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Draft Genome Sequence of a Novel *Coriobacteriaceae* sp. Strain, EMTCatB1, Reconstructed from the Metagenome of a Thermophilic Electromethanogenic Biocathode

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ABSTRACT A draft genome of *Coriobacteriaceae* sp. strain EMTCatB1 was determined through taxonomic binning of a metagenome of a thermophilic biocathode actively catalyzing electromethanogenesis. This genome will provide information about the biocathode ecosystem, as well as the natural diversity of the *Coriobacteriaceae* family.

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Electromethanogenesis is a bioelectrochemical process, in which direct reduction of CO_2 to methane is catalyzed by biocathodes (1). Recent studies have indicated that methanogens play a central role in the biocathode. However, the function(s) of other microbes colonizing on the biocathode have never been examined. The draft genome reported here was obtained from shotgun sequencing of the metagenome of thermophilic biocathodes actively catalyzing electromethanogenesis at 55°C for more than 60 days at a poised potential of −0.5 V versus the standard hydrogen electrode (2).

Sequencing of the metagenome was performed using an Illumina HiSeq 2000 platform (150-bp paired-end sequencing, two lanes). Sequence reads were trimmed after removal of adapter sequences by Cutadapt version 1.8.3 (3). Approximately 395 million trimmed reads (approx. 60 Gb) were used for phylogenetic and functional profiling of the metagenome. An initial metagenomic binning indicated that approximately 60% of the read sequences were derived from a single operational taxonomic unit, suggesting that the corresponding organism (named "EMTCatB1") plays a role in the biocathode ecosystem. To assemble the sequences from the microbe, the reads were down-sampled to 400 Mb, thereby reducing sequences originating from relatively minor species, and assembled using Velvet, followed by gap-closing with Sealer (4, 5). The resulting draft genome of strain EMTCatB1 is 1.84 Mb (G+C content, 67.2%) contained in a single circular scaffold with no gap, representing a circular chromosome. The scaffold was annotated with the Genaris Annotation System (Genaris, Inc., Kanagawa, Japan) (3), revealing a total of 1,710 features (1,660 protein-coding genes and 50 RNAs). Among the 1,660 proteins, 1,310 (79%) were assigned to different functional categories of NCBI Clusters of Orthologous Groups (COG) (6). The most abundant COG category was "Amino acid metabolism and transport" (132 proteins), followed by "General functional prediction only" (126 proteins) and "Translation" (126 proteins).

Phylogenetic analysis of the 16S and 23S rRNA genes and RpoB revealed that strain EMTCatB1 represents a distinct lineage deeply rooted within the family *Coriobacteriaceae* of the phylum *Actinobacteria*, showing, respectively, 88 to 90%, 82 to 85%, and 70 to 73% sequence identities to the cultured representatives, and thus likely belongs to a new genus. The members of *Coriobacteriaceae* are obligate anaerobes capable of

fermentation or anaerobic respiration (7). The latter metabolism is likely retained in the genome, which encodes homologs of enzymes required for hydrogen and formate oxidation (hydrogenases and formate dehydrogenases). Interestingly, those enzymes can mediate direct electron uptake at the cathode (8). Additionally, the draft genome encodes many putative redox proteins (18 c-type cytochromes and 24 ferredoxins) possibly involved in the electron transfer (9).

Members of the *Coriobacteriaceae* family are dominant bacteria of human gut microbiota and gain an increasing attention due to their roles in host metabolisms and as pathobionts (10). This is the first genome of *Coriobacteriaceae* from a non-host-related habitat and will be useful for understanding the biocathode ecosystem and diversity of the *Coriobacteriaceae* family.

Accession number(s). The *Coriobacteriaceae* sp. strain EMTCatB1 draft genome reported here is available in the DDBJ/EMBL/GenBank database under the accession number BDLO01000001.

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