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Draft Genome Sequence of the Arsenite-Oxidizing Strain *Aliihoeflea* sp. 2WW, Isolated from Arsenic-Contaminated Groundwater

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Here, we report the draft genome sequence of the arsenite-oxidizing bacterium *Aliihoeflea* sp. strain 2WW, which consists of a 4.15-Mb chromosome and contains different genes that are involved in arsenic transformations.

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Aliihoeflea sp. strain 2WW was isolated from a biofilter treating arsenic-contaminated groundwater in the city of Cremona (Lombardia, Italy). It is a strictly aerobic, mobile, and rod-shaped Gram-negative bacterium. Phylogenetic analysis of the 16S rRNA gene sequence showed that the strain is closely (98.7%) affiliated with *Aliihoeflea aestuarii* N8^T (1) within the family *Phyllobacteriaceae* in the class *Alphaproteobacteria*. Strain 2WW is highly arsenic resistant, with MIC values of >200 mM and 5 mM for arsenate [As(V)] and arsenite [As(III)], respectively. Under heterotrophic conditions, it can oxidize As(III) to As(V), with specific growth rates (h⁻¹) of 0.23, 0.13, and 0.006 at 30°C, 15°C, and 5°C, respectively. In growth experiments, As(III) was always oxidized to As(V) in the early exponential growth phase and the oxidation was complete within 24 h at 30°C, 96 h at 15°C, and 350 h at 5°C. Complete As(III) oxidation occurred in the pH range 5.0 to 8.0. The resting cells of an As(III)-induced culture of strain 2WW were able to oxidize completely 200 μg liter⁻¹ of As(III) in 8 h, while noninduced cells oxidized As(III) in 24 h.

The genome sequence of *Aliihoeflea* sp. strain 2WW was obtained by Illumina sequencing (Illumina, Inc., San Diego, CA), producing paired-end and mate-pair sequence reads of ~50 bp, with insert sizes of ~300 bp and ~4,000 bp, respectively. CLC Genomics Workbench version 5.5.1 (CLC bio, Aarhus, Denmark) was used to assemble the quality-filtered paired-end reads into 273 contigs. Subsequently, SSPACE Premium scaffolder version 2.0 (2) and GapFiller version 1.11 (3) were used to place the contigs into 10 gap-closed scaffolds with an average sequence size of 415,210 bp. This resulted in a draft genome of 4,152,101 bp and a G+C content of 64.4%. IMG/ER (4) and RAST (5) were used to annotate the draft genome. The genome contains 4,140 genes, including 65 RNA genes. It possesses two different arsenic islands, one including 4 genes of the *ars* operon for arsenic resistance [*arsR* for regulatory protein, *acr3* for arsenite efflux pump, *arsC* for arsenate reductase, and *arsH* for protein conferring high resistance

to As(V)], and the second containing an arsenite oxidase, *aioBA*. Phylogenetic analysis of *aioA* confirmed the phylogenetic affiliation with the *Alphaproteobacteria* and showed close affiliation with members of the family *Phyllobacteriaceae*, although 2WW is not chemoautotrophic. Although 2WW possesses *arsC*, normally retrieved in the *ars* operon of As(V)-resistant strains, it was not able to reduce As(V) to As(III). In addition, many genes encoding putative metal (lead, cadmium, zinc, mercury, copper, and chromium) transporters and cobalt-zinc-cadmium resistance protein (*CzcD*) were also identified on the genome.

Nucleotide sequence accession number. The draft genome sequence of *Aliihoeflea* sp. strain 2WW has been deposited in GenBank under the accession no. [AYOD00000000](https://www.ncbi.nlm.nih.gov/nuclseq/AYOD00000000).

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REFERENCES

1. Roh SW, Kim KH, Nam YD, Chang HW, Kim MS, Shin KS, Yoon JH, Oh HM, Bae JW. 2008. *Aliihoeflea aestuarii* gen. nov., sp. nov., a novel bacterium isolated from tidal flat sediment. *J. Microbiol.* 46:594–598.
2. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics* 27:578–579.
3. Boetzer M, Pirovano W. 2012. Toward almost closed genomes with GapFiller. *Genome Biol.* 13:R56. doi:10.1186/gb-2012-13-6-r56.
4. Markowitz VM, Chen IMA, Palaniappan K, Chu K, Szeto E, Grechkin Y, Ratner A, Jacob B, Huang J, Williams P, Huntemann M, Anderson I, Mavromatis K, Ivanova NN, Kyrpides NC. 2012. IMG: the integrated microbial genomes database and comparative analysis system. *Nucleic Acids Res.* 40:D115–D122. doi:10.1093/nar/gkr1044.
5. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. doi:10.1186/1471-2164-9-75.