



**HAL**  
open science

## Draft Genome Sequence of *Microbacterium oleivorans* Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil

Philippe Ortet, Nicolas Gallois, Laurie Piette, Justine Long, C. Berthomieu,  
J. Armengaud, mohamed Barakat, Virginie Chapon

► **To cite this version:**

Philippe Ortet, Nicolas Gallois, Laurie Piette, Justine Long, C. Berthomieu, et al.. Draft Genome Sequence of *Microbacterium oleivorans* Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil. *Genome Announcements*, 2017, 5 (14), pp.e00092-17. 10.1128/genomeA.00092-17. hal-01560969

**HAL Id: hal-01560969**

**<https://hal-amu.archives-ouvertes.fr/hal-01560969>**

Submitted on 12 Jul 2017

**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.



Distributed under a Creative Commons Attribution| 4.0 International License



# Draft Genome Sequence of *Microbacterium oleivorans* Strain A9, a Bacterium Isolated from Chernobyl Radionuclide-Contaminated Soil

Philippe Ortet,<sup>b</sup> Nicolas Gallois,<sup>a</sup> Laurie Piette,<sup>a</sup> Justine Long,<sup>b</sup> Catherine Berthomieu,<sup>a</sup> Jean Armengaud,<sup>c</sup> Mohamed Barakat,<sup>b</sup> Virginie Chapon<sup>a</sup>

CEA, CNRS, Aix-Marseille Université, UMR 7265 Biologie Végétale et Microbiologie Environnementales, Laboratoire des Interactions Protéine Métal, Saint-Paul-lez-Durance, France<sup>a</sup>; CEA, CNRS, Aix-Marseille Université, UMR 7265 Biologie Végétale et Microbiologie Environnementales, Laboratoire d'Écologie Microbienne de la Rhizosphère et d'Environnements Extrêmes, Saint-Paul-lez-Durance, France<sup>b</sup>; CEA, DRF/IBiTec-S/SPI/Li2D, BP 17171, Bagnols-sur-Cèze, France<sup>c</sup>

**ABSTRACT** Here, we present the draft genome sequence of *Microbacterium oleivorans* strain A9, a uranium-tolerant actinobacterium which has been isolated from radionuclide-contaminated soil from the Chernobyl exclusion zone. It is composed of 22 contigs totaling 2,954,335 bp and contains 2,813 coding DNA sequences, one cluster of rRNA genes, and 45 tRNA genes.

Members of the genus *Microbacterium* are rod-shaped, Gram-positive, and non-spore-forming actinobacteria. *Microbacterium*-related bacteria are apparently ubiquitous, since they have been detected in a wide variety of habitats, including soil (1), sediment (2), air (3), seawater (4), plants (5), jellyfish (6), insect gut (7), food (8), clinical specimens (9), polluted environments (10), and radionuclide-rich soils (11). At the time of this writing, there are more than 90 *Microbacterium* species with a valid name (12) and 129 complete or draft genomes (<https://gold.jgi.doe.gov>). Here, we report the draft genome sequence of *Microbacterium oleivorans* strain A9, which was isolated from a radionuclide-contaminated soil sample collected from trench T22 in the Chernobyl exclusion zone (13). This bacterium exhibits high uranium tolerance due to multiple detoxication mechanisms (14).

Bacteria were cultured in LB at 32°C until late-exponential-growth phase, and high-quality genomic DNA was extracted from cells using the DNeasy blood and tissue kit (Qiagen), according to the manufacturer's instructions for Gram-positive bacteria. The quality of the purified DNA was checked using a NanoDrop spectrophotometer (Thermo Scientific). Genomic DNA was sequenced on a HiSeq 2000 sequencing platform (Illumina) by the GenoScreen Company (Lille, France). *De novo* genome assembly was performed on the reads using ABySS (15).

