



Draft Genome Sequence of the Sulfate-Reducing Bacterium *Desulfotomaculum copahuensis* Strain CINDEFI1 Isolated from the Geothermal Copahue System, Neuquén, Argentina

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***Desulfotomaculum copahuensis* strain CINDEFI1 is a novel spore-forming sulfate-reducing bacterium isolated from the Copahue volcano area, Argentina. Here, we present its draft genome in which we found genes related with the anaerobic respiration of sulfur compounds similar to those present in the Copahue environment.**

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The geothermal Caviahue-Copahue system is a naturally extreme environment located in the northwest of Neuquén province, Argentina and dominated by Copahue volcano. The area is characterized by the presence of acidic, sulfur-rich and high-temperature hot springs that are potential sources of extremophilic microorganisms, with applications in various biotechnological processes, mainly those related with biomining and bioremediation (1, 2). Sulfate-reducing prokaryotes are of special interest since they can be used in heavy metals bioprecipitation processes. Copahue hot springs are enabling environments for the development of such microorganisms, and microorganisms with sulfate-reducing activity have already been detected in the anaerobic zones (3).

To date only three species of this genus have been isolated from terrestrial hot springs (4), the most recent being *Desulfotomaculum copahuensis* strain CINDEFI1 obtained from an acidic sediment from Las Máquinas hot spring (40°C, pH 2) at Copahue volcano. *D. copahuensis* strain CINDEFI1 is a spore-forming and slightly curved rod that grows optimally at 40°C and pH 7.0. It is an obligate anaerobe capable of heterotrophic growth using lactate, pyruvate as well as several sugars as carbon and energy sources. These compounds are incompletely oxidized to acetic acid (5).

Genomic DNA of *D. copahuensis* strain CINDEFI1 was extracted using a Promega Wizard genomic DNA purification kit (Promega) and sequenced using the Illumina HiSeq 2500 platform (Illumina, Inc., San Diego, CA, USA). Genome assembly was performed using CLC Genomics Workbench 7.5 which predicted a genome size of 3,628,787 bp in 375 contigs (largest: 228,398 bp, shortest: 2,008 bp, and N_{50} 50,475 bp) with a coverage of 55.76× and 47.7% G+C content. Annotation was performed with NCBI Prokaryotic Genome Annotation Pipeline 2.10 and RAST server (6). A total of 4,063 coding sequences (CDSs), and 59 structural

RNAs (51 tRNAs and 8 rRNAs) were predicted. Three percent of the CDSs were classified as hypothetical proteins and 96% as known enzymes.

The genome of *D. copahuensis* strain CINDEFI1 presents genes that might be involved in the metabolic features described previously for this strain. Key enzymes for sulfate reduction, such as sulfate adenylyltransferase (ATP-sulfurilase), adenosine-5'-phosphosulfate (APS) reductase, and dissimilatory sulfite reductase (DSR), were detected (7). Sugar metabolism can be inferred by the presence of all genes of the Embden-Meyerhof-Parnas pathway. Enzymes involved in the fermentation of sugar compounds and a putative pyruvate dehydrogenase complex were also found (8). Incomplete oxidation of organic compounds observed experimentally, can be confirmed by the absence of genes for key enzymes for the TCA cycle. On the other hand, genes codifying enzymes related with energy generation and conservation in Gram-positive sulfate-reducers, including *qmoAB* and *hdrBC* genes, which codify the Qmo complex and the soluble subunits of the heterodisulfide reductase B and C, respectively, were also found (7, 9). All protein sequences showed low e-values with corresponding proteins from *D. thermocisternum*, *D. nigrificans*, *D. gibsoniae*, and *D. reducens* in a BLASTp comparison (7, 10).

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. [LYVF00000000](https://www.ncbi.nlm.nih.gov/nuclink/LYVF00000000). The version described in this paper is version LYVF01000000.

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REFERENCES

1. Chiacchiarini P, Lavalle L, Giaveno A, Donati E. 2010. First assessment of acidophilic microorganisms from geothermal Copahue–Caviahue system. *Hydrometallurgy* 104:334–341. <http://dx.doi.org/10.1016/j.hydromet.2010.02.020>.
2. Varekamp D, Maartende Moor J, Merrill M, Colvin A, Goss A, Vroon P. 2006. Geochemistry and isotopic characteristics of the Caviahue–Copahue volcanic complex, Province of Neuquén, Argentina. *Geol Soc Am Spec Pap* 407:317–342.
3. Willis G, Hedrich S, Nancucheo I, Johnson DB, Donati ER. 2013. Microbial diversity in acidic anaerobic sediments at geothermal Caviahue–Copahue system, Argentina. *Adv Mater Res* 825:7–10. <http://dx.doi.org/10.4028/www.scientific.net/AMR.825.7>.
4. Amin O, Fardeau ML, 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^T. *Genome Announc* 1(1):e00114-12. <http://dx.doi.org/10.1128/genomeA.00114-12>.
5. Willis Poratti G. 2016. Biorremediación de metales pesados por sulfidogénesis utilizando comunidades y microorganismos sulfato-reductores. Ph.D. thesis. Facultad de Ciencias Exactas, Universidad Nacional de la Plata, La Plata, Argentina.
6. 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>.
7. Cardoso Pereira IA, Ramos AR, Grein F, Coimbra Marques M, Marques da Silva S, Santos Venceslau S. 2011. A comparative genomic analysis of energy metabolism in sulfate reducing bacteria and archaea. *Front Microbiol* 2:1–22.
8. Visser M, Parshina SN, Alves JI, Sousa DZ, Pereira IA, Muyzer G, Kuever J, Lebedinsky AV, Koehorst JJ, Worm P, Plugge CM, Schaap PJ, Goodwin LA, Lapidus A, Kyrpides NC, Detter JC, Woyke T, Chain P, Davenport KW, Spring S, Rohde M, Klenk HP, Stams AJM. 2014. Genome analysis of the carboxydrotrophic sulfate-reducers *Desulfotomaculum nigrificans* and *Desulfotomaculum carboxydivorans* and reclassification of *Desulfotomaculum carboxydivorans* as a later synonym of *Desulfotomaculum nigrificans*. *Stand Genomic Sci* 9:655–675. <http://dx.doi.org/10.4056/sigs.4718645>.
9. 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* 12:2738–2754. <http://dx.doi.org/10.1111/j.1462-2920.2010.02242.x>.
10. Kuever J, Visser M, Loeffler C, Boll M, Worm P, Sousa DZ, Plugge CM, Schaap PJ, Muyzer G, Pereira IA, Parshina SN, Goodwin LA, Kyrpides NC, Detter J, Woyke T, Chain P, Davenport KW, Rohde M, Spring S, Klenk HP, Stams AJM. 2014. Genome analysis of *Desulfotomaculum gibsoniae* strain Groll^T a highly versatile Gram-positive sulfate-reducing bacterium. *Stand Genomic Sci* 9:821–839. <http://dx.doi.org/10.4056/sigs.5209235>.