



HAL
open science

Whole-Genome Sequence of French Clinical *Olivibacter jilunii* Strain P8502

Hussein Anani, May Khodor, Didier Raoult, Pierre-Edouard Fournier

► **To cite this version:**

Hussein Anani, May Khodor, Didier Raoult, Pierre-Edouard Fournier. Whole-Genome Sequence of French Clinical *Olivibacter jilunii* Strain P8502. *Microbiology Resource Announcements*, 2019, 8 (31), 10.1128/MRA.00701-19 . hal-02481909

HAL Id: hal-02481909

<https://amu.hal.science/hal-02481909v1>

Submitted on 6 Nov 2024

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



Whole-Genome Sequence of French Clinical *Olivibacter jilunii* Strain P8502

Hussein Anani,^{a,b} May Khodor,^{b,c} Didier Raoult,^{b,c,d} Pierre-Edouard Fournier^{a,b}

^aAix Marseille Université, Institut de Recherche pour le Développement (IRD), Service de Santé des Armées, AP-HM, UMR Vecteurs Infections Tropicales et Méditerranéennes (VITROME), Institut Hospitalo-Universitaire Méditerranée Infection, Marseille, France

^bInstitut Méditerranée Infection, Marseille, France

^cAix-Marseille Université, Institut de Recherche pour le Développement (IRD), UMR Microbes Evolution Phylogeny and Infections (MEPHI), Institut Hospitalo-Universitaire Méditerranée-Infection, Marseille, France

^dSpecial Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

ABSTRACT In 2013, *Olivibacter jilunii* was reported as a bacterial species isolated from contaminated soil. In 2018, a clinical strain from the same species was isolated from the rectal swab of a Hajj pilgrim. Genome sequencing yielded 6,704,032 bp, with 41.2% G+C content, 5,406 protein-coding genes, and 54 predicted RNA genes in strain P8502.

In 2007, Ntougias et al. proposed the creation of a novel bacterial genus, *Olivibacter* gen. nov. (1), within the family *Sphingobacteriaceae* in the phylum *Bacteroidetes* (2). Currently, this genus includes nine species with validly published names (3), as follows: *Olivibacter sitiensis*, the first species of the *Olivibacter* genus that was isolated from alkaline olive oil mill wastes in the region of Sitia, Crete in Greece (1), *O. soli*, *O. ginsengisoli*, *O. terrae* (4), *O. oleidegradans* (5), *O. jilunii* (6), *O. composti* (7), *O. domesticus* (8), and *O. ginsenosidimutans* (8). In 2018, we isolated from a fecal sample of a healthy Hajj pilgrim strain P8502 using the culturomics approach, an approach based on the use of a large panel of growing conditions (9–11). Growth was obtained after 24 h of culture in 5% sheep blood-enriched Columbia agar (bioMérieux, Marcy l'Etoile, France) in a strict aerobic atmosphere at 37°C. This bacterium exhibited 99.53% 16S rRNA sequence similarity with *O. jilunii* strain 14-2A^T (=KCTC23098^T =CCTCAB2010105^T), its closest phylogenetic neighbor. *O. jilunii* strain 14-2A^T was isolated during the study of culturable heterotrophic bacteria in dichlorodiphenyltrichloroethane (DDT)-contaminated soil collected from a DDT production plant in Jiangsu, China (6). In our laboratory, DNA of *O. jilunii* strain P8502 was extracted using an EZ1 biorobot with the EZ1 DNA tissue kit (Qiagen). DNA was quantified by a Qubit assay with the high-sensitivity kit (Life Technologies, Carlsbad, CA, USA) at 0.2 µg/µl and was sequenced with the MiSeq platform (Illumina, Inc., San Diego, CA, USA). The DNA was fragmented and amplified by limited PCR (12 cycles), introducing dual-index barcodes and sequencing adapters. After purification on AMPure XP beads (Beckman Coulter, Inc., Fullerton, CA, USA), the libraries were normalized and pooled for sequencing on the MiSeq platform. Paired-end sequencing and automated cluster generation with dual-indexed 2 × 251-bp reads were performed during a 40-h run. Total information of 8.2 Gb was obtained from a 1,207,000/mm² cluster density with a cluster passing quality control filters of 89.3% (10,507.2 passed filtered reads). Reads were quality checked using FastQC and trimmed using Trimmomatic version 0.36.6 (12). MiSeq reads were assembled using the SPAdes version 3.5.0 software (13). The option “careful” was used in order to reduce the number of mismatches and short indels. Default parameters were applied for k values, i.e., k-mer values of 127, 99, 77, 55, 33, and 21. SSPACE (14) and GapFiller (15) were used to combine

