Check for updates

Whole-Genome Sequence of *Pseudomonas* sp. Strain 1239, Isolated from Soil in Western France

Julien Crovadore,ᵃ Damien Grizard,ᵇ Romain Chablais,ᵃ Bastien Cochard,ᵃ Philippe Blanc,ᶜ François Lefortᵃ

ᵃPlants and Pathogens Group, Research Institute Land Nature and Environment, hepia, HES-SO University of Applied Sciences and Arts Western Switzerland, Geneva, Switzerland
ᵇProxis Développement, Levallois-Perret, France
ᶜBioprox, Noyant, France

ABSTRACT We report here the draft genome sequence of *Pseudomonas* sp. strain 1239, a bacterium that is potentially usable as a biostimulant for agriculture or in depollution. Its genome encodes resistance to mercury, heavy metals, and several antibiotics. It is potentially able to produce marinocine, a broad-spectrum antibiotic.

*P*seudomonas spp. are aerobic rod-shaped and motile bacteria and ubiquitous residents of various terrestrial and aquatic environments (1). Very few are opportunistic pathogens of plants and animals. While most species are commensals, some are beneficial to plants (2–4) or usable in depollution (5, 6). *Pseudomonas* sp. strain 1239 was isolated from soil samples from the lower Loire Valley in western France and initially identified by biochemical profiling and morphology as *Pseudomonas fluorescens*, whereas 16S rRNA gene sequencing showed 99% shared identity with *Pseudomonas putida*.

DNA was extracted with a modified cetyltrimethylammonium bromide (CTAB) protocol (7) from a culture grown exponentially from a single colony in King B broth. A sequencing library was built with the TruSeq Nano DNA library preparation kit (Illumina, USA). Whole-genome sequencing (WGS) was performed using a MiniSeq high-output kit, within one Illumina MiniSeq run at 2×151-bp paired-end read length, and resulted in $309\times$ genome coverage. The overall quality metrics of the reads were assessed with FastQC version 0.11.5 (8). Genome assembly was computed with the SPAdes genome assembler 3.10 (9), with a setting of "paired-end assembly, careful mode," yielded 68 contigs ($\geq$ 200 bp), was ordered with BioEdit version 7.0.5 (10), and was analyzed with QUAST version 4.6.3 (11), with the setting of "QUAST: skip contigs shorter than 200 bp." The genome's total length is 6,024,399 bp, with a GC content of 64.03% and an N_{50} value of 244,210 bp.

A blast analysis of the complete 16S rRNA gene showed that this strain shares 82% identity with *Pseudomonas alkylphenolica* sp. nov. strain KL28 (12). Automated gene annotation carried out by the Prokaryotic Genome Annotation Pipeline (PGAP) version 4.1 (13) identified 5,538 coding sequences and 89 RNA genes, while RAST version 2.0 (14), using the ClassicRAST annotation scheme, detected 5,376 coding sequences and 76 RNA genes. RAST found a partial prophage genome (24 genes) on contig 61. PlasmidFinder version 1.3 (15) and plasmidSPAdes (16), both using default settings, did not detect any plasmids. Five genes code for auxin synthesis. Siderophore sensing, transport, and reception are encoded by 34 genes, while 26 other genes encode siderophore synthesis and secretion, with 19 genes arranged in a pyoverdin gene cluster. This strain also has two complete type II and VI secretion systems (T2SS and T6SS, respectively) organized in operons. Two genes, *lodA* and *lodB*, might encode the production of marinocine, a broad-spectrum antibiotic (17, 18). Degradation of aromatic compounds is suggested by 118 genes. Like *Pseudomonas putida* strain DRA525

(19), the presence of a mercury ion reductase gene and some genes of the mercury operon (*merA, merP, merT,* and *merR*) would ensure resistance to mercury. Similarly, multiple copies of the genes *arsB, arsC, arsH, arsR,* and *acr3* would provide resistance to arsenic. A putative resistance to heavy metals is provided by 73 genes, including multiple copies of the genes *czcD, czcA, czcC, cusB* or *czsB, cusA,* and *czrR* and genes coding for heavy metal sensor histidine kinases. A complete MexE-MexF-OprN multi-drug efflux system predicts tolerance to heavy metals and antibiotics. These characteristics make this strain interesting for agriculture and soil depollution.

