

# Draft Genome Sequence of the Gram-Positive Thermophilic Iron Reducer *Thermincola ferriacetica* Strain Z-0001<sup>T</sup>

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**A 3.19-Mbp draft genome of the Gram-positive thermophilic iron-reducing *Firmicutes* isolate from the *Peptococcaceae* family, *Thermincola ferriacetica* Z-0001, was assembled at ~100× coverage from 100-bp paired-end Illumina reads. The draft genome contains 3,274 predicted genes (3,187 protein coding genes) and putative multiheme *c*-type cytochromes.**

Received 10 August 2015 Accepted 13 August 2015 Published 24 September 2015

**Citation** Lusk BG, Badalamenti JP, Parameswaran P, Bond DR, Torres CI. 2015. Draft genome sequence of the Gram-positive thermophilic iron reducer *Thermincola ferriacetica* strain Z-0001<sup>T</sup>. *Genome Announc* 3(5):e01072-15. doi:10.1128/genomeA.01072-15.

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*Thermincola ferriacetica* strain Z-0001 (DSM 14005), first isolated from a terrestrial hydrothermal spring on Kunashir Island (Kurils) (1), is a Gram-positive, thermophilic (45°C to 70°C), spore-forming bacterium that is capable of dissimilatory metal reduction and anode respiration in a microbial electrochemical cell (MXC) (2–4) and is one of only a limited number of sequenced Gram-positive thermophilic bacteria that has been documented to perform extracellular electron transfer (EET) to insoluble metal substrates (5–7). Strain Z-0001 is capable of organotrophic growth with acetate and other organic compounds while reducing extracellular electron acceptors, including amorphous Fe(III)-hydroxide, magnetite, Mn(IV), anthraquinone-2,6-disulfonate (AQDS), and anodes in MXCs (1, 2, 4). Strain Z-0001 is also capable of chemolithoautotrophic growth, using molecular hydrogen as the electron donor and Fe(III) as the electron acceptor (1). In addition, strain Z-0001 produces H<sub>2</sub> and CO<sub>2</sub> while using CO as its electron donor and acquiring its carbon from acetate (1).

Among Gram-positive bacteria, little is known regarding the mechanism for EET or how the peptidoglycan layer impacts this pathway (8–10). Direct contact-dependent electron transfer has been suggested in *Thermincola potens* JR (11) with genetic evidence for the presence of *c*-type cytochromes (12), proteins which are responsible for EET in other metal-reducing bacteria (13). In contrast to *T. potens*, *T. ferriacetica* strain Z-0001 has been suggested to transfer electrons long range via an extracellular matrix (4), suggesting it may encode additional electron transfer capabilities. *Thermincola ferriacetica* has been reported to produce current densities up to 10 A·m<sup>-2</sup> despite having only half the cytochrome repertoire of *Geobacter sulfurreducens* (4, 14). Further genetic comparison of these strains could help elucidate the EET mechanism(s) of strain Z-0001.

The draft assembly presented here is from an axenic culture of electrode-grown *T. ferriacetica* strain Z-0001 cells in order to eliminate contamination by iron or anthraquinone 2,6,-disulfonate (AQDS). gDNA was collected and sequenced on an Illumina

HiSeq 2000 lane, yielding >45 million 2- × 100- bp reads. Raw reads were trimmed (sliding window 3 until quality >28) and down-sampled to provide 100× coverage for assembly using the a5 pipeline (26 Mart 2013 release [15]). The 3,196,047-bp draft genome assembly yielded 53 contigs >500 bp with an *N*<sub>50</sub> of 112112 bp, an *L*<sub>50</sub> of 8, and a G+C content of 45.69%.

The draft assembly was annotated using the JGI IMG/ER pipeline, yielding 51 tRNAs, 3,274 predicted genes (3,187 predicted protein coding genes), and 35 *c*-type cytochromes with three or more heme (CXXCH)-binding motifs. BLASTN sequence analysis of its 16S rRNA gene revealed 99.9% (1,436/1,438 nt) identity with *T. potens* JR and 99.7% (1,399/1,403 nt) identity with *Thermincola carboxydophila* (5, 16). *T. ferriacetica* contains two multiheme *c*-type cytochromes and 429 genes that are not present in *T. potens*. However, based on an average nucleotide identity (ANI) of 98.3% between their genomes, these two organisms may be members of the same species (17).

**Nucleotide sequence accession numbers.** This whole-genome shotgun project for *T. ferriacetica* strain Z-0001 has been deposited at DDBJ/EMBL/GenBank under the accession number [LGTE000000000](https://www.ncbi.nlm.nih.gov/nuccore/LGTE000000000). The version described in this paper is version [LGTE010000000](https://www.ncbi.nlm.nih.gov/nuccore/LGTE010000000). The raw and adaptor trimmed Illumina reads were submitted to SRA under accession number [SRX1100231](https://www.ncbi.nlm.nih.gov/sra/SRX1100231).

## ACKNOWLEDGMENTS

B.G.L., P.P., and C.I.T. were supported by Office of Naval Research grant no. N000141210344. Additional support and Illumina sequencing were provided by the Swette Center for Environmental Biotechnology at Arizona State University.

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