AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

High-Quality Draft Genome Sequence of *Pseudomonas wadenswilerensis* CCOS 864^T

Dominik Rutz,[a,b] David Frasson,[b] Martin Sievers,[b] Jochen Blom,[c] Fabio Rezzonico,[a] Joël F. Pothier,[a] Theo H. M. Smits[a]

[a]Environmental Genomics and Systems Biology Research Group, Institute of Natural Resource Sciences, Zurich University of Applied Sciences (ZHAW), Wädenswil, Switzerland

[b]Microbiology and Molecular Biology Research Group, Institute of Chemistry and Biotechnology, Zurich University of Applied Sciences (ZHAW), Wädenswil, Switzerland

[c]Bioinformatics and Systems Biology, Justus-Liebig-Universität, Giessen, Germany

ABSTRACT *Pseudomonas wadenswilerensis* CCOS 864^T was isolated in 2014 from forest soil. The organism belongs taxonomically to the *Pseudomonas putida* group, members of which have been well studied for their potential in biotechnological applications. We present here the draft genome sequence of *P. wadenswilerensis* CCOS 864^T.

The genus *Pseudomonas* belongs to the gamma subclass of *Proteobacteria* and forms a large taxonomic grouping of species (1, 2). Members of this genus appear as Gram negative and are involved in a highly diverse range of activities (2). Pseudomonads can be isolated from many different environmental sources, including soil, water, plants, animals, and air (3). Over the years, members of the *Pseudomonas putida* group were studied because of their usage as an efficient cell factory in industrial biotechnological applications (4). Nowadays, *Pseudomonas* spp. are used for the production of bio-based polymers, small-molecular-weight chiral compounds, heterologous proteins, biosurfactants, and several biotechnologically important enzymes (lipases, proteases, and amylases) (3–5). In 2014, a new species of *Pseudomonas* was isolated during the search for novel biocatalysts. The isolate, identified as *Pseudomonas wadenswilerensis* CCOS 864^T, was obtained from soil samples collected in the Riedholz Forest in Richterswil, Switzerland (6).

Genomic DNA of *P. wadenswilerensis* CCOS 864^T, grown overnight at 28°C in LB medium, was isolated using the NucleoSpin tissue kit (Macherey-Nagel, Düren, Germany) and fragmented using the Covaris E220 ultrasonicator (average target size, 550 bp). Library preparation was done using the Illumina NeoPrep library system according to the manufacturer's instructions. Genome sequencing was done at Zurich University of Applied Sciences (ZHAW) using an Illumina MiSeq instrument (2 × 300-bp reads) with a total output of 1,960,890 reads (6). For *de novo* assembly, the SeqMan NGen software version 12.1.0 (DNASTAR, Madison, WI) with standard settings was used. After several assembly steps, a final 18 contigs and an N_{50} value of 532,738 bp were obtained. The final assembly had a total length of 5,966,942 bp and a G+C content of 63.39%. After annotation in GenDB (7), comparative genomics to related pseudomonads was performed in EDGAR version 2.3 (8).

By determination of the genome-to-genome distances values (GGDC) based on *in silico* DNA-DNA hybridization (DDH) (9) and calculation of average nucleotide identities (ANIb) with JSpeciesWS version 3.0.20 (10), we confirmed the species delineation against other species of the *P. putida* group. An average ANIb result of 92.39% ± 0.03% and GGDC of 51.2% ± 0.1% DDH were obtained with three genomes from the species *Pseudomonas donghuensis* (11, 12), while all other members of the *P. putida* group had lower ANIb and GGDC values. Therefore, the genome sequence confirms that *P.*

Received 13 August 2018 **Accepted** 1 October 2018 **Published** 25 October 2018

Citation Rutz D, Frasson D, Sievers M, Blom J, Rezzonico F, Pothier JF, Smits THM. 2018. High-quality draft genome sequence of *Pseudomonas wadenswilerensis* CCOS 864^T. Microbiol Resour Announc 7:e01059-18. https://doi.org/10.1128/MRA.01059-18.

