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GENOME SEQUENCES

Draft Genome Sequence of *Citrobacter gillenii* MBT-C3, Isolated from Lamb's Lettuce

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ABSTRACT The genome of the streptomycin-resistant *Citrobacter gillenii* strain MBT-C3, isolated from lamb's lettuce in Germany, was sequenced. Sequence analysis showed the assembled draft genome size to be 5,167,205 bp, containing a predicted total of 5,011 protein-encoding genes, 8 rRNAs, and 71 tRNAs.

Citrobacter spp. are opportunistic human pathogens which can cause serious diseases in neonates, children, and immunocompromised patients (1, 2). *Citrobacter* spp. occur in the soil, in water, in food, and in the gastrointestinal tract in humans and animals and have been reported to cause diseases, such as sepsis and respiratory and urinary tract infections (2). The microbiological and medical importance of these bacteria stems from not only their pathogenicity but also the appearance of strains with multiple resistance to antibiotics used in therapy.

Currently, the genus *Citrobacter* comprises 15 species, of which *C. gillenii* was first described by Brenner et al. (3). Before that time, this species was known as *Citrobacter* genomospecies 10, and strains of this species were isolated from human and animal stool, human urine, and human blood (4). The most recently described *Citrobacter* species is *C. portucalensis*, which was isolated from a water well sample collected in Cantanhede, a city in the Centro Region of Portugal, in 2017 (5). We recently reported the draft genome sequence of a multidrug-resistant *C. portucalensis* strain isolated from vegetables (*Piper guineense,* also known as Ashanti pepper or uziza) in Africa (6). In this study, we sequenced the genome of a novel streptomycin-resistant *C. gillenii* strain, MBT-C3, isolated from lamb's lettuce grown in Germany.

The *Citrobacter gillenii* MBT-C3 strain was grown overnight in brain heart infusion (BHI) broth, and the genomic DNA was extracted using the ZR fungal/bacterial DNA miniprep kit (Zymo Research, Freiburg, Germany) and quantified using a Qubit 3 fluorometer (Invitrogen, Darmstadt, Germany). For sequencing, the Nextera XT DNA library preparation kit and the MiSeq reagent kit version 2 were used, according to the manufacturers' instructions, using a MiSeq sequencer (Illumina, Munich, Germany). Raw sequencing data were quality trimmed using Trimmomatic (7); the 401,324 filtered paired-end reads (2 × 250 bp) and 46,088 filtered unpaired-end reads (250 bp) were *de novo* assembled into 37 contigs, with a total length of 5,167,205 bp and a G+C content of 52.52 mol%, using SPAdes version 3.12.0 (8). The assembled genome showed 24-fold coverage, and the N_{50} value was 413,666 bp. The genome annotation was performed automatically with RAST (9), and a manual comparison of predicted open reading frames (ORFs) with proteins was carried out using PATRIC (10). The genome sequence annotation showed 5,011 predicted genes, 71 tRNA, 6 5S rRNA, 1 16S rRNA, and 1 23S rRNA gene. None of the contigs were identified as a plasmid-related sequence by the PlasmidFinder pipeline (11). In addition, *in silico* DNA-DNA hybridization was carried out using the Genome-to-Genome Distance Calculator (GGDC) (12). The results showed that the *C. gillenii* MBT-C3 genome was distinct from the genomes of representative strains of related species (i.e., *Citrobacter braakii* CIP 104554^{T}, *Citrobacter werkmanii*

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BF6^T, *C. freundii* ATCC 8090^T, and *C. portucalensis* A60^T), with similarity values of 31.6%, 31.5%, 31.4%, and 31.7%, respectively.

Data availability. The whole-genome shotgun project of *C. gillenii* MBT-C3 has been deposited at DDBJ/ENA/GenBank under the accession no. QVEK00000000 (BioProject no. PRJNA485440).

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REFERENCES

1. Badger JL, Stins MF, Kim KS. 1999. *Citrobacter freundii* invades and replicates in human brain microvascular endothelial cells. Infect Immun 67:4208–4215.
2. Liu L, Lan R, Liu L, Wang Y, Zhang Y, Wang Y, Xu J. 2017. Antimicrobial resistance and cytotoxicity of *Citrobacter* spp. in Maanshan Anhui Province, China. Front Microbiol 8:1357. https://doi.org/10.3389/fmicb.2017.01357.
3. Brenner DJ, O'Hara CM, Grimont PA, Janda JM, Falsen E, Aldova E, Ageron E, Schindler J, Abbott SL, Steigerwalt AG. 1999. Biochemical identification of *Citrobacter* species defined by DNA hybridization and description of *Citrobacter gillenii* sp. nov. (formerly *Citrobacter* genomospecies 10) and *Citrobacter murliniae* sp. nov. (formerly *Citrobacter* genomospecies 11). J Clin Microbiol 37:2619–2624.
4. Brenner DJ, Grimont PAD, Steigerwalt AG, Fanning GR, Ageron E, Riddle CF. 1993. Classification of citrobacteria by DNA hybridization: designation of *Citrobacter farmeri* sp. nov., *Citrobacter youngae* sp. nov., *Citrobacter braakii* sp. nov., *Citrobacter werkmanii* sp. nov., *Citrobacter sedlakii* sp. nov., and three unnamed *Citrobacter genomospecies*. Int J Syst Bacteriol 43:645–658. https://doi.org/10.1099/00207713-43-4-645.
5. Ribeiro TG, Goncalves BR, da Silva MS, Novais A, Machado E, Carrico JA, Peixe L. 2017. *Citrobacter portucalensis* sp. nov., isolated from an aquatic sample. Int J Syst Evol Microbiol 67:3513–3517. https://doi.org/10.1099/ijsem.0.002154.
6. Igbinosa EO, Rathje J, Habermann D, Brinks E, Cho G-S, Franz CMAP. 2018. Draft genome sequence of multidrug-resistant strain *Citrobacter portucalensis* MBTC-1222, isolated from uziza (*Piper guineense*) leaves in Nigeria. Genome Announc 6:e00123-18. https://doi.org/10.1128/genomeA.00123-18.
7. 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.
8. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski 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.
9. 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. https://doi.org/10.1186/1471-2164-9-75.
10. Wattam AR, Abraham D, Dalay O, Disz TL, Driscoll T, Gabbard JL, Gillespie JJ, Gough R, Hix D, Kenyon R, Machi D, Mao C, Nordberg EK, Olson R, Overbeek R, Pusch GD, Shukla M, Schulman J, Stevens RL, Sullivan DE, Vonstein V, Warren A, Will R, Wilson MJC, Yoo HS, Zhang C, Zhang Y, Sobral BW. 2014. PATRIC, the bacterial bioinformatics database and analysis resource. Nucleic Acids Res 42:D581–D591. https://doi.org/10.1093/nar/gkt1099.
11. Carattoli A, Zankari E, García-Fernández A, Voldby Larsen M, Lund O, Villa L, Møller Aarestrup F, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. Antimicrob Agents Chemother 58:3895–3903. https://doi.org/10.1128/AAC.02412-14.
12. 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.