

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

Xiuli Hao, Yanbing Lin, Laurel Johnstone, Guanghui Liu,
Gejiao Wang, Gehong Wei, Timothy McDermott and
Christopher Rensing
J. Bacteriol. 2012, 194(4):903. DOI: 10.1128/JB.06585-11.

Updated information and services can be found at:
<http://jb.asm.org/content/194/4/903>

	<i>These include:</i>
REFERENCES	This article cites 8 articles, 3 of which can be accessed free at: http://jb.asm.org/content/194/4/903#ref-list-1
CONTENT ALERTS	Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), more»

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

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

Xiuli Hao,^{a,b} Yanbing Lin,^{a,b} Laurel Johnstone,^c Guanghui Liu,^{d,e} Gejiao Wang,^d Gehong Wei,^a Timothy McDermott,^e and Christopher Rensing^b

College of Life Sciences, State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A & F University, Yangling, Shaanxi, China^a; Department of Soil, Water and Environmental Science,^b University of Arizona Genetics Core,^c The University of Arizona, Tucson, Arizona, USA; State Key Laboratory of Agricultural Microbiology, College of Life Science and Technology, Huazhong Agricultural University, Wuhan, People's Republic of China^d; and Department of Land Resources and Environmental Sciences, Montana State University, Bozeman, Montana, USA^e

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 metalloids) 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](http://www.ncbi.nlm.nih.gov/GenBank/AGVZ00000000). The version described in this paper is the first version, [AGVZ01000000](http://www.ncbi.nlm.nih.gov/GenBank/AGVZ01000000).

ACKNOWLEDGMENTS

This work was supported by projects from National Science Foundation of China (31125007, 30970003, and 30900215), the 973 Project of China (2010CB126502), and U.S. National Science Foundation grants MCB-0817170 and EAR-0745956 to T.R.M.

Sequencing was performed at the University of Arizona Genetics Core facility.

REFERENCES

1. Aziz R, et al. 2008. The RAST Server: rapid annotations using subsystems technology. *BMC Genomics* 9:75.
2. Badri DV, Weir TL, van der Lelie D, Vivanco JM. 2009. Rhizosphere chemical dialogues: plant-microbe interactions. *Curr. Opin. Biotechnol.* 20:642–650.
3. Escobar MA, Dandekar AM. 2003. *Agrobacterium tumefaciens* as an agent of disease. *Trends Plant Sci.* 8:380–386.
4. Goodner B, et al. 2001. Genome sequence of the plant pathogen and biotechnology agent *Agrobacterium tumefaciens* C58. *Science* 294:2323–2328.
5. Hilgers MT, Ludwig ML. 2001. Crystal structure of the quorum-sensing protein LuxS reveals a catalytic metal site. *Proc. Natl. Acad. Sci. U. S. A.* 98:11169–11174.
6. Hopkins DL. 2004. Management of bacterial diseases: chemical methods. Taylor & Francis, London, United Kingdom.
7. Kashyap DR, Botero LM, Franck WL, Hassett DJ, McDermott TR. 2006. Complex regulation of arsenite oxidation in *Agrobacterium tumefaciens*. *J. Bacteriol.* 188:1081–1088.
8. Liu G, et al. A periplasmic arsenite-binding protein involved in regulating arsenite oxidation. *Environ. Microbiol.*, in press.
9. Macur RE, Jackson CR, Botero LM, McDermott TR, Inskeep WP. 2004. Bacterial populations associated with the oxidation and reduction of arsenic in an unsaturated soil. *Environ. Sci. Technol.* 38:104–111.
10. Margulies M, et al. 2005. Genome sequencing in open microfabricated high density picoliter reactors. *Nature* 437:376.

Received 24 November 2011 Accepted 30 November 2011

Address correspondence to C. Rensing, reningc@ag.arizona.edu, or T. McDermott, timmcder@montana.edu.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.06585-11