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GENOME SEQUENCES

Draft Genome Sequence of Multidrug-Resistant *Enterococcus faecium* Strain E1298, with a Sequence Type 1274 Profile, Recovered from the Cloacal Microbiome of a Tropical Screech Owl (*Megascops choliba*) in Rio de Janeiro, Brazil

Andréa Andrade Rangel Freitas,[a] Stephanie Silva Rodrigues Souza,[a,b] Adriana Rocha Faria,[a,c] Paul J. Planet,[d,e,f] Vânia Lúcia Carreira Merquior,[b] Lúcia Martins Teixeira[a]

[a]Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
[b]Faculdade de Ciências Médicas, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
[c]Faculdade de Medicina, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, Brazil
[d]Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, USA
[e]Pediatric Infectious Disease Division, Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, USA
[f]Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, New York, USA

ABSTRACT Here, we present the draft genome sequence of *Enterococcus faecium* strain E1298, a representative of the clonal complex 17 (CC17), identified as sequence type 1274 (ST1274) and resistant to multiple classes of antimicrobials, isolated from the cloaca of a tropical screech owl (*Megascops choliba*) in Rio de Janeiro, Brazil.

Certain multidrug-resistant lineages of *Enterococcus faecium* are recognized as important agents of health care-associated infections and public health threats (1–3). Most of these lineages belong to clonal complex 17 (CC17), which is disseminated throughout the world (3–5). Carriage of high-risk *E. faecium* strains by wild birds has been recently reported (6–8), but the role of birds in the dissemination of these microorganisms is still uncertain.

Here, we present the draft genome sequence of *Enterococcus faecium* E1298, a multidrug-resistant strain belonging to sequence type 1274 (ST1274), a member of CC17 (http://pubmlst.org/efaecium). The strain was isolated from a tropical screech owl (*Megascops choliba*), a common owl in urban environments, that was admitted in October 2013 to a wildlife rehabilitation center in Rio de Janeiro, Brazil. A cloacal content sample was collected using a swab (Transystem with Amies medium; Copan, Brescia, Italy) and inoculated into Enterococcosel broth (BD Microbiology Systems, Cockeysville, MD, USA). After incubation for 24 h at 37°C, an aliquot of the broth culture was streaked onto an Enterococcosel agar plate (BD Microbiology Systems) and incubated under the same conditions.

For DNA extraction, a single bacterial colony grown on a blood agar plate was inoculated into 5 ml of tryptic soy broth and incubated overnight at 37°C. Genomic DNA was obtained from 1.5 ml of that culture using a Wizard genomic DNA purification kit (Promega, Madison, WI, USA), prepped using the Nextera XT kit, and sequenced on a HiSeq 2500 sequencer (Illumina, Inc., San Diego, CA, USA) with 125-bp paired-end reads. A total of 344,111 paired-end Illumina reads and 51,960,761 bp were obtained. Reads were trimmed using Trimmomatic 0.38 (9), and quality metrics were assessed by FastQC v0.11.18 (10). High-quality reads were assembled by the autoassembly strategy and annotated using the RAST tool kit (RASTtk) in the genome annotation service of the Pathosystems Resource Integration Center (PATRIC 3.4.11) (11), leading to the predic-

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Address correspondence to Lúcia Martins Teixeira, lmt2@micro.ufrj.br.

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tion of 51 tRNAs and 3 rRNAs and the identification of 2,945 coding sequences (CDS). The draft genome has a total size of 2,897,331 bp with a G+C content of 37.79% and consists of 117 contigs (N_{50} length of 59,074 bp), with a coverage of 18×.

A comparison of amino acid polymorphisms detected in the C-terminal region of PBP5 (coded by the *pbp5* gene) with a reference sequence (GenBank accession number X84860) showed the polymorphisms Met485Ala, Ala499Thr, Glu629Val, and Pro667Ser and the insertion of serine after position 466, associated, when combined, with high-level resistance to β-lactam antibiotics in *E. faecium* strains from animals and humans (1, 12). Alignment of the *parC* and *gyrA* genes with the *E. faecium* DO genome (GenBank accession number CP003583) and quinolone resistance-determining regions (QRDRs) (GenBank accession numbers AF060881 and AB017811) revealed single amino acid polymorphisms in codons 82 (Ser to Ile) and 84 (Ser to Arg), respectively.

