



**HAL**  
open science

## Genome Sequence of the Sulfate-Reducing Bacterium *Desulfotomaculum hydrothermale* Lam5(T).

Oulfat Amin, Marie-Laure Fardeau, Odile Valette, Agnès Hirschler-Réa,  
Valérie Barbe, Claudine Médigue, Benoit Vacherie, Bernard Ollivier, Philippe  
N Bertin, Alain Dolla

► **To cite this version:**

Oulfat Amin, Marie-Laure Fardeau, Odile Valette, Agnès Hirschler-Réa, Valérie Barbe, et al.. Genome Sequence of the Sulfate-Reducing Bacterium *Desulfotomaculum hydrothermale* Lam5(T).. *Genome Announcements* , 2013, 1 (1), epub ahead of print. 10.1128/genomeA.00114-12 . hal-00807485

**HAL Id: hal-00807485**

**<https://hal.science/hal-00807485>**

Submitted on 3 Apr 2013

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# Genome Sequence of the Sulfate-Reducing Bacterium *Desulfotomaculum hydrothermale* Lam5<sup>T</sup>

Oulfat Amin,<sup>a</sup> Marie-Laure Fardeau,<sup>a</sup> Odile Valette,<sup>b</sup> Agnès Hirschler-Réa,<sup>a</sup> Valérie Barbe,<sup>c</sup> Claudine Médigue,<sup>d</sup> Benoit Vacherie,<sup>c</sup> Bernard Ollivier,<sup>a</sup> Philippe N. Bertin,<sup>e</sup> Alain Dolla<sup>b</sup>

Aix-Marseille Université, Université Sud Toulon, CNRS/INSU, IRD, MIO-UM110, Marseille, France<sup>a</sup>; Aix-Marseille Université, CNRS, LCB-UMR7283, Marseille, France<sup>b</sup>; Laboratoire de Finition CEA, Institut de Génomique-Génomscope, Évry, France<sup>c</sup>; Laboratoire d'Analyses Bioinformatiques pour la Génomique et le Métabolisme (LABGeM), Génomscope-IG-CEA, Évry, France<sup>d</sup>; CNRS, UMR7156, Université Louis Pasteur, Strasbourg, France<sup>e</sup>

**Here, we report the draft genome sequence of *Desulfotomaculum hydrothermale*, a sulfate-reducing, spore-forming bacterium isolated from a Tunisian hot spring. The genome is composed of 2.7 Mb, with a G+C content of 49.48%, and it contains 2,643 protein-coding sequences.**

Received 8 November 2012 Accepted 12 November 2012 Published 24 January 2013

**Citation** Amin O, Fardeau M-L, Valette O, Hirschler-Réa A, Barbe V, Médigue C, Vacherie B, Ollivier B, Bertin PN, Dolla A. 2013. Genome sequence of the sulfate-reducing bacterium *Desulfotomaculum hydrothermale* LAM5<sup>T</sup>. *Genome Announc.* 1(1):e00114-12. doi:10.1128/genomeA.00114-12.

**Copyright** © 2013 Amin et al. This is an open-access article distributed under the terms of the [Attribution 3.0 Unported Creative Commons License](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Alain Dolla, [dolla@imm.cnrs.fr](mailto:dolla@imm.cnrs.fr).

Members of the genus *Desulfotomaculum* are sulfate-reducing, spore-forming Gram-positive bacteria that are widely distributed within mesothermic and thermal ecosystems (1). Evidence of their presence in terrestrial geothermal hot springs has been obtained several times using molecular approaches (2), but only three species of this genus have been isolated so far, the most recent being *Desulfotomaculum hydrothermale* (3). Here, we report the first draft genome sequence of a *Desulfotomaculum* species isolated from a terrestrial hot spring in Tunisia: *D. hydrothermale*. The strain was shown to reductively detoxify arsenate [As(V)], in the presence of pyruvate as an electron donor, without evidence for any respiration using As(V) as a terminal electron acceptor (3). Because arsenic is known to be present in hot springs (4), information regarding the genome sequence of *D. hydrothermale* may be useful in understanding the As-detoxifying process developed in *Desulfotomaculum* species.

A Sanger/pyrosequencing hybrid approach was used for the whole-genome sequencing. A shotgun library was constructed with 10-kb fragments of genomic DNA in vector pCNS (derived from pSU). Sequencing with vector-based primers was carried out using the ABI 3730 Applied sequencer, and a total of 6,421 reads (~1.6-fold coverage) were analyzed and assembled with Newbler (a Roche assembler), with 341,086 single reads (~26-fold coverage) and 106,386 mate-paired 8-kb reads obtained with Genome Sequencer version FLX and Titanium (Roche Applied Science), respectively. The finishing step was achieved by using primer walks, PCRs, and *in vitro* transposition technologies. For quality assessment, 5,501,511 (36-nucleotide) Illumina reads (~70-fold coverage) were mapped using Soap1 (<http://soap.genomics.org.cn/>) on the 16 consensus contigs. The draft genome sequence consists of 2,706,432 bases with a G+C content of 49.48%, and it contains 2,643 candidate protein-encoding genes, in addition to 60 tRNA and 3 16S rRNA genes.

