

Complete Genome Sequence of the Electricity-Producing “*Thermincola potens*” Strain JR[∇]

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“*Thermincola potens*” strain JR is one of the first Gram-positive dissimilatory metal-reducing bacteria (DMRB) for which there is a complete genome sequence. Consistent with the physiology of this organism, preliminary annotation revealed an abundance of multiheme *c*-type cytochromes that are putatively associated with the periplasm and cell surface in a Gram-positive bacterium. Here we report the complete genome sequence of strain JR.

“*Thermincola potens*” strain JR, a Gram-positive anaerobe isolated from a thermophilic microbial fuel cell (MFC), constituted a dominant member of the current-producing bacterial community (10). Strain JR is a *Thermincola* species in the phylum *Firmicutes* belonging to the family *Peptococcaceae* in the order *Clostridiales*. It shares 99% 16S rRNA gene sequence identity with the two known members of the *Thermincola* genus, *T. carboxdophilia* and *T. ferriacetica* (8, 12). This strain coupled acetate oxidation to reduction of the insoluble electron acceptors MFC anodes and hydrous ferric oxide (HFO) (10). Strain JR is also capable of growth with CO as the sole electron donor and carbon source.

This member of the *Firmicutes* is the first MFC isolate and *Thermincola* species to have its genome sequenced and is one of only a few bacteria in the *Peptococcaceae* to have its genome sequenced (5, 11). Genomic analysis will aid elucidation of electron transfer mechanisms by strain JR, contributing to the knowledge of extracellular respiration by Gram-positive bacteria. By comparing these mechanisms to those in Gram-negative organisms, the conserved and disparate aspects of this seminal metabolism can be identified. This will include analysis of the *c*-type cytochrome gene makeup of the genome, especially the increased number of proteins with double heme (CXXCH) motifs and multiple heme binding domains compared to the nearest phylogenetic neighbors with sequenced genomes (4, 6, 7). *c*-type cytochromes are essential for the reduction of insoluble electron acceptors by model Gram-negative bacteria, such as *Geobacter* or *Shewanella* species (3, 9); however, their role in Gram-positive mineral respiration is still unknown.

Joint Genome Institute (JGI) sequencing used a combination of 454 and Illumina techniques with 27× coverage. All library construction and sequencing techniques are available at

<http://www.jgi.doe.gov/>. Illumina reads were assembled into 121 contigs using Velvet 0.7.1.18 (13) and shredded into 1-kb pseudoreads (with 100-bp overlap). The pseudoreads were incorporated into a hybrid 454/Illumina assembly using the parallel Phrap assembler (CodonCode Corporation, Dedham, MA) (1, 2). Misassemblies were corrected with Dupfinisher (C. S. Han and P. Chain, presented at the 2006 International Conference on Bioinformatics and Computational Biology). Gene modeling was performed using Prodigal (<http://prodigal.ornl.gov/>), and resulting protein translations were assigned by comparisons to Pfam, KEGG, and COGs databases using BLASTP or HMMER. The complete genome was a single circular chromosome of approximately 3,036,819 bp with an average G+C content of 45.9%. A total of 2,963 protein-encoding genes were predicted, and 393 (6.9%) had no similarity to public database sequences.

Nucleotide sequence accession number. The genome sequence of *Thermincola potens* strain JR reported in this paper has been deposited in the GenBank database under accession number NC_014152.

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