Editor John J. Dennehy, Queens College

Address correspondence to Joël F. Pothier, joel.pothier@zhaw.ch.

wadenswilerensis CCOS 864^T constitutes a separate species distinguishable from other members of the *P. putida* group. The analysis of the genome content will still show the unique properties of this strain.

Data availability. The draft genome sequence of *P. wadenswilerensis* CCOS 864^T has been deposited in DDBJ/EMBL/GenBank under the BioProject number PRJEB27830 and the sequence accession number UIDD00000000. The version described in this paper is version UIDD01000000. Raw sequence reads (Illumina) have been deposited in the Sequence Read Archive under the accession number ERR2814815.

ACKNOWLEDGMENT

This study was supported by the Department of Life Sciences and Facility Management of the Zurich University of Applied Sciences (ZHAW) in Wädenswil, Switzerland.

REFERENCES

1. Palleroni NJ. 2015. Genus I. *Pseudomonas*, p 323–379. *In* Brenner DJ, Krieg NR, Staley JT, Garrity GM (ed), Bergey's manual of systematics of archaea and bacteria. John Wiley & Sons, Chichester, United Kingdom.
2. Timmis KN. 2002. *Pseudomonas putida*: a cosmopolitan opportunist *par excellence*. Environ Microbiol 4:779–781. https://doi.org/10.1046/j.1462-2920.2002.00365.x.
3. Peix A, Ramírez-Bahena M-H, Velázquez E. 2018. The current status on the taxonomy of *Pseudomonas* revisited: an update. Infect Genet Evol 57:106–116. https://doi.org/10.1016/j.meegid.2017.10.026.
4. Poblete-Castro I, Becker J, Dohnt K, dos Santos VM, Wittmann C. 2012. Industrial biotechnology of *Pseudomonas putida* and related species. Appl Microbiol Biotechnol 93:2279–2290. https://doi.org/10.1007/s00253-012-3928-0.
5. Kahlon RS. 2016. *Pseudomonas* for industrial biotechnology, p 282–327. *In* Kahlon RS (ed), *Pseudomonas*: molecular and applied biology. Springer, New York, NY.
6. Frasson D, Opoku M, Picozzi T, Torossi T, Balada S, Smits THM, Hilber U. 2017. *Pseudomonas wadenswilerensis* sp. nov. and *Pseudomonas reidholzensis* sp. nov., two novel species within the *Pseudomonas putida* group isolated from forest soil. Int J Syst Evol Microbiol 67:2853–2861. https://doi.org/10.1099/ijsem.0.002035.
7. Meyer F, Goesmann A, McHardy A, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A. 2003. GenDB—an open source genome annotation system for prokaryote genomes. Nucleic Acids Res 31:2187–2195. https://doi.org/10.1093/nar/gkg312.
8. Blom J, Kreis J, Spänig S, Juhre T, Bertelli C, Ernst C, Goesmann A. 2016. EDGAR 2.0: an enhanced software platform for comparative gene content analyses. Nucleic Acids Res 44:W22–W28. https://doi.org/10.1093/nar/gkw255.
9. Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. 2013. Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics 14:60. https://doi.org/10.1186/1471-2105-14-60.
10. Richter M, Rosselló-Móra R, Oliver Glöckner F, Peplies J. 2016. JSpeciesWS: a Web server for prokaryotic species circumscription based on pairwise genome comparison. Bioinformatics 32:929–931. https://doi.org/10.1093/bioinformatics/btv681.
11. Gao J, Xie G, Peng F, Xie Z. 2015. *Pseudomonas donghuensis* sp. nov., exhibiting high-yields of siderophore. Antonie Van Leeuwenhoek 107:83–94. https://doi.org/10.1007/s10482-014-0306-1.
12. Krzyzanowska DM, Ossowicki A, Jafra S. 2014. Genome sequence of *Pseudomonas* sp. strain P482, a tomato rhizosphere isolate with broad-spectrum antimicrobial activity. Genome Announc 2:e00394-14. https://doi.org/10.1128/genomeA.00394-14.