Genome Sequence of the Arsenite-Oxidizing Strain *Agrobacterium tumefaciens* 5A

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Microbial transformations of arsenic influence its mobility and toxicity. We report the draft genome sequence of the arsenite-oxidizing strain *Agrobacterium tumefaciens* 5A isolated from an As-contaminated soil in the Madison River Valley, MT. A large number of metal (or metalloid) resistance genes, especially contributing to arsenite oxidation, were identified.

The alphaproteobacterium *Agrobacterium tumefaciens* is best known as a soilborne phytopathogen and is widely used in plant transgenics (3). *A. tumefaciens* is also reported to be metal resistant because it is commonly exposed to high levels of metal ions for agricultural pathogen management (6). We report the draft genome of the arsenite [As(III)]-oxidizing *A. tumefaciens* strain 5A isolated from an As-enriched Typic Calciaquoll soil collected from an irrigated pasture in the Madison River Valley, MT (9). Complex regulation of arsenite oxidation, including As(III)-sensing, three-component signal transduction, and quorum sensing are involved (7, 8). Prior to this genome report, only a single *A. tumefaciens* whole-genome sequence (strain C58) had been published (4).

The *A. tumefaciens* strain 5A genome was sequenced using the 454 GS FLX sequencer (10) and assembled with GS *de novo* assembler (Newbler), version 2.3. The Rapid Annotation Subsystem Technology (RAST) server (1) was used for functional annotation. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for submission (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The draft genome consists of 59 contigs (5,743,748 bp) with an 18-fold genome coverage (58.58% G+C). At least two copies of 5S, one copy of 23S, and three copies of 16S rRNAs and 49 tRNA genes were predicted by RAST. A total of 5,580 protein-coding sequences (CDSs) were annotated, and an additional 1,440 did not match annotated proteins. Based on BLASTp with KEGG Orthology (KO) (http://www.genome.jp/kegg), strain 5A contains 2,390 orthologs (bit score, >60) to *A. tumefaciens* C58, and 4,524 proteins were assigned to COG families by PGAAP.

The strain 5A genome carries genes involved in As(III) oxidation. Transposon mutagenesis and reverse transcriptase PCR data identified an *aio* operon (*aioX-aioS-aioR-aioA-aioB-cytc2*) involved in As(III) oxidation (7). The expression of *aioS* was reduced by the interruption of *aioR*, and expression of *aioAB* was induced by As(III). AioR appears to be autoregulatory and partially controls the expression of the *aio* operon. Complementation of an *aioR*::Tn5B22 mutant [As(III) oxidation minus] required the entire *aio* region, indicating genes in the *aio* operon are part of a common transcriptional unit (7). Thus far, it appears that there are at least two separate regulatory circuits controlling the expression of the *aio* operon: (i) a two-component signal transduction system, AioS and AioR, which recently has been shown to include AioX as a putative periplasmic signal receptor (8); and (ii) quorum sensing, which is normally involved in virulence of plants (2, 5), is also involved in regulating As(III) oxidation in *A. tumefaciens* 5A (7).

Nucleotide sequence accession numbers. The draft genome sequence has been deposited in GenBank under accession no. AGVZ00000000. The version described in this paper is the first version, AGVZ01000000.

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