

Draft Genome Sequence of *Empedobacter* (Formerly *Wautersiella*) *falsenii* comb. nov. Wf282, a Strain Isolated from a Cervical Neck Abscess

German Matías Traglia,^a Chelsea Dixon,^f Kevin Chiem,^f Marisa Almuzara,^b Claudia Barberis,^b Sabrina Montaña,^a Cindy Merino,^f María Alejandra Mussi,^e Marcelo E. Tolmasky,^f Andres Iriarte,^{c,d} Carlos Vay,^b María Soledad Ramírez^f

Instituto de Microbiología y Parasitología Médica (IMPAM, UBA-CONICET), Buenos Aires, Argentina^a; Laboratorio de Bacteriología Clínica, Departamento de Bioquímica Clínica, Hospital de Clínicas José de San Martín, Facultad de Farmacia y Bioquímica, Buenos Aires, Argentina^b; Departamentos de Bioquímica y Genómica Microbianas and Genómica, IIBCE, Montevideo, Uruguay^c; Departamento de Desarrollo Biotecnológico, Facultad de Medicina, Instituto de Higiene, UdelaR, Montevideo, Uruguay^d; Centro de Estudios Fotosintéticos y Bioquímicos (CEFOBI- CONICET), Rosario, Argentina^e; Department of Biological Science, Center for Applied Biotechnology Studies, California State University Fullerton, Fullerton, California, USA^f

***Empedobacter* (formerly *Wautersiella*) *falsenii* comb. nov. strain Wf282 was isolated from a cervical neck abscess sample from an 18-year-old female patient. The isolate was resistant to many antibiotics, including meropenem and colistin. The total DNA from the multidrug-resistant *E. falsenii* comb. nov. Wf282 clinical isolate was sequenced.**

Received 18 February 2015 Accepted 23 February 2015 Published 2 April 2015

Citation Traglia GM, Dixon C, Chiem K, Almuzara M, Barberis C, Montaña S, Merino C, Mussi MA, Tolmasky ME, Iriarte A, Vay C, Ramírez MS. 2015. Draft genome sequence of *Empedobacter* (formerly *Wautersiella*) *falsenii* comb. nov. Wf282, a strain isolated from a cervical neck abscess. *Genome Announc* 3(2):e00235-15. doi:10.1128/genomeA.00235-15.

Copyright © 2015 Traglia et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to María Soledad Ramírez, msramirez@fullerton.edu.

Empedobacter (formerly *Wautersiella*) *falsenii* comb. nov. was first described in 2006 and renamed in 2014 (1, 2). Its phenotype resembles members of the genera *Chryseobacterium* and *Empedobacter*. *E. falsenii* comb. nov. is a nonmotile Gram-negative rod that grows aerobically at 20, 30, and 37°C on standard medium, such as tryptic soy agar or blood agar. In the year 2012, the first isolation of *Wautersiella falsenii* from a urine sample of an infant with a complicated urinary tract infection was described (3).

E. falsenii comb. nov. strain Wf282 was isolated from a cervical neck abscess sample from an 18-year-old female patient who was admitted to the otolaryngology service with acute otitis media. The nonfermenting Gram-negative rods were identified as *E. falsenii* using a matrix-assisted laser desorption/ionization-time of flight mass spectrometer (MALDI-TOF MS) (Bruker, Germany), with a score of 2.074 (probable species-level identification). Antibiotic susceptibility testing was performed using the Vitek 2 system, employing the panel AST-079 (Gram-negative susceptibility [GNS] card). The MIC results were interpreted using the CLSI breakpoints (4) for other non-*Enterobacteriaceae*, except for ampicillin, cephalothin, and cefoxitin, for which those for *Enterobacteriaceae* were used. *E. falsenii* comb. nov. strain Wf282 was resistant to ampicillin (≥ 32 $\mu\text{g/ml}$), ampicillin-sulbactam (≥ 32 $\mu\text{g/ml}$), cephalothin (≥ 32 $\mu\text{g/ml}$), meropenem (≥ 16 $\mu\text{g/ml}$), and colistin (8 $\mu\text{g/ml}$); intermediate to piperacillin-tazobactam (64 $\mu\text{g/ml}$), cefotaxime (16 $\mu\text{g/ml}$), ceftazidime (16 $\mu\text{g/ml}$), imipenem (8 $\mu\text{g/ml}$), and ciprofloxacin (2 $\mu\text{g/ml}$); and susceptible to cefepime (4 $\mu\text{g/ml}$), amikacin (8 $\mu\text{g/ml}$), gentamicin (2 $\mu\text{g/ml}$), and trimethoprim-sulfamethoxazole (2 $\mu\text{g/ml}$).

Whole-genome shotgun sequencing was performed using Illumina MiSeq-I, using Nextera XT libraries for sample prep-

aration. The reads were assembled with the Ray assembler (<http://denovoassembler.sourceforge.net>). A total of 1,076,192 high-quality paired-end reads were produced, with an average insertion size of 825 bp. *De novo* assembly was performed with the SPAdes assembler version 3.1.0 (5), using a preassembly approach with Velvet (6). Of the generated reads, 99.9% were mapped, resulting in a mean nucleotide coverage of $65\times$ (and a *k*-mer coverage of 29.9). The corrected reads showed an average length of 230 bp. The assembled contigs sum 3,738,626 base pairs, with an N_{50} contig size of 113,944 (max length, 279,129) and a G+C content of 32.24%.

Since this isolate is resistant to many antibiotics, including meropenem and colistin, the future detailed analysis of the genome of this strain (Wf282) might lead us to find novel antibiotic resistance traits that may explain its phenotype, as well as its potential role as a reservoir of antibiotic resistance genes.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JSYQ000000000](https://www.ncbi.nlm.nih.gov/nuclseq/JSYQ000000000). The version described in this paper is version JSYQ01000000.

ACKNOWLEDGMENTS

G.M.T. and S.M. have doctoral fellowships from CONICET. This study was supported by grants to C.V. from UBACyT 2014–2017, Buenos Aires, Argentina, and by Public Health Service grant 2R15AI047115-04 from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, to M.E.T.

REFERENCES

1. Kämpfer P, Avesani V, Janssens M, Charlier J, De Baere T, Vaneechoutte M. 2006. Description of *Wautersiella falsenii* gen. nov., sp. nov., to accommodate clinical isolates phenotypically resembling members of the genera

- Chryseobacterium* and *Empedobacter*. Int J Syst Evol Microbiol 56: 2323–2329. <http://dx.doi.org/10.1099/ijs.0.64393-0>.
2. Zhang RG, Tan X, Liang Y, Meng TY, Liang HZ, Lv J. 2014. Description of *Chishuiella changwenlii* gen. nov., sp. nov., isolated from freshwater, and transfer of *Wautersiella falsenii* to the genus *Empedobacter* as *Empedobacter falsenii* comb. nov. Int J Syst Evol Microbiol 64:2723–2728. <http://dx.doi.org/10.1099/ijs.0.063115-0>.
3. Van der Velden LB, de Jong AS, de Jong H, de Gier RP, Rentenaar RJ. 2012. First report of a *Wautersiella falsenii* isolated from the urine of an infant with pyelonephritis. Diagn Microbiol Infect Dis 74:404–405. <http://dx.doi.org/10.1016/j.diagmicrobio.2012.08.008>.
4. Clinical and Laboratory Standard Institute. 2013. Performance standards for antimicrobial susceptibility testing; 23rd informational supplement M100-S23. Clinical and Laboratory Standard Institute, Wayne, PA.
5. 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. <http://dx.doi.org/10.1089/cmb.2012.0021>.
6. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.