

# Draft Genome Sequence of *Nitriicola* sp. Strain A-D6, an Arsenic-Resistant Gammaproteobacterium Isolated from a Salt Flat

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**We report *Nitriicola* sp. strain A-D6, which was characterized as an arsenic-resistant bacterium isolated from the Ascotán Salt Flat in northern Chile. The size of the genome is 3,795,776 bp, with a G+C content of 49.96%. Genes for the arsenic-resistant Ars system and arsenic oxidation have been encoded.**

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Arsenic (As) is a ubiquitous element present in the environment in different forms (1). Inorganic arsenic, most often in trivalent or pentavalent form, is the most abundant species of As in nature and is commonly present in soil, water, and food (2). This metalloid is extremely toxic to living organisms and its toxicity is primarily based on its chemical speciation. However, some microorganisms cope with arsenic toxicity in a variety of different ways (1, 3, 4). Such microorganisms therefore play an important role in the arsenic geocycle (5).

*Nitriicola* sp. strain A-D6 was isolated from Salar de Ascotán, a circum-neutral and arsenic-containing salt flat environment in northern Chile. The *Nitriicola* genus comprises aerobic and Gram-negative bacteria belonging to the *Gammaproteobacteria* subdivision (6). This report can shed light on the molecular mechanisms involved in arsenic metabolism in this bacterium and its role in the biogeochemical cycle of arsenic in this extreme environment.

The genome of strain A-D6 was sequenced using the Ion Torrent PGM platform and single-end libraries. The low-quality sequences were examined by FastQC (version 0.10.1; Babraham Institute [<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/>]) and then trimmed by Trimmomatic version 0.32 (7) before assembly. The trimmed sequence were assembled *de novo* using a coverage assembled of 40×, with Mira assembler version 4.0.2 (8) and the CAP3 (9) program. This resulted in 117 contigs. Contig sizes range from 850 to 121,978 bp ( $N_{50}$ , 52,683 bp). The length of the total draft genome of *Nitriicola* sp. strain A-D6 is 3,795,776 bp, with a G+C content of 49.96%.

The annotation of the assembled genome was submitted to the RAST (Rapid Annotation using Subsystem Technology) server (10). The tRNA genes were detected by tRNAscan-SE version 1.23 (11) and the rRNA with RNAmmer (12). The draft genome was shown to encode 43 tRNA sequences, one complete 5S-16S-23S operon, and 4,401 protein-coding genes, 22.27% of which were assigned hypothetical functions. This hypothetical set was assigned to 4 clusters of orthologous groups that comprise a meta-

bolic cluster with 662 genes, a genetic information processing cluster with 187 genes, an environmental information processing cluster with 272 genes, and a cellular process cluster with 99 genes.

The genes responsible for arsenic metabolism include arsenite oxidase small subunit (*aioA*) and large subunit (*aioB*), and an *azu* gene encoding for the physiological electron acceptor azurin (13). The genes responsible for arsenic resistance include an Ars system (*arsRDACH*). ArsC from the Ars system is a cytoplasmic arsenate reductase that reduces As(V) to As(III) (1). ArsD represses upper expression levels of the *ars* operon in the absence of As(III). ArsA is an ATPase that converts membrane potential to ATP, which is usually hydrolyzed by ArsB, making As(III) efflux more efficient. ArsB is an integral membrane protein that pumps As(III) out of the cell (1), however a canonical *arsB* gene is not encoded in the genome of this bacterium. Interestingly, *Nitriicola* sp. has a gene that encodes for the Acr3 extrusion pump (14). Thus, *Nitriicola* sp. strain A-D6 possesses a complete set of genes for dissimilatory oxidation and a system for reducing and extruding arsenic.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JRLB000000000](https://www.ncbi.nlm.nih.gov/nuccore/JRLB000000000). The version described in this paper is version [JRLB010000000](https://www.ncbi.nlm.nih.gov/nuccore/JRLB010000000).

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## REFERENCES

- Slyemi D, Bonnefoy V. 2012. How prokaryotes deal with arsenic. *Environ. Microbiol. Rep.* 4:571–586. <http://dx.doi.org/10.1111/j.1758-2229.2011.00300.x>.
- Cohen SM, Arnold LL, Eldan M, Lewis AS, Beck BD. 2006. Methylated arsenicals: the implications of metabolism and carcinogenicity studies in rodents to human risk assessment. *Crit. Rev. Toxicol.* 36:99–133. <http://dx.doi.org/10.1080/10408440500534230>.

3. Páez-Espino D, Tamames J, De Lorenzo V, Cánovas D. 2009. Microbial responses to environmental arsenic. *BioMetals* 22:117–130. <http://dx.doi.org/10.1007/s10534-008-9195-y>.
4. Tsai SL, Singh S, Chen W. 2009. Arsenic metabolism by microbes in nature and the impact on arsenic remediation. *Curr. Opin. Biotechnol.* 20:659–667. <http://dx.doi.org/10.1016/j.copbio.2009.09.013>.
5. Mukhopadhyay R, Rosen BP, Phung LT, Silver S. 2002. Microbial arsenic: from geocycles to genes and enzymes. *FEMS Microbiol. Rev.* 26: 311–325. <http://dx.doi.org/10.1111/j.1574-6976.2002.tb00617.x>.
6. Dimitriu PA, Shukla SK, Conradt J, Márquez MC, Ventosa A, Maglia A, Peyton BM, Pinkart HC, Mormile MR. 2005. *Nitrincola lacisaponensis* gen. nov., sp. nov., a novel alkaliphilic bacterium isolated from an alkaline, saline lake. *Int. J. Syst. Evol. Microbiol.* 55:2273–2278. <http://dx.doi.org/10.1099/ijs.0.63647-0>.
7. Lohse M, Bolger AM, Nagel A, Fernie AR, Lunn JE, Stitt M, Usadel B. 2012. RobiNA: a user-friendly, integrated software solution for RNA-Seq-based transcriptomics. *Nucleic Acids Res.* 40:W622–W627. <http://dx.doi.org/10.1093/nar/gks540>.
8. Chevreaux B, Wetter T, Suhai S. 1999. Genome sequence assembly using trace signals and additional sequence information, p 45–56. *In* Proceedings of the German conference on bioinformatics (GCB) 99, Hannover, Germany.
9. Huang X, Madan A. 1999. CAP3: a DNA sequence assembly program. *Genome Res.* 9:868–877. <http://dx.doi.org/10.1101/gr.9.9.868>.
10. 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. <http://dx.doi.org/10.1186/1471-2164-9-75>.
11. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955–964. <http://dx.doi.org/10.1093/nar/25.5.0955>.
12. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108. <http://dx.doi.org/10.1093/nar/gkm160>.
13. Anderson GL, Williams J, Hille R. 1992. The purification and characterization of arsenite oxidase from *Alcaligenes faecalis*, a molybdenum-containing hydroxylase. *J. Biol. Chem.* 267:23674–23682.
14. Mansour NM, Sawhney M, Tamang DG, Vogl C, Saier MH Jr. 2007. The bile/arsenite/riboflavin transporter (BART) superfamily. *FEBS J.* 274: 612–629.