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GENOME ANNOUNCEMENT

Genome Sequence of the Facultative Anaerobic Arsenite-Oxidizing and Nitrate-Reducing Bacterium *Acidovorax* sp. Strain NO1

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***Acidovorax* sp. strain NO1, isolated from gold mine soil, was shown to be a facultative anaerobic arsenite-oxidizing and nitrate-reducing bacterium. The reported draft genome predicts the presence of genes involved in arsenic metabolism, nitrate reduction, phosphate transport, and multiple metal resistances and indicates putative horizontal gene transfer events.**

Acidovorax sp. strain NO1 was isolated from arsenic-contaminated soil of a gold mine in Daye, Hubei Province, China. It is highly arsenic resistant, with MICs of 20 mM and 200 mM for As(III) and As(V), respectively. Strain NO1 oxidized As(III) to As(V) aerobically and anaerobically with efficiencies of 121.7 μM h^{-1} OD^{-1} and 61.7 μM h^{-1} OD^{-1}, respectively (where OD is optical density). It also reduced NO_3^- to NO_2^- under anaerobic conditions with an efficiency of 206.0 μM h^{-1} OD^{-1}. *Acidovorax* sp. NO1 grew aerobically using 3-hydroxybenzoic acid as the sole carbon source. Strain NO1 was identified as a member of the genus *Acidovorax* using 16S rRNA sequence, fatty acid, and physiological/biochemical analyses.

Acidovorax is a bacterial genus whose main characteristics are that it is Gram-negative, has a motile rod with polar flagella, and is oxidase positive (13, 14). The sequenced genomes of *Acidovorax* members can be further separated into two groups, four environmental species, including those from soil and water habitats (NZ_ACQT00000000) (4, 6, 7), and three plant pathogens that cause fruit blotch or brown stripe (ADCB01000000) (3, 15), which makes the *Acidovorax* genus a good candidate for genome comparison to explore its different physiological and ecological roles.

The whole genomic sequence of *Acidovorax* sp. NO1, sequenced by a Roche 454 genome sequencer (GS) FLX instrument (9) and assembled by Roche GS Assembler version 2.0.01 software, contains 5,012,610 bp distributed in 167 contigs. The approximate genome coverage was 19 fold. CLC Sequence Viewer version 6.5.4 (CLC Bio) showed that *Acidovorax* sp. NO1 has an average GC content of 64.36%. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline predicted 4,732 genes, with 46 tRNA genes, 1 rRNA gene, and 4,682 protein-coding genes (CDS), of which 3,816 were assigned to the clusters of orthologous groups (COG; http://www.ncbi.nlm.nih.gov/COG/). Genome comparison with reciprocal best BLAST demonstrated that *Acidovorax* sp. NO1 was most closely related to *A. radicis* strain N35 (3,050 CDS; E value, <1e−5; coverage, >50%; identity, >30%) (7), followed by *A. delafieldii* strain 2AN (2,845 CDS; NZ_ACQT00000000), *Acidovorax* sp. strain JS42 (2,532 CDS) (6), *A. ebreus* strain TPSY (2,531 CDS) (4), *A. avenae* ATCC 19860 (2,492 CDS; ADCB01000000), and *A. citrulli* strain AAC00-1 (2,481 CDS) (3).

Among all the sequenced *Acidovorax* strains, only strain NO1 has an *aio* operon responsible for arsenite oxidation (*aioR-aioS-aioX-aioA-aioB-aioD-aioC*) (5, 8, 9), found on contig 81 (AGTS01000077) with two adjacent arsenic resistance *ars* operons (*arsH-arsC-acr3-arsC-arsR* and *arsR-arsC-arsD-arsA-CBS-arsB*) (1, 8, 10) and a phosphate transport *pst* operon (*pstS-pstC-pstA-pstB-phoU-phoR*) (2, 8, 10). There is another *ars* operon (*acr3-arsC-arsR*) located on contig 75 (AGTS01000071). Both the *arsR-arsC-arsD-arsA-CBS-arsB* and *acr3-arsC-arsR* operons display putative horizontal gene transfer (HGT) origins. In addition to the *pst* cluster in the vicinity of the *aio* operon, strain NO1 has a *pst* cluster (*pstS-pstC-pstA-pstB-phoU-phoB-phoR*) on contig 147 (AGTS01000143) which is conserved in other *Acidovorax* strains that have only one *pst* cluster.

In contrast to other environmental *Acidovorax* strains that have a complete set of denitrification pathway genes (*nar*, *nir*, *nor*, and *nos*), strain NO1 contains *nar*, *nor*, and *nos* genes but lacks *nir*, which encodes nitrite reductase; in this way, it is the same as the arsenite-oxidizing strain MLHE-1 (11, 12).

Nucleotide sequence accession numbers. The draft genome sequence of *Acidovorax* sp. NO1 has been deposited in DDBJ/EMBL/GenBank under accession number AGTS00000000. The version described in this paper is the first version, AGTS01000000.

ACKNOWLEDGMENTS

This work was supported by the National Natural Science Foundation of China (31170106).

Sequencing was performed at the University of Arizona Genetics Core.

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Received 25 December 2011 **Accepted** 9 January 2012

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doi:10.1128/JB.06814-11

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