Genome sequence of the acid-tolerant Desulfovibrio sp. DV isolated from the sediments of a Pb-Zn mine tailings dam in the Chita region, Russia

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Abstract
Here we report the draft genome sequence of the acid-tolerant Desulfovibrio sp. DV isolated from the sediments of a Pb-Zn mine tailings dam in the Chita region, Russia. The draft genome has a size of 4.9 Mb and encodes multiple K⁺-transporters and proton-consuming decarboxylases. The phylogenetic analysis based on concatenated ribosomal proteins revealed that strain DV clusters together with the acid-tolerant Desulfovibrio sp. TomC and Desulfovibrio magneticus. The draft genome sequence and annotation have been deposited at GenBank under the accession number MLBG00000000.

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1. Direct link to deposited data
https://www.ncbi.nlm.nih.gov/nuccore/MLBG00000000.

2. Introduction
The sulfate-reducing bacteria (SRB) are important components of microbial communities in mine drainage waters and sediments. These types of environments are often characterized by low pH values and high concentration of dissolved metals originating from the oxidation of residual sulfide minerals in mine waste. SRB can be exploited to mitigate acid mine drainage (AMD) by metal precipitation as insoluble sulfides and proton consumption due to the biogenic H₂S production [1,2]. However, only few acidophilic/acid-tolerant SRB have been isolated and characterized. The only two validly described, moderately acidophilic SRB isolated from AMD belong to the genus Desulfosporosinus [3,4]. At least six different phyla contain prokaryotes capable of dissimilatory sulfate reduction. The majority of known species belong to Firmicutes, including the genera Desulfosporosinus and Desulfotomaculum, and to Deltaproteobacteria. The deltaproteobacterial Desulfovibrio spp. are prospective for bioremediation purposes due to their relatively fast growth (compared to other SRB), tolerance to oxygen [5] and, of all SRB, the best understood metabolic features and stress response mechanisms [6]. However, the metal-tolerant Desulfovibrio isolates characterized so far do not tolerate low pH values [7–9]. Recently the first acid-tolerant member of Desulfovibrio, Desulfovibrio sp. TomC, was isolated and its genome was made available [10]. Here we report the draft genome sequence of a novel acid-tolerant strain DV, which was isolated from the sediments of a Pb-Zn mine waste at Novii Akatui, Chita region, Russia. The 16S rRNA sequencing and phylogenetic analysis showed that strain DV belongs to the genus Desulfovibrio and its closest relative is Desulfovibrio sp. TomC (Karnachuk et al., unpublished). The genome sequence will allow to verify the phylogenetic relationships of the two strains and other Desulfovibrio isolates and to explore the mechanisms, which enable these bacteria to withstand low pH values.
3. Experimental design, materials and methods

3.1. Sequencing and assembly of the Desulfovibrio sp. DV genome

Genomic DNA was isolated from Desulfovibrio sp. DV biomass using the SDS-CTAB method [11]. The shotgun genomic DNA library was sequenced with a Roche Genome Sequencer FLX using the Titanium XL+ protocol. The reads were de novo assembled into contigs using the Newbler Assembler version 2.9 (454 Life Sciences, Branford, CT). The draft genome of Desulfovibrio sp. DV consists of 199 contigs longer than 500 bp, with a total length of 4,848,582 bp. The total length of all 219 obtained contigs is 4,854,132 bp. The N50 contig size of the genome is 34,234 bp. Gene search and annotation were performed using the RAST server [12] following manual curation.

3.2. Features of the Desulfovibrio sp. DV genome

The draft genome of Desulfovibrio sp. DV of 4.9 Mb is smaller by comparison to 5.07 Mb of Desulfovibrio sp. TomC [10] and 5.25 Mb of Desulfovibrio magneticus RS-1 [13], but approximately the same size as 4.8 Mb of Desulfovibrio cf. magneticus IFRC170 (NZ_JACG00000000). The GC content of the genome is 62.95%. The genome includes 4350 protein-coding genes, 48 tRNA genes, and 3 rRNA genes. The phylogenetic analysis of 36 ribosomal proteins showed that Desulfovibrio sp. DV is more closely related to Desulfovibrio magneticus than Desulfovibrio TomC [10] and 5.25 Mb of Desulfovibrio IFRC170.

The evolutionary history was inferred using the Neighbor-Joining method [14]. The optimal tree with the sum of branch length = 1.872 8742 is shown. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [15]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [16] and are in the units of the number of amino acid substitutions per site. The analysis involved 16 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 4398 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [17].

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