



# Draft Genome Sequence of the UV-Resistant Antarctic Bacterium *Sphingomonas* sp. Strain UV9

Juan J. Marizcurrena,<sup>a</sup> Danilo Morales,<sup>a</sup> Pablo Smircich,<sup>b,c</sup> Susana Castro-Sowinski<sup>a,d</sup>

<sup>a</sup>Section Biochemistry, Faculty of Sciences, Universidad de la República, Iguá, Montevideo, Uruguay

<sup>b</sup>Laboratory of Molecular Interactions, Faculty of Sciences, Universidad de la República, Iguá, Montevideo, Uruguay

<sup>c</sup>Department of Genomics, Instituto de Investigaciones Biológicas Clemente Estable, MEC, Montevideo, Uruguay

<sup>d</sup>Molecular Microbiology, Instituto de Investigaciones Biológicas Clemente Estable, MEC, Montevideo, Uruguay

**ABSTRACT** We report the draft genome sequence of the Antarctic UV-resistant bacterium *Sphingomonas* sp. strain UV9. The strain has a genome size of 4.25 Mb, a 65.62% GC content, and 3,879 protein-coding sequences. Among others, genes encoding the resolving of the DNA damage produced by the UV irradiation were identified.

Bacteria from the genus *Sphingomonas* are *Alphaproteobacteria* (family *Sphingomonadaceae*) with 127 described species. They are found in a broad range of environments, such as soils, fresh and marine waters, and plants, and in humans acting as opportunistic pathogens (1–6). *Sphingomonas* strains also colonize extreme environments, including Antarctica, volcano lakes, contaminated soils, and highly UV-irradiated places (6–8). They are Gram-negative, rod-shaped, chemoheterotrophic, strictly aerobic, and non-spore-forming bacteria (9).

This work reports the draft genome sequence of the UV-resistant bacterium *Sphingomonas* sp. strain UV9. The isolation and growth conditions for UV9 were previously described (7). Total DNA was extracted using the fungal/bacterial DNA miniprep purification kit (Zymo Research, catalog number D6005). The library preparation was performed using the Accel-NGS 2S PCR-free DNA library kit (Swift Biosciences, MI) and was sequenced at Macrogen using the HiSeq 2000/2500 technology platform with 101-bp paired-end read strategy. At least 13.7 million reads were obtained. Their quality was evaluated with FastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) and assembled *de novo* using SPAdes (<http://cab.spbu.ru/software/spades/>) with the repeat resolution and mismatch correction settings enabled. The draft genome consists of ca. 4.25 Mb, including 62 contigs of above 1,000 bp, with a GC content of 65.62% and an  $N_{50}$  contig length of 1.26 Mb ( $L_{50}$  of 2 Mb) and 40× final coverage. The genome was annotated and the functions of genes were predicted and compared using the Rapid Annotations using Subsystems Technology (RAST) (10) and NCBI Prokaryotic Genome Annotation Pipeline (PGAP) servers. The predicted genes were functionally categorized using the SEED subsystems (11) at the RAST server. Proteins that conserve functional domains were identified using the NCBI conserved domain search service (CD-Search) (12).

The genome was predicted to have at least 3,879 protein-coding sequences (CDS) (1,274 were considered hypothetical, and 1,750 CDSs were classified into 209 subsystems), 50 tRNAs, 1 copy each of 23S rRNA-, 16S rRNA-, and 5S rRNA-encoding genes, and 86 pseudogenes. UV9 has the genomic information for the production of three photolyases, enzymes responsible for photorepairing the DNA damage caused by UV irradiation (13). These include two photolyases that repair the cyclobutane pyrimidine dimers (CPD-photolyase) and one that repairs 6,4 photoproducts (6,4-photolyase); both

**Citation** Marizcurrena JJ, Morales D, Smircich P, Castro-Sowinski S. 2019. Draft genome sequence of the UV-resistant Antarctic bacterium *Sphingomonas* sp. strain UV9. *Microbiol Resour Announc* 8:e01651-18. <https://doi.org/10.1128/MRA.01651-18>.

**Editor** John J. Dennehy, Queens College

**Copyright** © 2019 Marizcurrena et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Susana Castro-Sowinski, [scs@icien.edu.uy](mailto:scs@icien.edu.uy).