Citation Anani H, Khodor M, Raoult D, Fournier P-E. 2019. Whole-genome sequence of French clinical *Olivibacter jilunii* strain P8502. *Microbiol Resour Announc* 8:e00701-19. <https://doi.org/10.1128/MRA.00701-19>.

Editor Frank J. Stewart, Georgia Institute of Technology

Copyright © 2019 Anani 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 Pierre-Edouard Fournier, pierre-edouard.fournier@univ-amu.fr.

Received 26 June 2019

Accepted 8 July 2019

Published 1 August 2019

contigs, using default parameters. The draft genome sequence of *O. jilunii* strain P8502 is composed of 23 contigs (N_{50} , 537,034 bp; L_{50} , 4) and 21 scaffolds (N_{50} , 643,697 bp; L_{50} , 3), for a total of 6,704,032 bp with 42.1% G+C content. Annotation using Prokka (version 1.12) (16) predicted 5,524 genes, including 5,406 protein-coding genes, 3,498 of which (63.32%) are assigned to clusters of orthologous groups. In addition, 51 RNA genes were detected (6 rRNAs and 45 tRNAs). In addition, 43 resistance genes are predicted, including 3 genes associated with antibiotic resistance (tetracycline). No toxin/antitoxin module or bacteriocin-associated gene could be found.

Data availability. The draft genome and read sequences (raw sequences) of *O. jilunii* strain P8502 have been deposited at GenBank/EBI under the accession numbers [UWUA01000001](https://www.ncbi.nlm.nih.gov/nuccore/UWUA01000001) to [UWUA01000023](https://www.ncbi.nlm.nih.gov/nuccore/UWUA01000023) and [ERR3393031](https://www.ncbi.nlm.nih.gov/nuccore/ERR3393031), respectively.

ACKNOWLEDGMENTS

This study was supported by the Méditerranée Infection Foundation, the National Research Agency, under the program “Investissements d’avenir,” reference ANR-10-IAHU-03, and by Région Provence Alpes Côte d’Azur and European funding FEDER PRIMI.

We declare no financial or nonfinancial competing interests.

