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Complete Genome Sequences of *Arcobacter butzleri* ED-1 and *Arcobacter* sp. Strain L, Both Isolated from a Microbial Fuel Cell

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Arcobacter butzleri **strain ED-1 is an exoelectrogenic epsilonproteobacterium isolated from the anode biofilm of a microbial fuel cell.** ***Arcobacter*** **sp. strain L dominates the liquid phase of the same fuel cell. Here we report the finished and annotated genome sequences of these organisms.**

Arcobacter butzleri strain ED-1 is a microaerobic exoelectrogenic epsilonproteobacterium isolated from the electrode of an acetate-fed microbial fuel cell (MFC) (1). It was the first epsilonproteobacterium demonstrated to act as an exoelectrogen and can readily transfer electrons to an external solid electron acceptor as a pure culture when supplied with acetate as the sole carbon source. The liquid phase of the same laboratory MFC was dominated by a different *Arcobacter* sp., strain L (1); together, these two *Arcobacter* spp. made up >90% of the fuel cell community. The 16S rRNA gene sequence of *A. butzleri* ED-1 is identical to that in the sequenced genome of *A. butzleri* strain RM4018 (4), while that of *Arcobacter* sp. strain L is more closely related to those of other *Arcobacter* spp. such as *Arcobacter nitrofigilis* (1). Neither the interspecies interactions between the *Arcobacter* spp. nor the mechanism by which *A. butzleri* ED-1 transfers electrons from acetate to the electrode has been characterized. We therefore carried out whole-genome sequencing of these two *Arcobacter* species as a tool for investigating these questions.

The complete genome sequences of *A. butzleri* ED-1 and *Arcobacter* sp. strain L were determined using a combination of the Sanger method (ABI 3730xl sequencers) and 454 pyrosequencing (GS-FLX sequencers). We generated 13,300 (3730xl) and 493,869 (GS-FLX) sequences from the ED-1 genome and 18,223 (3730xl) and 244,537 (GS-FLX) sequences from the *Arcobacter* sp. strain L genome. The 454 pyrosequencing reads were first assembled using the Newbler assembler software according to the supplier's protocol, and then 366 (strain ED-1) and 214 (strain L) of the GS-FLX contigs were imported into the Sanger data as "pseudoreads" using the Phred/Phrap/Consed system (2). The hybrid assembly of the Sanger and 454 data eventually generated 26 (strain ED-1) and 20 (strain L) contigs. Gap closing and resequencing of low-quality regions in the assembled data were performed by PCR, primer walking, and direct sequencing of appropriate plasmid clones. The overall accuracy of the finished sequence was estimated to have an error rate of <1 per 10,000 bases (Phrap score of ≥40). Prediction and annotation of protein-coding genes were performed as described previously (3, 5).

The ED-1 genome consists of a circular 2,256,675-bp chromosome with a G+C content of 27.1% and contains 2,158 predicted protein-coding genes. We could assign known functions to 1,454 (67%) of them, 639 (30%) as conserved hypothetical genes and 65 (3%) as novel hypothetical genes. ED-1 and RM4018 share 1,950 orthologous genes. The *Arcobacter* sp. strain L genome consists of a circular 2,945,673-bp chromosome (G+C content, 26.6%) containing 2,845 predicted protein-coding genes and a small plasmid (1,989 bp; G+C content, 46.6%) containing three protein-coding genes. We could assign known functions to 1,812 (64%) of them, 748 (26%) as conserved hypothetical genes and 288 (10%) as novel hypothetical genes. The *Arcobacter* sp. strain L genome also contains the region (2,051 bp) known as clustered regularly interspersed short palindromic repeats (CRISPR). *Arcobacter* ED-1 and *Arcobacter* sp. strain L encode five rRNA gene operons (5S, 16S, and 23S rRNAs), and there were 53 tRNA genes in the ED-1 genome and 56 in that of *Arcobacter* sp. strain L. *Arcobacter* ED-1 and *Arcobacter* sp. strain L share 1,744 orthologous genes.

Nucleotide sequence accession numbers. The sequence data for the *A. butzleri* ED-1 chromosome and the *Arcobacter* sp. strain L chromosome and plasmid have been deposited in GenBank/DDBJ/EMBL under accession numbers AP012047, AP012048, and AP012049, respectively.

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