J.J.M. and D.M. contributed equally to this work.

**Received** 10 December 2018

**Accepted** 23 January 2019

**Published** 14 February 2019

photoproducts halt RNA polymerase II during transcription or DNA polymerase during replication (14). These enzymes may have different functional antenna chromophores, 8-hydroxy-7,8-didemethyl-5-deazariboflavin (MTHF) and/or 6,7-dimethyl-8-ribityllumazine (DMRL), as the biosynthetic pathways were found. UV9 also shows a UvrABC system (14) (excinuclease ABC), as is found in the gamma radiation-resistant *Hymenobacter sedentarius* (15) and *Deinococcus swuensis* (16) bacteria, and an ATP-dependent DNA helicase UvrD/PcrA (essential during replication, recombination, and repair of UV damage) (17). It also contains a copy of the *radA* gene (which fills a gap using the information from the undamaged DNA strand) and the DNA mismatch repair proteins MutL/MutS (which identify and correct errors made during the replication). UV9 has genetic information for the synthesis of bacteriorhodopsin, a light-driven proton pump. Finally, UV9 harbors heavy metal resistance genes, including those for cobalt, zinc, cadmium, chromium, and arsenic, and employs the toxin-antitoxin system (RelEB and VapC), including specific proteases such as Lon, ClpXP, or ClpAP that commonly degrade the antidote (18). Thus, strain UV9 could be a model for studying bacterial UV resistance.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [SCIN00000000](https://doi.org/10.1093/jks.064828-0). The version described in this paper is version SCIN01000000.

## ACKNOWLEDGMENTS

We thank the Uruguayan Antarctic Institute for logistical support during our stay in the Antarctic Base Artigas. S.C.-S., P.S., and J.J.M. are members of the National Research System (SNI [Sistema Nacional de Investigadores]).

This work was partially supported by PEDECIBA (Programa de Desarrollo de las Ciencias Básicas) and ANII (Agencia Nacional de Investigación e Innovación, project FMV\_3\_2016\_1\_1226654). The work of J.J.M. was supported by ANII and CAP (Comisión Académica de Posgrado, UdelaR).

