



5-28-2020

Draft Genome Sequence of *Enterococcus faecalis* UMB1309, Isolated from Catheterized Urine

Adam Schwartz
Loyola University Chicago

Taylor Miller-Ensminger
Loyola University Chicago

Adelina Voukadinova
Loyola University Chicago

Alan J. Wolfe
Loyola University Chicago, awolfe@luc.edu

Catherine Putonti
Loyola University Chicago, cputonti@luc.edu

Follow this and additional works at: https://ecommons.luc.edu/bioinformatics_facpub



Part of the [Bioinformatics Commons](#), and the [Biology Commons](#)

Recommended Citation

Schwartz, Adam; Miller-Ensminger, Taylor; Voukadinova, Adelina; Wolfe, Alan J.; and Putonti, Catherine. Draft Genome Sequence of *Enterococcus faecalis* UMB1309, Isolated from Catheterized Urine. *Microbiology Resource Announcements*, 9, : , 2020. Retrieved from Loyola eCommons, Bioinformatics Faculty Publications, <http://dx.doi.org/10.1128/MRA.00406-20>


This Article is brought to you for free and open access by the Faculty Publications and Other Works by Department at Loyola eCommons. It has been accepted for inclusion in Bioinformatics Faculty Publications by an authorized administrator of Loyola eCommons. For more information, please contact ecommons@luc.edu.



This work is licensed under a [Creative Commons Attribution 4.0 International License](#).
© Schwartz et al., 2020.



Draft Genome Sequence of *Enterococcus faecalis* UMB1309, Isolated from Catheterized Urine

Adam Schwartz,^a Taylor Miller-Ensminger,^b Adelina Voukadinova,^b Alan J. Wolfe,^c  Catherine Putonti^{a,b,c,d}

^aDepartment of Biology, Loyola University Chicago, Chicago, Illinois, USA

^bBioinformatics Program, Loyola University Chicago, Chicago, Illinois, USA

^cDepartment of Microbiology and Immunology, Stritch School of Medicine, Loyola University Chicago, Maywood, Illinois, USA

^dDepartment of Computer Science, Loyola University Chicago, Chicago, Illinois, USA

ABSTRACT A strain of *Enterococcus faecalis* was isolated from catheterized urine. Here, we present the draft genome sequence of this isolate, *E. faecalis* UMB1309. Analysis of the genome revealed multiple genes coding for virulence factors, as well as genes associated with antibiotic resistance.

Enterococcus faecalis has long been identified as a commensal organism found in the gastrointestinal tract of healthy individuals and as a low-grade opportunistic pathogen (1–3) associated with endocarditis, urinary tract infections (UTIs), sepsis, bacteremia, and meningitis (2–4). Over the past 50 years, however, the emergence of multidrug-resistant strains of enterococci has contributed to its rise to become the third leading cause of nosocomial infections today (1–5). Of all nosocomial infections caused by *E. faecalis*, UTIs are the most common (3, 6). Here, we present the draft genome of *E. faecalis* UMB1309, which was isolated from the catheterized urine of a woman with a UTI.

E. faecalis UMB1309 was isolated from a catheterized urine specimen from a woman seeking clinical care at the Loyola University Medical Center Female Pelvic Medicine and Reconstructive Surgery Center (Maywood, IL, USA) as part of a previous institutional review board (IRB)-approved study (7). This strain was isolated using the expanded quantitative urinary culture (EQUC) protocol (8). Matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry was used to determine the genus and species of the isolate following a previously published protocol (8). The isolate was then stored at -80°C . The isolate was streaked onto a Columbia nalidixic acid (CNA) agar plate and incubated at 35°C with 5% CO_2 for 24 h. A single colony was selected and added to liquid brain heart infusion (BHI) medium, which was then incubated again under the aforementioned conditions. DNA was extracted using a Qiagen DNeasy blood and tissue kit following the manufacturer's protocol for Gram-positive bacteria with the following modifications: we used $230\ \mu\text{l}$ of lysis buffer ($180\ \mu\text{l}$ of 20 mM Tris-Cl, 2 mM sodium EDTA, and 1.2% Triton X-100 and $50\ \mu\text{l}$ of lysozyme) in step 2 and altered the incubation time in step 5 to 10 min. DNA was quantified using a Qubit fluorometer. The DNA was sequenced at the Microbial Genomic Sequencing Center at the University of Pittsburgh. DNA was enzymatically fragmented using an Illumina tagmentation enzyme, and then indices were attached using PCR. The DNA library was sequenced using a NextSeq 550 flow cell; this produced 2,145,494 pairs of 150-bp reads. Raw reads were quality controlled by trimming using Sickle v1.33 (<https://github.com/najoshi/sickle>). The genome was then assembled using SPAdes v3.13.0 (9) with the only-assembler option for k values of 55, 77, 99, and 127 and annotated using PATRIC v3.6.3 (10). The publicly available genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (11). The genome

Citation Schwartz A, Miller-Ensminger T, Voukadinova A, Wolfe AJ, Putonti C. 2020. Draft genome sequence of *Enterococcus faecalis* UMB1309, isolated from catheterized urine. Microbiol Resour Annuoc 9:e00406-20. <https://doi.org/10.1128/MRA.00406-20>.

