

Complete Genome Sequence of *Geobacter anodireducens* SD-1^T, a Salt-Tolerant Exoelectrogenic Microbe in Bioelectrochemical Systems

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Strain SD-1 is the type strain of the species *Geobacter anodireducens*, which was originally isolated from a microbial fuel cell reactor in the United States. The characteristic of this bacterium is its high electrochemical activity. Here, we report the fully assembled genome and plasmid sequence of *G. anodireducens* SD-1^T.

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Geobacter anodireducens SD-1 (=CGMCC 1.12536 = KCTC 4672), the type strain of the species *G. anodireducens*, was first isolated from a mature anode biofilm in a bioelectrochemical system (BES) based on its current generation capability (1, 2). Compared to the type exoelectrogenic microbes of *Geobacter sulfurreducens* PCA and *Geobacter metallireducens* GS-15, strain SD-1 showed higher electrochemical activity in BESs (1–3). The extracellular electron transfer (EET) of anode microbes has been studied intensely in the past decade (4). However, our understanding of how microorganisms transfer electrons to/from electrodes is still incomplete, and only a few different microbes have been genetically studied. To facilitate genetic studies of the EET mechanism, we assembled and annotated the genome of *G. anodireducens* SD-1^T.

The *G. anodireducens* SD-1^T genome was sequenced using ABI PGM. A 3-kb mate-pair library and a 200-bp library were prepared from sheared genomic DNA using the 5500 SOLiD mate-paired library kit and Ion Xpress Plus fragment library kit, respectively. Subread filtering from 2 libraries yielded 1.4 Gbp of sequence. The sequences were checked, trimmed, and assembled in Genomics Workbench 6.0 (CLC bio, Aarhus, Denmark). The complete genome of SD-1^T was obtained, consisting of a circular chromosome of 3,555,507 bp in length (average coverage, 261×) and a circular plasmid of 110,507 bp (average coverage, 160×), with G+C contents of 61% and 52.17%, respectively. The NCBI staff used the Prokaryotic Genome Annotation Pipeline (PGAP) (<http://ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) to complete the annotation; there are 3,407 predicted genes in the genome, including 2,802 protein-coding genes, 547 pseudogenes, 48

tRNA-coding genes, 6 rRNA-coding genes, 4 noncoding RNA (ncRNA), and 1 clustered regularly interspaced short palindromic repeat (CRISPR) array.

Nucleotide sequence accession numbers. The *G. anodireducens* SD-1^T genome sequence and annotation data are available from GenBank under accession numbers [CP014963](https://ncbi.nlm.nih.gov/nuccore/CP014963) and [CP014964](https://ncbi.nlm.nih.gov/nuccore/CP014964).

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