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Draft Genome Sequence of *Desulfuromonas acetexigens* Strain 2873, a Novel Anode-Respiring Bacterium

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ABSTRACT Here, we report the draft genome sequence of *Desulfuromonas acetexigens* strain 2873, which was originally isolated from digester sludge from a sewage treatment plant in Germany. This bacterium is capable of anode respiration with high electrochemical activity in microbial electrochemical systems. The draft genome contains 3,376 predicted protein-coding genes and putative multiheme c-type cytochromes.

Desulfuromonas acetexigens strain 2873 (DSM 1397), first isolated from digester sludge from the Göttingen, Germany, sewage treatment plant (1), is a Gram-negative, non-spore-forming anaerobic bacterium that is capable of chemoor-ganotrophic growth on acetate as the energy and carbon source with elemental sulfur, fumarate, or malate as electron acceptors (1). Recently, its high abundance in mixed-culture anodic biofilms of current-generating microbial electrochemical systems (MESs) (2–4) suggests its role in current generation. Pure culture studies in MESs confirmed that *D. acetexigens* strain 2873 is capable of extracellular electron transfer (EET) to the anode, which serves as the electron acceptor, producing high peak current densities of 7 to 9 A/m² in a very short growth period with acetate as the electron donor (5, 6). However, our understanding of how *D. acetexigens* strain 2873 transfers electrons to and from electrodes is lacking, and sequencing and analysis of its genome could help elucidate its EET mechanism(s).

Here, we assembled and annotated a draft genome of *D. acetexigens* strain 2873. Genomic DNA extracted from strain 2873 was prepared for genome sequencing using the Illumina Nextera DNA library preparation kit (Illumina, Inc.), following the manufacturer's instructions. Sequencing was performed on Illumina MiSeq instruments at DNASense Aps (Aalborg, Denmark) using the MiSeq reagent kit version 3 (Illumina, Inc.), yielding 2.7 million paired-end reads. Raw reads were quality trimmed using Trimmomatic version 0.36 (7), and the trimmed paired-end Illumina reads were *de novo* assembled using SPAdes version 3.7.1 (8). The genome assembly produced 41 contigs with a total length of 3,683,125 bp (G+C content, 60.3%) and an N_{50} of 301,105 bp.

The assembled genome was annotated using Prokka version 1.11 (9), with the genome of *Geobacter sulfurreducens* PCA (NC_002939) (10), a well-known model organism in the field of microbial electrochemistry, used as a reference for annotation. Annotation revealed two rRNA operons, six rRNA genes, 56 tRNA genes, and 3,376 predicted protein-coding genes. Among the predicted protein-coding genes, those encoding for c-type cytochromes are of primary interest. Based on the methodology of Methé et al. (10), all predicted proteins containing putative heme-binding motifs were screened using PROSITE (11) with the following motifs: PS51007, cytochrome c family; PS51008, multiheme cytochrome c family; PS51009, cytochrome c class II; and PS51010, cytochrome f family. In addition, the proteins were annotated using the genome of

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G. sulfurreducens PCA (NC_002939) as a reference to ensure consistent cytochrome annotation. Cytochrome annotation revealed the presence of 39 putative multiheme c-type cytochromes, including the outer membrane c-type cytochromes, OmcS and OmcE, which have been reported to play a key role in current generation in *G. sulfurreducens* (12). Further analyses of functional annotations, metabolic pathways, and comparative genomics are under way and will be included in a future publication.

Accession number(s). The *D. acetexigens* genome sequence has been deposited in the European Nucleotide Archive under the accession numbers [FOJJ01000001](#) to [FOJJ01000041](#).

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