Data availability. This whole-genome shotgun project was deposited at DDBJ/EMBL/GenBank under the accession number NFSA00000000. The version described in this paper is the first version, NFSA01000000. The 68 contigs have been deposited under the accession numbers NFSA01000001 to NFSA01000068. Raw sequencing data sets have been registered in the NCBI Sequence Read Archive database (20) under the accession number SRR5515064.

REFERENCES

1. Peix A, Ramírez-Bahena M-H, Velázquez E. 2009. Historical evolution and current status of the taxonomy of genus *Pseudomonas*. Infect Genet Evol 9:1132–1147. https://doi.org/10.1016/j.meegid.2009.08.001.
2. Weller DM. 2007. *Pseudomonas* biocontrol agents of soilborne pathogens: looking back over 30 years. Phytopathology 97:250–256. https://doi.org/10.1094/PHYTO-97-2-0250.
3. Beneduzi A, Ambrosini A, Passaglia LMP. 2012. Plant growth-promoting rhizobacteria (PGPR): their potential as antagonists and biocontrol agents. Genet Mol Biol 35:1044–1051. https://doi.org/10.1590/S1415-47572012000600020.
4. Haas D, Défago G. 2005. Biological control of soil-borne pathogens by fluorescent pseudomonads. Nat Rev Microbiol 3:307–319. https://doi.org/10.1038/nrmicro1129.
5. Karigar CS, Rao SS. 2011. Role of microbial enzymes in the bioremediation of pollutants: a review. Enzyme Res 2011:805187. https://doi.org/10.4061/2011/805187.
6. Peixoto RS, Vermelho AB, Rosado AS. 2011. Petroleum-degrading enzymes: bioremediation and new prospects. Enzyme Res 2011:475193. https://doi.org/10.4061/2011/475193.
7. Lefort F, Douglas GC. 1999. An efficient micro-method of DNA isolation from mature leaves of four hardwood tree species *Acer*, *Fraxinus*, *Prunus* and *Quercus*. Ann Forest Sci 56:259–263.
8. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.
9. Bankevich A, Nurk S, Antipov D, Gurevich A, Dvorkin M, Kulikov A, Lesin V, Nikolenko S, Pham S, Prjibelski A, Pyshkin A, Sirotkin A, Vyahhi N, Tesler G, Alekseyev M, Pevzner P. 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.
10. Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser 41:95–98.
11. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
12. Mulet M, Sánchez D, Lalucat J, Lee K, García-Valdés E. 2015. *Pseudomonas alkylphenolica* sp. nov., a bacterial species able to form special aerial structures when grown on p-cresol. Int J Syst Evol Microbiol 65:4013–4018. https://doi.org/10.1099/ijsem.0.000529.
13. 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.
14. Aziz RK, Bartels D, Best AA, 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 9:75–90. https://doi.org/10.1186/1471-2164-9-75.
15. Carattoli A, Zankari E, Garcia-Fernandez A, Voldby Larsen M, Lund O, Villa L, Aarestrup FM, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. Agents Chemother Antimicrob 58:3895–3903. https://doi.org/10.1128/AAC.02412-14.
16. Antipov D, Hartwick N, Shen M, Raiko M, Lapidus A, Pevzner P. 2016. plasmidSPAdes: assembling plasmids from whole genome sequencing data. Bioinformatics 32:3380–3387. https://doi.org/10.1093/bioinformatics/btw493.
17. Lucas-Elio P, Hernandez P, Sanchez-Amat A, Solano F. 2005. Purification and partial characterization of marinocine, a new broad-spectrum antibacterial protein produced by *Marinomonas mediterranea*. Biochim Biophys Acta 1721:193–203. https://doi.org/10.1016/j.bbagen.2004.11.002.
18. Lucas-Elío P, Gómez D, Solano F, Sanchez-Amat A. 2006. The antimicrobial activity of marinocine, synthesized by *Marinomonas mediterranea*, is due to hydrogen peroxide generated by its lysine oxidase activity. J Bacteriol 188:2493–2501. https://doi.org/10.1128/JB.188.7.2493-2501.2006.
19. Drace K, Giangiuli S, LeSar C, Kiefer AM. 2018. Draft genome sequence of mercury-resistant *Pseudomonas putida* strain DRA525. Genome Announc 6:e00370-18. https://doi.org/10.1128/genomeA.00370-18.
20. Leinonen R, Sugawara H, Shumway M. 2011. The Sequence Read Archive. Nucleic Acids Res 39:D19–D21. https://doi.org/10.1093/nar/gkq1019.