

Lawrence Berkeley National Laboratory

LBL Publications

Title

Complete Genome Sequence for Asinibacterium sp. Strain OR53 and Draft Genome Sequence for Asinibacterium sp. Strain OR43, Two Bacteria Tolerant to Uranium

Permalink

<https://escholarship.org/uc/item/89c4s3qq>

Journal

Microbiology Resource Announcements, 8(14)

ISSN

2576-098X

Authors

Brzoska, Ryann M
Huntemann, Marcel
Clum, Alicia
et al.

Publication Date

2019-04-04


DOI

10.1128/mra.01701-18

Peer reviewed



Complete Genome Sequence for *Asinibacterium* sp. Strain OR53 and Draft Genome Sequence for *Asinibacterium* sp. Strain OR43, Two Bacteria Tolerant to Uranium

Ryann M. Brzoska,^a Marcel Huntemann,^b Alicia Clum,^b Amy Chen,^b Nikos Kyrpides,^b Krishnaveni Palaniappan,^b Natalia Ivanova,^b Natalia Mikhailova,^b Galina Ovchinnikova,^b Neha Varghese,^b Supratim Mukherjee,^b  T. B. K. Reddy,^b Chris Daum,^b Nicole Shapiro,^b Tanja Woyke,^b Annette Bollmann^a

^aDepartment of Microbiology, Miami University, Oxford, Ohio, USA

^bDOE Joint Genome Institute, Walnut Creek, California, USA

ABSTRACT *Asinibacterium* sp. strains OR43 and OR53 belong to the phylum *Bacteroidetes* and were isolated from subsurface sediments in Oak Ridge, TN. Both strains grow at elevated levels of heavy metals. Here, we present the closed genome sequence of *Asinibacterium* sp. strain OR53 and the draft genome sequence of *Asinibacterium* sp. strain OR43.

Asinibacterium sp. strains OR43 and OR53 (formerly *Sediminibacterium* sp. strains OR43 and OR53) are Gram-negative, nonmotile, aerobic bacteria. The type strain *Asinibacterium lactis* was isolated from donkey milk powder (1). Closely related genera include *Sediminibacterium*, *Vibrionimonas*, and *Hydrothalea* (2–6). Related sequences (16S rRNA) were detected ubiquitously in the environment but most notably in sites contaminated with hydrocarbons, heavy metals, and/or radionucleotides (7–14). The genome sequences will provide insight into the potential role of *Asinibacterium* sp. strains OR43 and OR53 in the bioremediation of heavy metals.

Asinibacterium sp. strains OR43 and OR53 were isolated from the contaminated subsurface sediment at the Integrated Field Research Challenge (IFRC) in Oak Ridge, TN, with the diffusion chamber approach (7). Both strains have a very similar physiology and are able to grow in the presence of uranium equal to the concentrations in their original environment (7, 15) (R. M. Brzoska and A. Bollmann, unpublished data). Prior to DNA isolation, the strains were grown in 0.1× Luria-Bertani broth at 27°C (7). Genomic DNA was isolated with the JETFLEX genomic DNA purification kit from GenoMed (Loehne, Germany) according to the manufacturer's recommendations. Genome sequence data for both genomes were obtained with the Illumina HiSeq 2000 platform with paired-end technology (2 × 150 bp) (16). The data produced 18,342,342 reads generating 3,005 Mbp (strain OR43) and 21,794,720 reads generating 3,269 Mbp (strain OR53). The genome sequences were assembled with ALLPATHS version R37654 (strain OR43) and version R39750 (strain OR53) (17), Velvet version 1.1.05 (18), and Phrap version 4.24 (High Performance Software LLC) (only strain OR53). Prodigal 2.5 was used for gene calling (19). The genomes were annotated with the DOE Joint Genome Institute (JGI) Annotation Pipeline (20, 21) and further analyzed with the Integrated Microbial Genomes and Microbiomes database and comparative analysis system (IMG/M) at the Joint Genome Institute in Walnut Creek, CA (22).

The genome size for *Asinibacterium* sp. strain OR43 was 3,768,016 bp in 12 scaffolds with a GC content of 45.7%, and that for *Asinibacterium* sp. strain OR53 was 3,715,967 bp in 1 scaffold with a GC content of 45.4%. *Asinibacterium* sp. strain OR43 had 2,473 proteins with predicted functions out of 3,284 protein-coding se-

Citation Brzoska RM, Huntemann M, Clum A, Chen A, Kyrpides N, Palaniappan K, Ivanova N, Mikhailova N, Ovchinnikova G, Varghese N, Mukherjee S, Reddy TBK, Daum C, Shapiro N, Woyke T, Bollmann A. 2019. Complete genome sequence for *Asinibacterium* sp. strain OR53 and draft genome sequence for *Asinibacterium* sp. strain OR43, two bacteria tolerant to uranium. *Microbiol Resour Announc* 8:e01701-18. <https://doi.org/10.1128/MRA.01701-18>.