A total of 18,500,514 reads were obtained, with a mean read length of 100 bases. These reads were assembled into a set of 104 contigs for a total of 2.99 Mbp sequence by the assembler, with k-mer optimal size set to 64. Of those 104 contigs, only the 22 contigs with sequence length longer than 500 bp were retained. The largest contig was 553,625 bp, and the  $N_{50}$  parameter was 205,808 bp. The genome size was estimated at 2.95 Mbp. According to our assembly, the G+C content was 68.33%, a value in accordance with the phylogenetic position of *Microbacterium* within the *Actinobacteria* phylum (16). Taxonomic assignment at the species level was provided by the NCBI using the average nucleotide identity, as described by Federhen et al. (17). Genome annotation was performed with the NCBI Prokaryotic Genome Annotation Pipeline (18), which reported the prediction of 2,813 protein-coding genes, 15 pseudogenes, one

Received 6 February 2017 Accepted 7 February 2017 Published 6 April 2017

**Citation** Ortet P, Gallois N, Piette L, Long J, Berthomieu C, Armengaud J, Barakat M, Chapon V. 2017. Draft genome sequence of *Microbacterium oleivorans* strain A9, a bacterium isolated from Chernobyl radionuclide-contaminated soil. *Genome Announc* 5:e00092-17. <https://doi.org/10.1128/genomeA.00092-17>.

**Copyright** © 2017 Ortet 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 Philippe Ortet, [philippe.ortet@cea.fr](mailto:philippe.ortet@cea.fr), or Virginie Chapon, [virginie.chapon@cea.fr](mailto:virginie.chapon@cea.fr).

complete rRNA cluster, three noncoding RNAs (ncRNAs), and 45 tRNA genes. Annotation of regulatory proteins was accomplished using the P2RP Web server (19), which identified genes encoding 58 two-component system proteins (30 histidine kinases, 26 response regulators, and two histidine phosphotransferases) and 180 transcription factors.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [MTIO000000000](https://doi.org/10.1099/MTIO000000000). The version described in this paper is the first version, MTIO01000000.

## ACKNOWLEDGMENTS

This study was financed by the Toxicology Program of the French Alternative Energies and Atomic Energy Commission (CEA) and by the NEEDS-PF Resources Program (CEA, CNRS, AREVA). Nicolas Gallois is the recipient of a Ph.D. grant funded by the CEA.

