehydrogenase. *C. acetobutylicum* and *C. carboxidivorans* (5.6 Mbp), which is closely related to *C. drakei*, also possess this enzyme (10). An in-depth study of the metabolic pathway would enable application of *C. drakei* as a potential industrial platform for utilization of cellulose-derived sugars such as xylose, arabinose, and rhamnose (11).

Nucleotide sequence accession numbers. The draft genome sequence of *C. drakei* has been deposited at the DDBJ/EMBL/GenBank database under the accession no. [JIBU000000000](https://www.ncbi.nlm.nih.gov/nuccore/JIBU000000000). The version described in this paper is the first version, [JIBU010000000](https://www.ncbi.nlm.nih.gov/nuccore/JIBU010000000).

ACKNOWLEDGMENTS

This work was supported by the Intelligent Synthetic Biology Center of Global Frontier Project 2011-0031957 through the National Research Foundation of Korea (NRF), funded by the Ministry of Science, ICT, and Future Planning.

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