## REFERENCES

- Leung KT, Chang YJ, Gan YD, Peacock A, Macnaughton SJ, Stephen JR, Burkhalter RS, Flemming CA, White DC. 1999. Detection of Sphingomonas spp in soil by PCR and sphingolipid biomarker analysis. *J Ind Microbiol Biotechnol* 23:252–260. <https://doi.org/10.1038/sj.jim.2900677>.
- Asker D, Beppu T, Ueda K. 2007. Sphingomonas jaspsi sp. nov., a novel carotenoid-producing bacterium isolated from Misasa, Tottori, Japan. *Int J Syst Evol Microbiol* 57:1435–1441. <https://doi.org/10.1099/ijs.0.64828-0>.
- Amato P, Parazols M, Sancelme M, Laj P, Mailhot G, Delort AM. 2007. Microorganisms isolated from the water phase of tropospheric clouds at the Puy de Dôme: major groups and growth abilities at low temperatures. *FEMS Microbiol Ecol* 59:242–254. <https://doi.org/10.1111/j.1574-6941.2006.00199.x>.
- Khan AL, Waqas M, Kang SM, Al-Harrasi A, Hussain J, Al-Rawahi A, Al-Khiziri S, Ullah I, Ali L, Jung HY, Lee IJ. 2014. Bacterial endophyte Sphingomonas sp. LK11 produces gibberellins and IAA and promotes tomato plant growth. *J Microbiol* 52:689–695. <https://doi.org/10.1007/s12275-014-4002-7>.
- Ryan MP, Adley CC. 2010. Sphingomonas paucimobilis: a persistent Gram-negative nosocomial infectious organism. *J Hosp Infect* 75: 153–157. <https://doi.org/10.1016/j.jhin.2010.03.007>.
- Farias ME, Revale S, Mancini E, Ordoñez O, Turjanski A, Cortez N, Vazquez MP. 2011. Genome sequence of Sphingomonas sp. S17, isolated from an alkaline, hyperarsenic, and hypersaline volcano-associated lake at high altitude in the Argentinean Puna. *J Bacteriol* 193:3686–3687. <https://doi.org/10.1128/JB.05225-11>.
- Marizcurrena JJ, Morel MA, Braña V, Morales D, Martínez-López W, Castro-Sowinski S. 2017. Searching for novel photolyases in UVC-resistant Antarctic bacteria. *Extremophiles* 21:409–418. <https://doi.org/10.1007/s00792-016-0914-y>.
- Merroun ML, Nedelkova M, Ojeda JJ, Reitz T, Fernández ML, Arias JM, Romero-González M, Selenska-Pobell S. 2011. Bio-precipitation of uranium by two bacterial isolates recovered from extreme environments as estimated by potentiometric titration, TEM and X-ray absorption spectroscopic analyses. *J Hazard Mater* 197:1–10. <https://doi.org/10.1016/j.jhazmat.2011.09.049>.
- Brenner D, Krieg N, Staley J. 2005. Bergey's manual of systematic bacteriology, vol. 2: the proteobacteria, part C—the alpha-, beta-, delta-, and epsilonproteobacteria. Springer, New York, NY.
- Aziz RK, Bartels D, Best A, 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. <https://doi.org/10.1186/1471-2164-9-75>.
- Overbeek R, Begley T, Butler RM, Choudhuri JV, Chuang HY, Cohoon M, de Crécy-Lagard V, Diaz N, Disz T, Edwards R, Fonstein M, Frank ED, Gerdes S, Glass EM, Goemann A, Hanson A, Iwata-Reuyl D, Jensen R, Jamshidi N, Krause L, Kubal M, Larsen N, Linke B, McHardy AC, Meyer F, Neuweger H, Olsen G, Olson R, Osterman A, Portnoy V, Pusch GD, Rodionov DA, Rückert C, Steiner J, Stevens R, Thiele I, Vassieva O, Ye Y, Zagnitko O, Vonstein V. 2005. The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Res* 33:5691–5702. <https://doi.org/10.1093/nar/gki866>.
- Marchler-Bauer A, Derbyshire MK, Gonzales NR, Lu S, Chitsaz F, Geer LY, Geer RC, He J, Gwadz M, Hurwitz DI, Lanczycki CJ, Lu F, Marchler GH, Song JS, Thanki N, Wang Z, Yamashita RA, Zhang D, Zheng C, Bryant SH. 2015. CDD: NCBI's conserved domain database. *Nucleic Acids Res* 43: D222–D226. <https://doi.org/10.1093/nar/gku1221>.
- Sancar GB, Sancar A. 2006. Purification and characterization of DNA photolyases. *Methods Enzymol* 408:121–156. [https://doi.org/10.1016/S0076-6879\(06\)08009-8](https://doi.org/10.1016/S0076-6879(06)08009-8).
- Budden T, Bowden NA. 2013. The role of altered nucleotide excision repair and UVB-induced DNA damage in melanomagenesis. *Int J Mol Sci* 14:1132–1151. <https://doi.org/10.3390/ijms14011132>.
- Kim MK, Kang MS, Srinivasan S, Lee DH, Lee SY, Jung HY. 2017. Complete genome sequence of *Hymenobacter sedentarius* DG5BT, a bacterium

- resistant to gamma radiation. *Mol Cell Toxicol* 13:199–205. <https://doi.org/10.1007/s13273-017-0021-x>.
16. Kim MK, Srinivasan S, Back C-G, Joo ES, Lee S-Y, Jung H-Y. 2015. Complete genome sequence of *Deinococcus swuensis*, a bacterium resistant to radiation toxicity. *Mol Cell Toxicol* 11:315–321. <https://doi.org/10.1007/s13273-015-0031-5>.
  17. Lee JY, Yang W. 2006. UvrD helicase unwinds DNA one base pair at a time by a two-part power stroke. *Cell* 127:1349–1360. <https://doi.org/10.1016/j.cell.2006.10.049>.
  18. Buts L, Lah J, Dao-Thi MH, Wyns L, Loris R. 2005. Toxin-antitoxin modules as bacterial metabolic stress managers. *Trends Biochem Sci* 30:672–679. <https://doi.org/10.1016/j.tibs.2005.10.004>.