REFERENCES

- Ntougias S, Fasseas C, Zervakis GI. 2007. *Olivibacter sitiensis* gen. nov., sp. nov., isolated from alkaline olive-oil mill wastes in the region of Sitia. *Int J Syst Evol Microbiol* 57:398–404. <https://doi.org/10.1099/ijs.0.64561-0>.
- Steyn PL, Segers P, Vancanneyt M, Sandra P, Kersters K, Joubert JJ. 1998. Classification of heparinolytic bacteria into a new genus, *Pedobacter*, comprising four species: *Pedobacter heparinus* comb. nov., *Pedobacter piscium* comb. nov., *Pedobacter africanus* sp. nov. and *Pedobacter saltans* sp. nov. Proposal of the family Sphingobacteriaceae fam. nov. *Int J Syst Bacteriol* 48:165–177. <https://doi.org/10.1099/00207713-48-1-165>.
- Parte AC. 2018. LPSN—List of Prokaryotic names with Standing in Nomenclature (bacterio.net), 20 years on. *Int J Syst Evol Microbiol* 68:1825–1829. <https://doi.org/10.1099/ijsem.0.002786>.
- Wang L, Ten LN, Lee H-G, Im W-T, Lee S-T. 2008. *Olivibacter soli* sp. nov., *Olivibacter ginsengisoli* sp. nov. and *Olivibacter terrae* sp. nov., from soil of a ginseng field and compost in South Korea. *Int J Syst Evol Microbiol* 58:1123–1127. <https://doi.org/10.1099/ijs.0.65299-0>.
- Szabó I, Szoboszlay S, Kriszt B, Hahn J, Harkai P, Baka E, Tancsics A, Kaszab E, Privler Z, Kukolya J. 2011. *Olivibacter oleidegradans* sp. nov., a hydrocarbon-degrading bacterium isolated from a biofilter clean-up facility on a hydrocarbon-contaminated site. *Int J Syst Evol Microbiol* 61:2861–2865. <https://doi.org/10.1099/ijs.0.026641-0>.
- Chen K, Tang S-K, Wang G-L, Nie G-X, Li Q-F, Zhang J-D, Li W-J, Li S-P. 2013. *Olivibacter jilunii* sp. nov., isolated from DDT-contaminated soil. *Int J Syst Evol Microbiol* 63:1083–1088. <https://doi.org/10.1099/ijs.0.042416-0>.
- Lin Y, Hameed A, Chiu KY, Liu YC, Hsu YH, Lai WA, Young CC. 2017. *Olivibacter composti* sp. nov., isolated from compost collected at a greenhouse. *Int J Syst Evol Microbiol* 67:148–152. <https://doi.org/10.1099/ijsem.0.001593>.
- Siddiqi MZ, Liu Q, Lee SY, Choi KD, Im WT. 2018. *Olivibacter ginsenosidimitans* sp. nov., with ginsenoside converting activity isolated from compost, and reclassification of *Pseudosphingobacterium domesticum* as *Olivibacter domesticum* comb. nov. *Int J Syst Evol Microbiol* 68:2509–2514. <https://doi.org/10.1099/ijsem.0.002819>.
- Lagier J-C, Armougom F, Million M, Hugon P, Pagnier I, Robert C, Bittar F, Fournous G, Gimenez G, Maraninchi M, Trape J-F, Koonin EV, La Scola B, Raoult D. 2012. Microbial culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect* 18:1185–1193. <https://doi.org/10.1111/1469-0691.12023>.
- Lagier J-C, Hugon P, Khelaifia S, Fournier P-E, La Scola B, Raoult D. 2015. The rebirth of culture in microbiology through the example of culturomics to study human gut microbiota. *Clin Microbiol Rev* 28:237–264. <https://doi.org/10.1128/CMR.00014-14>.
- Lagier J-C, Khelaifia S, Alou MT, Ndongo S, Dione N, Hugon P, Caputo A, Cadoret F, Traore SI, Seck EH, Dubourg G, Durand G, Mourembou G, Guilhot E, Togo A, Bellali S, Bachar D, Cassir N, Bittar F, Delerce J, Mailhe M, Ricaboni D, Bilen M, Dangui Nieko NPM, Dia Badiane NM, Valles C, Mouelhi D, Diop K, Million M, Musso D, Abrahão J, Azhar EI, Bibi F, Yasir M, Diallo A, Sokhna C, Djossou F, Vitton V, Robert C, Rolain JM, La Scola B, Fournier P-E, Levasseur A, Raoult D. 2016. Culture of previously uncultured members of the human gut microbiota by culturomics. *Nat Microbiol* 1:16203. <https://doi.org/10.1038/nmicrobiol.2016.203>.
- Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics* 27:578–579. <https://doi.org/10.1093/bioinformatics/btq683>.
- Boetzer M, Pirovano W. 2012. Toward almost closed genomes with Gap-Filler. *Genome Biol* 13:R56. <https://doi.org/10.1186/gb-2012-13-6-r56>.
- Torsten S. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <https://doi.org/10.1093/bioinformatics/btu153>.