Editor Jason E. Stajich, University of California, Riverside

Copyright © 2019 Brzoska 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 Annette Bollmann, bollmaa@miamioh.edu.

Received 19 December 2018

Accepted 27 February 2019

Published 4 April 2019

quences, while *Asinibacterium* sp. strain OR53 had 2,464 proteins with predicted functions out of 3,281 protein-coding sequences. The genomes contained predicted heavy-metal efflux pumps and sensing proteins. The average nucleotide identity (ANI) between the genomes was calculated with the Microbial Species Identifier (MiSI) method (23) at 96.4%, which indicated that the genomes were the same species and very closely related. Further analysis is needed to determine the mechanism of *Asinibacterium* spp. to withstand and grow in the presence of uranium.

Data availability. This whole-genome project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [ATYE00000000](https://doi.org/10.1099/ijs.0.047639-0) (*Asinibacterium* sp. strain OR43) and [AZXP00000000](https://doi.org/10.1099/ijs.0.047639-0) (*Asinibacterium* sp. strain OR53). The raw reads were deposited in the SRA under [SRP078705](https://doi.org/10.1099/ijs.0.047639-0) (*Asinibacterium* sp. strain OR53) and [SRP078706](https://doi.org/10.1099/ijs.0.047639-0) (*Asinibacterium* sp. strain OR43).

ACKNOWLEDGMENTS

This work was conducted by the U.S. Department of Energy Joint Genome Institute, a DOE Office of Science User Facility, which is supported by the Office of Science of the U.S. Department of Energy under contract number DE-AC02-05CH11231.

We thank Eveline Brambilla (Leibniz Institute DSMZ–German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany) for her help with the isolation of the genomic DNA.

