

Genome Sequence of the Highly Efficient Arsenite-Oxidizing Bacterium *Achromobacter arsenitoxydans* SY8

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We report the draft genome sequence of *Achromobacter arsenitoxydans* SY8, the first reported arsenite-oxidizing bacterium belonging to the genus *Achromobacter* and containing a genomic arsenic island, an intact type III secretion system, and multiple metal(loid) transporters. The genome may be helpful to explore the mechanisms intertwining metal(loid) resistance and pathogenicity.

Achromobacter bacteria are Gram-negative, strictly aerobic, rod-shaped cells that do not produce pigment on agar and can use xylose and glucose as the sole carbon sources. Some members of the genus *Achromobacter* are common inhabitants of the human intestinal tract, and these bacteria may become opportunistic pathogens (e.g., causing bacteremia, meningitis, and urinary tract infection) (7, 10). Four *Achromobacter* members have been sequenced, including one strain isolated from polychlorinated biphenyl-contaminated soil (*A. xylosoxidans* A8, GenBank accession number CP002287) (16) and three clinical isolates (*A. xylosoxidans* AXX-A [GenBank accession number AFRQ00000000], *A. xylosoxidans* C54 [GenBank accession number ACRC00000000], and *A. piechaudii* ATCC 43553 [GenBank accession number ADMS00000000]).

Achromobacter arsenitoxydans SY8 was isolated from arsenic-contaminated soil of a pig farm (5, 6) and assigned to the *Achromobacter* genus based on 16S rRNA gene similarity and physiological/biochemical analyses. The MIC for arsenite was 18 mM in CDM medium (5). It could oxidize arsenite to arsenate with efficiencies of up to 721.1 $\mu\text{M h}^{-1} \text{OD}_{600}$ (optical density at 600 nm)⁻¹ (6).

Whole-genome shotgun sequencing was performed using Roche 454 GS-FLX-TM (11). The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) was used for genome annotation. The automatic outputs were modified manually based on Blastp/rps-BLAST and COG analyses through Artemis software (15) and the Cognitor tool, respectively (17). Genome comparative analysis was performed using the SEED Viewer (4) and Local BLAST (3). GC content was analyzed using CLC Sequence Viewer version 5.6.4 (CLCbio).

The draft genome was assembled into 105 contigs with a genome size of 6,156,664 bp and a genome coverage of 24-fold using GS De Novo Assembler (Newbler) version 2.5.3. It had a GC content of 66.0%, 5,655 putative coding sequences (CDS), 57 tRNA genes, and 5 scattered rRNA genes. The genome of *A. arsenitoxydans* SY8 was most similar to that of *A. piechaudii* ATCC 43553 (78.9% identity), followed by those of *A. xylosoxidans* A8 (78.2%), *A. xylosoxidans* C54 (78.0%), and *A. xylosoxidans* AXX-A (76.2%), based on ortholog CDS analysis.

Genome analysis indicated that *A. arsenitoxydans* SY8 possessed a genomic “arsenic island” with 37 genes on contig 00053

(GenBank accession number AGUF01000052), including three arsenic resistance operons (*arsR-arsC1-arsD-arsA-arsB*, *arsR-arsO-arsC2-mfs-arsH1*, and *arsR-acr3-mfs-arsC3-arsH2*) (1, 6, 12), an arsenite oxidation operon (*aioX-aioS-aioR-aioA-aioB-aioC-aioD*) (6, 8, 9, 12, 13), and an operon encoding proteins putatively involved in phosphate uptake (*pstS-pstC-pstB-pstA*). Such an extensive arsenic island was absent in the other four sequenced *Achromobacter* genomes. In addition, many genes encoding putative metal (copper, mercury, chromate, and zinc) transporters were also identified on the genome.

SY8's genome harbored an intact type III secretion system (30 genes) in contig 00052 (GenBank accession number AGUF01000051) and displayed synthetic conservation with amino acid identities of 74.2%, 51.2%, and 50.9% to *A. xylosoxidans* AXX-A, *Bordetella bronchiseptica* RB50 (2, 14), and *A. xylosoxidans* C54, respectively. Such an intact type III secretion system was absent in *A. piechaudii* ATCC 43553 and *A. xylosoxidans* A8. Furthermore, strain SY8 contained several virulence factors, implicating cell adhesion and endotoxin, exotoxin, and serum resistance (2, 14), indicating the possibility that it could be an opportunistic pathogen. The draft genome of strain SY8 provides information to explore the metal(loid) resistance mechanisms, as well as pathogenic analysis.

Nucleotide sequence accession numbers. The draft genome sequence of strain SY8 has been deposited at DDBJ/EMBL/GenBank under accession number AGUF00000000. The version described in this paper is the first version, AGUF01000000.

ACKNOWLEDGMENTS

This work was supported by the National Natural Science Foundation of China (grant 30970075).

Sequencing was performed at the University of Arizona Genetics Core.

Received 7 December 2011 Accepted 12 December 2011

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doi:10.1128/JB.06667-11

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