Using the ResFinder 3.1 tool (13), we identified the following genes: *ant(6)-Ia*, *aph(2′)-Id*, *aph(3′)-III*, and *sat-4* (aminoglycoside resistance); *msrC* and *erm(B)* (macrolide, lincosamide, and streptogramin B resistance); *lnu*(B) (lincosamide resistance); and *tet*(M) (tetracycline resistance). The *acm* and *efaAfm* virulence genes were identified by VirulenceFinder 2.0 (14). Plasmids of the rep1, repUS15, and rep14 families were detected using PlasmidFinder 2.0 (15), and Phast (16) predicted two incomplete prophage regions. No sequences associated with a CRISPR region were identified by using the CRISPRFinder (17).

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number RCFR00000000. The version described in this paper is the first version, RCFR01000000. Raw sequence reads have been deposited in the NCBI Sequence Read Archive (SRA) under the BioProject accession number PRJNA494878.

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REFERENCES

1. Torres C, Alonso CA, Ruiz-Ripa L, León-Sampedro R, Del Campo R, Coque TM. 2018. Antimicrobial resistance in *Enterococcus* spp. of animal origin. Microbiol Spectr 6:ARBA-0032-2018. https://doi.org/10.1128/microbiolspec.ARBA-0032-2018.
2. Guzman Prieto AM, van Schaik W, Rogers MRC, Coque TM, Baquero F, Corander J, Willems RJL. 2016. Global emergence and dissemination of enterococci as nosocomial pathogens: attack of the clones? Front Microbiol 7:788. https://doi.org/10.3389/fmicb.2016.00788.
3. Lee T, Pang S, Abraham S, Coombs GW. 2019. Antimicrobial resistant CC17 *Enterococcus faecium*: the past, the present and the future. J Glob Antimicrob Resist 16:36–47. https://doi.org/10.1016/j.jgar.2018.08.016.
4. Homan WL, Tribe D, Poznanski S, Li M, Hogg G, Spalburg E, Van Embden JD, Willems RJ. 2002. Multilocus sequence typing scheme for *Enterococcus faecium*. J Clin Microbiol 40:1963–1971. https://doi.org/10.1128/JCM.40.6.1963-1971.2002.
5. Santos BA, Oliveira JS, Cardoso NT, Barbosa AV, Superti SV, Teixeira LM, Neves FPG. 2017. Major globally disseminated clonal complexes of antimicrobial resistant enterococci associated with infections in cancer patients in Brazil. Infect Genet Evol 55:56–62. https://doi.org/10.1016/j.meegid.2017.08.027.
6. Oravcová V, Peixe L, Coque TM, Novais C, Francia MV, Literák I, Freitas AR. 2018. Wild corvid birds colonized with vancomycin-resistant *Enterococcus faecium* of human origin harbor epidemic *vanA* plasmids. Environ Int 118:125–133. https://doi.org/10.1016/j.envint.2018.05.039.
7. Silva V, Igrejas G, Carvalho I, Peixoto F, Cardoso L, Pereira JE, del Campo R, Poeta P. 2018. Genetic characterization of *vanA-Enterococcus faecium* isolates from wild red-legged partridges in Portugal. Microb Drug Resist 24:89–94. https://doi.org/10.1089/mdr.2017.0040.
8. Roberts MC, No DB, Marzluff JM, Delap JH, Turner R. 2016. Vancomycin resistant *Enterococcus* spp. from crows and their environment in metropolitan Washington State, USA: is there a correlation between VRE positive crows and the environment? Vet Microbiol 194:48–54. https://doi.org/10.1016/j.vetmic.2016.01.022.
9. 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.
10. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. http://www.bioinformatics.babraham.ac.uk/projects/fastqc.
11. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource center. Nucleic Acids Res 45:D535–D542. https://doi.org/10.1093/nar/gkw1017.
12. Galloway-Peña JR, Rice LB, Murray BE. 2011. Analysis of PBP5 of early U.S. isolates of *Enterococcus faecium*: sequence variation alone does not

explain increasing ampicillin resistance over time. Antimicrob Agents Chemother 55:3272–3277. https://doi.org/10.1128/AAC.00099-11.
13. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 67:2640–2644. https://doi.org/10.1093/jac/dks261.
14. Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM. 2014. Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic *Escherichia coli*. J Clin Microbiol 52:1501–1510. https://doi.org/10.1128/JCM.03617-13.
15. 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.
16. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. Nucleic Acids Res 39:W347–W352. https://doi.org/10.1093/nar/gkr485.
17. Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res 35:W52–W57. https://doi.org/10.1093/nar/gkm360.