The mechanism of microbe-mediated metal reduction, studied mainly in *Geobacter* and *Shewanella* species, involves *c*-type

cytochromes (5, 6). For *Desulfotomaculum reducens*, it has been hypothesized that an integral membrane multiheme *c*-type cytochrome (Dred\_0700-0701) is involved in the reduction of metals such as Fe(III) and U(VI) (7). Inspection of the draft genome sequence of *D. hydrothermale* suggests the absence of *c*-type cytochromes and the absence of an identified ortholog of Dred\_0700-0701, even though the strain is able to reduce Fe(III) to Fe(II) (3). Metal reduction in this strain would use a different pathway, which needs to be specified. The *D. hydrothermale* genome encodes an arsenite resistance protein (DESHYv2\_110039) that exhibits homology to the intrinsic membrane protein ArsB (8). A gene (DESHYv2\_110038) encoding a transcriptional regulator belonging to the AsrR family (9) was found immediately upstream from *asrB*. Even if no homolog to the arsenate reductase gene *asrC* (10) has been identified so far, this gene cluster could be of great importance for arsenite reduction and for the tolerance capacity of this strain.

Insights into the arsenite resistance process of *Desulfotomaculum* species could be gained through comparative genomics and biochemical analyses of the arsenite resistance mechanisms, which are in progress in our laboratories.

**Nucleotide sequence accession numbers.** The whole-genome shotgun project has been deposited at DDBL/EMBL/Genbank under the accession no. [CAOS01000001](https://www.ncbi.nlm.nih.gov/nuccore/CAOS01000001) to [CAOS01000016](https://www.ncbi.nlm.nih.gov/nuccore/CAOS01000016).

## ACKNOWLEDGMENTS

Financial support came from the Université de Strasbourg (UDS), the Consortium National de Recherche en Génomique (CNRG), and the CNRS.

## REFERENCES

1. Kuever J, Rainey FA. 2009. Genus II. *Desulfotomaculum* C, Postgate. 1965. 361AL, p 989–996. In De Vos P, Garrity GM, Jones D, Krieg NR, Ludwig W, Rainey FA, Schleifer KH, Whitman WB (ed), *Bergey's manual of systematic bacteriology*, vol 3, 2nd ed. Springer Verlag, New York, NY.
2. Fishbain S, Dillon JG, Gough HL, Stahl DA. 2003. Linkage of high rates

- of sulfate reduction in Yellowstone hot springs to unique sequence types in the dissimilatory sulfate respiration pathway. *Appl. Environ. Microbiol.* 69(6):3663–3667.
3. Haouari O, Fardeau ML, Cayol JL, Casiot C, Elbaz-Poulichet F Hamdi M, Joseph M, Ollivier B. 2008. *Desulfotomaculum hydrothermale* sp. nov., a thermophilic sulfate-reducing bacterium isolated from a terrestrial Tunisian hot spring. *Int. J. Syst. Evol. Microbiol.* 58(Pt 11):2529–2535.
  4. Mandal BK, Suzuki KT. 2002. Arsenic round the world: a review. *Talanta* 58(1):201–235.
  5. Weber KA, Achenbach LA, Coates JD. 2006. Microorganisms pumping iron: anaerobic microbial iron oxidation and reduction. *Nat. Rev. Microbiol.* 4(10):752–764.
  6. Beliaev AS, Saffarini DA, McLaughlin JL, Hunnicutt D. 2001. MtrC, an outer membrane decahaem c cytochrome required for metal reduction in *Shewanella putrefaciens* MR-1. *Mol. Microbiol.* 39(3):722–730.
  7. Junier P, Junier T, Podell S, Sims DR, Detter JC, Lykidis A, Han CS, Wigginton NS, Gaasterland T, Bernier-Latmani R. 2010. The genome of the gram-positive metal- and sulfate-reducing bacterium *Desulfotomaculum reducens* strain MI-1. *Environ. Microbiol.* 12(10):2738–2754.
  8. Prakash S, Cooper G, Singhi S, Saier MH, Jr. 2003. The ion transporter superfamily. *Biochim. Biophys. Acta* 1618(1):79–92.
  9. Wu J, Rosen BP. 1991. The ArsR protein is a trans-acting regulatory protein. *Mol. Microbiol.* 5(6):1331–1336.
  10. Messens J, Silver S. 2006. Arsenate reduction: thiol cascade chemistry with convergent evolution. *J. Mol. Biol.* 362(1):1–17.