Draft Genome Sequence of the Anaerobic Arsenite-Oxidizing *Halomonas* sp. Strain ANAO-440, Isolated from an Alkaline Saline Lake in Khovsgol, Mongolia

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**ABSTRACT** The draft genome sequence of *Halomonas* sp. strain ANAO-440 contains 3,866 predicted protein-coding sequences. This strain is capable of anaerobic arsenite oxidation and encodes an *arxA*-type arsenite oxidase within the *arxB2AB1CD* gene island. This genome sequence provides valuable information regarding the physiological diversity of Arx-dependent arsenite-oxidizing microorganisms.

*Halomonas* sp. strain ANAO-440 is a heterotrophic arsenite-oxidizing halophile isolated from an alkaline saline lake located in the northern region of Khovsgol, Mongolia. Strain ANAO-440 was able to oxidize arsenite anaerobically coupled to nitrate reduction and was shown to contain an *arxA*-type arsenite oxidase gene. Arx is a recently identified group of arsenite oxidases, originally characterized in chemoautotrophic arsenite oxidizers from Mono Lake (Mono County, CA, USA). The haloalkaliphilic strain *Alkalilimnicola ehrlichii* MLHE-1 catalyzes arsenite oxidation coupled to nitrate reduction, and the anoxygenic phototroph *Ectothiorhodospira* sp. strain PHS-1 oxidizes arsenite during photosynthesis. Therefore, the genome sequence of strain ANAO-440 would provide useful information regarding ArxA-type arsenite oxidation in heterotrophic bacteria.

Strain ANAO-440 was grown as previously described (1), and genomic DNA was extracted using a MoBio power soil kit (Qiagen). A paired-end library (insert size, ~ 350 bp) was prepared using a NEBNext Ultra DNA library prep kit for Illumina (New England Biolabs), and genome sequencing was performed on a HiSeq X sequencing platform (Illumina, San Diego, CA) at the National Institute for Environmental Studies. Overall, 14,972,975 raw paired-end reads were generated (150-bp paired-end format), and low-quality sequences (Q ≤ 13) were removed using the Trim_Reads tool implemented in CLC Genomic Workbench (GW) 20.0.2 (Qiagen). The sequences were assembled de novo in slow mode in GW using default parameters, except for the minimum contig length (500 bp) and word size (30); the assembly resulted in 64 contigs with an N50 value of 193,648 bp and a maximum contig length of 449,532 bp. The draft genome sequence of strain ANAO-440 was 4,309,801 bp long with 534.0x genome coverage and a G+C content of 62.6%. Annotation was conducted using the NCBI Prokaryotic Genome Annotation Pipeline (8) and GhostKOALA in KEGG (9), resulting in 3,866 predicted protein-coding sequences, 60 tRNAs, and 5 rRNAs (1 copy of 5S, and 2 copies each of 16S and 23S). BLASTn analysis of the 16S rRNA gene showed that this strain is closely related to other *Halomonas* strains (sequence identity, >97%), such as *Halomonas chromatiyields* strain AGD 8-3 (GenBank accession number CP014226.1).

The draft genome sequence of ANAO-440 contained the *arx* gene island, *arxB2ABCD*, which was previously identified in *Ectothiorhodospira* sp. strain PHS-1 and *A. ehrlichii* MLHE-1 (2, 7). However, the *arxSR* genes encoding putative regulatory proteins that were found adjacent to the *arxB2ABCD* gene islands in PHS-1 and MLHE-1 (7) were absent from the *arx* gene island.
island in ANAO-440, possibly indicating the presence of a distinct regulatory mechanism for arx genes in this heterotrophic arsenite-oxidizing *Halomonas* strain. Additionally, the functional genes encoding enzymes in the denitrification pathway (*narGHI*, *napAB*, *nirS*, *norBC*, and *nosZ*) were present in the draft genome sequence, while lacking either the dissimilatory arsenate reductase gene *arr* or the *aioA*-type arsenate oxidase gene. The draft genome sequence of *Halomonas* sp. strain ANAO-440 provides valuable information regarding Arx-dependent arsenite oxidation in phylogenetically and physiologically diverse microorganisms.

**Data availability.** The draft genome sequence was deposited in GenBank under accession number JAHXBV000000000, BioProject accession number PRJNA670823, BioSample accession number SAMN20309323, and SRA accession number SRR15204658.

**ACKNOWLEDGMENTS**

This work was supported by the Japan Society for the Promotion of Science (JSPS) KAKENHI (grant numbers 19KK0270, 19H04302, and 18K19879 to N.H.) and the Environmental Genomics Promotion Project of the National Institute for Environmental Studies.

We thank Yuri Sakai and Yurie Matsuda for technical assistance.

**REFERENCES**