## REFERENCES

1. Yoon JH, Schumann P, Kang SJ, Lee CS, Lee SY, Oh TK. 2009. *Microbacterium insulae* sp. nov., isolated from soil. *Int J Syst Evol Microbiol* 59:1738–1742. <https://doi.org/10.1099/ijss.0.007591-0>.
2. Mawlankar RR, Mual P, Sonalkar VV, Thorat MN, Verma A, Srinivasan K, Dastager SG. 2015. *Microbacterium enclense* sp. nov., isolated from sediment sample. *Int J Syst Evol Microbiol* 65:2064–2070. <https://doi.org/10.1099/ijss.0.000221>.
3. Zlamala C, Schumann P, Kämpfer P, Valens M, Rosselló-Mora R, Lubitz W, Busse HJ. 2002. *Microbacterium aerolatum* sp. nov., isolated from the air in the ‘Virgilkapelle’ in Vienna. *Int J Syst Evol Microbiol* 52:1229–1234. <https://doi.org/10.1099/00207713-52-4-1229>.
4. Kim KK, Lee KC, Oh HM, Lee JS. 2008. *Microbacterium aquimaris* sp. nov., isolated from seawater. *Int J Syst Evol Microbiol* 58:1616–1620. <https://doi.org/10.1099/ijss.0.65763-0>.
5. Alves A, Correia A, Igual JM, Trujillo ME. 2014. *Microbacterium endophyticum* sp. nov. and *Microbacterium halimionae* sp. nov., endophytes isolated from the salt-marsh plant *Halimione portulacoides* and emended description of the genus *Microbacterium*. *Syst Appl Microbiol* 37:474–479. <https://doi.org/10.1016/j.syapm.2014.08.004>.
6. Kaur G, Mual P, Kumar N, Verma A, Kumar A, Krishnamurthi S, Mayilraj S. 2016. *Microbacterium aureliae* sp. nov., a novel actinobacterium isolated from *Aurelia aurita*, the moon jellyfish. *Int J Syst Evol Microbiol* 66:4665–4670. <https://doi.org/10.1099/ijsem.0.001407>.
7. Kim DY, Shin DH, Jung S, Kim H, Lee JS, Cho HY, Bae KS, Sung CK, Rhee YH, Son KH, Park HY. 2014. Novel alkali-tolerant GH10 endo-beta-1,4-xylanase with broad substrate specificity from *Microbacterium trichothecenolyticum* HY-17, a gut bacterium of the mole cricket *Gryllotalpa orientalis*. *J Microbiol Biotechnol* 24:943–953. <https://doi.org/10.4014/jmb.1405.05032>.
8. Kim YJ, Roh SW, Jung MJ, Kim MS, Park EJ, Bae JW. 2011. *Microbacterium mitrae* sp. nov., isolated from salted turban shell. *Int J Syst Evol Microbiol* 61:399–403. <https://doi.org/10.1099/ijss.0.021519-0>.
9. Clermont D, Diard S, Bouchier C, Vivier C, Bimet F, Motreff L, Welker M, Kallow W, Bizet C. 2009. *Microbacterium binotii* sp. nov., isolated from human blood. *Int J Syst Evol Microbiol* 59:1016–1022. <https://doi.org/10.1099/ijss.0.003160-0>.
10. Anand S, Bala K, Saxena A, Schumann P, Lal R. 2012. *Microbacterium amylolyticum* sp. nov., isolated from soil from an industrial waste site. *Int J Syst Evol Microbiol* 62:2114–2120. <https://doi.org/10.1099/ijss.0.034439-0>.
11. Mondani L, Piette L, Christen R, Bachar D, Berthomieu C, Chapon V. 2013. *Microbacterium lemovicicum* sp. nov., a bacterium isolated from a natural uranium-rich soil. *Int J Syst Evol Microbiol* 63:2600–2606. <https://doi.org/10.1099/ijss.0.048454-0>.
12. Euzéby JP. 1997. List of bacterial names with standing in nomenclature: a folder available on the Internet. *Int J Syst Bacteriol* 47:590–592. <https://doi.org/10.1099/00207713-47-2-590>.
13. Chapon V, Piette L, Vesvres M-H, Coppin F, Marrec CL, Christen R, Theodorakopoulos N, Février L, Levchuk S, Martin-Garin A, Berthomieu C, Sergeant C. 2012. Microbial diversity in contaminated soils along the T22 trench of the Chernobyl experimental platform. *Appl Geochem* 27:1375–1383. <https://doi.org/10.1016/j.apgeochem.2011.08.011>.
14. Theodorakopoulos N, Chapon V, Coppin F, Floriani M, Vercouter T, Sergeant C, Camilleri V, Berthomieu C, Février L. 2015. Use of combined microscopic and spectroscopic techniques to reveal interactions between uranium and *Microbacterium* sp. A9, a strain isolated from the Chernobyl exclusion zone. *J Hazard Mater* 285:285–293. <https://doi.org/10.1016/j.jhazmat.2014.12.018>.
15. Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. 2009. ABySS: a parallel assembler for short read sequence data. *Genome Res* 19:1117–1123. <https://doi.org/10.1101/gr.089532.108>.
16. Ventura M, Canchaya C, Tauch A, Chandra G, Fitzgerald GF, Chater KF, van Sinderen D. 2007. Genomics of *Actinobacteria*: tracing the evolutionary history of an ancient phylura. *Microbiol Mol Biol Rev* 71:495–548. <https://doi.org/10.1128/MMBR.00005-07>.
17. Federhen S, Rossello-Mora R, Klenk H-P, Tindall BJ, Konstantinidis KT, Whitman WB, Brown D, Labeda D, Ussery D, Garrity GM, Colwell RR, Hasan N, Graf J, Parte A, Yarza P, Goldberg B, Sichtig H, Karsch-Mizrachi I, Clark K, McVeigh R, Pruitt KD, Tatusova T, Falk R, Turner S, Madden T, Kitts P, Kimchi A, Klimke W, Agarwala R, DiCuccio M, Ostell J. 2016. Meeting report: GenBank Microbial Genomic Taxonomy Workshop (12–13 May, 2015). *Stand Genomic Sci* 11:15.
18. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
19. Barakat M, Ortet P, Whitworth DE. 2013. P2RP: a Web-based framework for the identification and analysis of regulatory proteins in prokaryotic genomes. *BMC Genomics* 14:269. <https://doi.org/10.1186/1471-2164-14-269>.