REFERENCES

- Lee D-G, Park J-M, Kang H, Hong S-Y, Lee KR, Chang H-B, Trujillo ME. 2013. *Asinibacterium lactis* gen. nov., sp. nov., a member of the family Chitinophagaceae, isolated from donkey (*Equus asinus*) milk. *Int J Syst Evol Microbiol* 63:3180–3185. <https://doi.org/10.1099/ijs.0.047639-0>.
- Albert RA, Zitomer D, Dollhopf M, Schauer-Gimenez AE, Struble C, King M, Son S, Langer S, Busse H-J. 2014. Proposal of *Vibrionimonas magnilacihabitans* gen. nov., sp. nov., a curved Gram-stain-negative bacterium isolated from lake water. *Int J Syst Evol Microbiol* 64:613–620. <https://doi.org/10.1099/ijs.0.056663-0>.
- Qu J-H, Yuan H-L. 2008. *Sediminibacterium salmoneum* gen. nov., sp. nov., a member of the phylum Bacteroidetes isolated from sediment of a eutrophic reservoir. *Int J Syst Evol Microbiol* 58:2191–2194. <https://doi.org/10.1099/ijs.0.65514-0>.
- Kim Y-J, Nguyen N-L, Weon H-Y, Yang D-C. 2013. *Sediminibacterium ginsengisoli* sp. nov., isolated from soil of a ginseng field, and emended descriptions of the genus *Sediminibacterium* and of *Sediminibacterium salmoneum*. *Int J Syst Evol Microbiol* 63:905–912. <https://doi.org/10.1099/ijs.0.038554-0>.
- Kämpfer P, Lodders N, Falsen E. 2011. *Hydrotalea flava* gen. nov., sp. nov., a new member of the phylum Bacteroidetes and allocation of the genera *Chitinophaga*, *Sediminibacterium*, *Lacibacter*, *Flaviumibacter*, *Flavisolibacter*, *Niabella*, *Niastella*, *Segetibacter*, *Parasegetibacter*, *Terrimonas*, *Ferruginibacter*, *Filimonas* and *Hydrotalea* to the family Chitinophagaceae fam. nov. *Int J Syst Evol Microbiol* 61:518–523. <https://doi.org/10.1099/ijs.0.023002-0>.
- Albuquerque L, Rainey FA, Nobre MF, da Costa MS. 2012. *Hydrotalea sandarakina* sp. nov., isolated from a hot spring runoff, and emended descriptions of the genus *Hydrotalea* and the species *Hydrotalea flava*. *Int J Syst Evol Microbiol* 62:1603–1608. <https://doi.org/10.1099/ijs.0.034496-0>.
- Bollmann A, Palumbo AV, Lewis K, Epstein SS. 2010. Isolation and physiology of bacteria from contaminated subsurface sediments. *Appl Environ Microbiol* 76:7413–7419. <https://doi.org/10.1128/AEM.00376-10>.
- Ayarza JM, Figuerola ELM, Erijman L. 2014. Draft genome sequences of type strain *Sediminibacterium salmoneum* NJ-44 and *Sediminibacterium* sp. strain C3, a novel strain isolated from activated sludge. *Genome Announc* 2:e01073-13. <https://doi.org/10.1128/genomeA.01073-13>.
- Singleton DR, Richardson SD, Aitken MD. 2011. Pyrosequence analysis of bacteria communities in aerobic bioreactors treating polycyclic aromatic hydrocarbon-contaminated soil. *Biodegradation* 22:1061–1073. <https://doi.org/10.1007/s10532-011-9463-3>.
- Abulencia CB, Wyborski DL, Garcia JA, Podar M, Chen W, Chang SH, Chang HW, Watson D, Brodie EL, Hazen TC, Keller M. 2006. Environmental whole-genome amplification to access microbial populations in contaminated sediments. *Appl Environ Microbiol* 72:3291–3301. <https://doi.org/10.1128/AEM.72.5.3291-3301.2006>.
- Laplante K, Sébastien B, Derome N. 2013. Parallel changes of taxonomic interaction networks in lacustrine bacterial communities by a polymetallic perturbation. *Evol Appl* 6:643–659. <https://doi.org/10.1111/eva.12050>.
- Al-Awadhi H, Dashti N, Khanafer M, Al-Mailem D, Ali N, Radwan S. 2013. Bias problems in culture-independent analysis of environmental bacterial communities: a representative study of hydrocarbonoclastic bacteria. *SpringerPlus* 2:369. <https://doi.org/10.1186/2193-1801-2-369>.
- Dhal PK, Islam E, Kazy SK, Sar P. 2011. Culture-independent molecular analysis of bacteria diversity in uranium-ore-/mine waste-contaminated and non-contaminated sites from uranium mines. *3 Biotech* 1:261–272. <https://doi.org/10.1007/s13205-011-0034-4>.
- Callbeck CM, Agrawal A, Voordouw G. 2013. Acetate production from oil under sulfate-reducing conditions in bioreactors injected with sulfate and nitrate. *Appl Environ Microbiol* 79:5059–5068. <https://doi.org/10.1128/AEM.01251-13>.
- Brzoska RM, Bollmann A. 2016. The long-term effect of uranium and pH on the community composition of an artificial consortium. *FEMS Microbiol Ecol* 92:fiv158. <https://doi.org/10.1093/femsec/fiv158>.
- Bennett S. 2004. Solexa Ltd. *Pharmacogenomics* 5:433–438. <https://doi.org/10.1517/14622416.5.4.433>.
- MacCallum I, Przybylski D, Gnerre S, Burton J, Shlyakhter I, Gnirke A, Malek J, McKernan K, Ranade S, Shea TP, Williams L, Young S, Nusbaum C, Jaffe DB. 2009. ALLPATHS 2: small genomes assembled accurately and with high continuity from short paired reads. *Genome Biol* 10:R103. <https://doi.org/10.1186/gb-2009-10-10-R103>.
- Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <https://doi.org/10.1101/gr.074492.107>.
- Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <https://doi.org/10.1186/1471-2105-11-119>.
- Huntmann M, Ivanova NN, Mavromatis K, Tripp HJ, Paez-Espino D, Palaniappan K, Szeto E, Pillay M, Chen I-MA, Pati A, Nielsen T, Markowitz VM, Kyrpides NC. 2015. The standard operating procedure of the DOE-JGI Microbial Genome Annotation Pipeline (MGAP v.4). *Stand Genomic Sci* 10:86. <https://doi.org/10.1186/s40793-015-0077-y>.
- Chen I-MA, Markowitz VM, Palaniappan K, Szeto E, Chu K, Huang J, Ratner A, Pillay M, Hadjithomas M, Huntmann M, Mikhailova N, Ovchinnikova G, Ivanova NN, Kyrpides N. 2016. Supporting community annotation and user collaboration in the integrated microbial genomes

- (IMG) system. *BMC Genomics* 17:307. <https://doi.org/10.1186/s12864-016-2629-y>.
22. Chen I-MA, Chu K, Palaniappan K, Pillay M, Ratner A, Huang J, Hunt-emann M, Varghese N, White JR, Seshadri R, Smirnova T, Kirton E, Jungbluth SP, Woyke T, Eloe-Fadrosh EA, Ivanova NN, Kyrpides NC. 2019. IMG/M v.5.0: an integrated data management and comparative analysis system for microbial genomes and microbiomes. *Nucleic Acids Res* 47:D666–D677. <https://doi.org/10.1093/nar/gky901>.
23. Varghese NJ, Mukherjee S, Ivanova N, Konstantinidis KT, Mavrommatis K, Kyrpides NC, Pati A. 2015. Microbial species delineation using whole genome sequences. *Nucleic Acids Res* 43:6761–6771. <https://doi.org/10.1093/nar/gkv657>.