Editor David A. Baltrus, University of Arizona

Copyright © 2020 Schwartz 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 Catherine Putonti, cputonti@luc.edu.

Received 13 April 2020

Accepted 8 May 2020

Published 28 May 2020

coverage was calculated using BMap v38.47 (<https://sourceforge.net/projects/bbmap>). Unless otherwise noted, default parameters were used for each software tool.

The *E. faecalis* UMB1309 draft genome is 3,046,929 bp assembled in 32 contigs and has a GC content of 37.20%. The genome coverage was 173×, and the N_{50} score was 283,553 bp. The PGAP annotation identified 2,892 protein-coding genes, 55 tRNAs, and 5 complete rRNAs (3 5S rRNAs, 1 16S rRNA, and 1 23S rRNA). PATRIC annotation included multiple putative virulence factors, including collagen-binding adhesins, PrgB (associated with cellular aggregation), and other cell wall surface anchor proteins. PATRIC also identified genes conferring antibiotic resistance, including *Isa(A)* (associated with macrolide resistance) and *tet(M)* (associated with tetracycline resistance). Despite the prevalence of *E. faecalis* infections, the role of this bacterium in the urinary tract is not well understood (4, 6). Further genomic analysis of *E. faecalis* can reveal insights into these mechanisms and ultimately aid in the development of effective treatments against *E. faecalis* UTIs.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under accession no. [JAAUWG000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAAUWG000000000). The version described in this paper is the first version (accession no. [JAAUWG010000000](https://www.ncbi.nlm.nih.gov/nuccore/JAAUWG010000000)). The raw sequencing reads have been deposited in the SRA under accession no. [SRR11441014](https://www.ncbi.nlm.nih.gov/sra/SRR11441014).

ACKNOWLEDGMENTS

This work was conducted as part of the Loyola University Chicago's Department of Biology Bacterial Genomics course. For prior patient recruitment, we acknowledge the Loyola Urinary Education and Research Collaborative and the patients who provided the samples for this study.

REFERENCES

- Lebreton F, Willems RJL, Gilmore MS. 2014. *Enterococcus* diversity, origins in nature, and gut colonization, p 5–64. In Gilmore MS, Clewell DB, Ike Y, Shankar N (ed), *Enterococci: from commensals to leading causes of drug resistant infection*. Massachusetts Eye and Ear Infirmary, Boston, MA.
- Murray BE. 1990. The life and times of the *Enterococcus*. *Clin Microbiol Rev* 3:46–65. <https://doi.org/10.1128/cmr.3.1.46>.
- Sood S, Malhotra M, Das BK, Kapil A. 2008. Enterococcal infections and antimicrobial resistance. *Indian J Med Res* 128:111–121.
- Fiore E, Van Tyne D, Gilmore M. 2019. Pathogenicity of enterococci. *Microbiol Spectr* 7:10.1128/microbiolspec.GPP3-0053-2018. <https://doi.org/10.1128/microbiolspec.GPP3-0053-2018>.
- Hidron AI, Edwards JR, Patel J, Horan TC, Sievert DM, Pollock DA, Fridkin SK. 2008. NHSN annual update: antimicrobial-resistant pathogens associated with healthcare-associated infections: annual summary of data reported to the National Healthcare Safety Network at the Centers for Disease Control and Prevention, 2006–2007. *Infect Control Hosp Epidemiol* 29:996–1011. <https://doi.org/10.1086/591861>.
- Kau AL, Martin SM, Lyon W, Hayes E, Caparon MG, Hultgren SJ. 2005. *Enterococcus faecalis* tropism for the kidneys in the urinary tract of C57BL/6J mice. *Infect Immun* 73:2461–2468. <https://doi.org/10.1128/IAI.73.4.2461-2468.2005>.
- Price TK, Dune T, Hilt EE, Thomas-White KJ, Kliethermes S, Brincat C, Brubaker L, Wolfe AJ, Mueller ER, Schreckenberger PC. 2016. The clinical urine culture: enhanced techniques improve detection of clinically relevant microorganisms. *J Clin Microbiol* 54:1216–1222. <https://doi.org/10.1128/JCM.00044-16>.
- Hilt EE, McKinley K, Pearce MM, Rosenfeld AB, Zilliox MJ, Mueller ER, Brubaker L, Gai X, Wolfe AJ, Schreckenberger PC. 2014. Urine is not sterile: use of enhanced urine culture techniques to detect residential bacterial flora in adult female bladder. *J Clin Microbiol* 52:871–876. <https://doi.org/10.1128/JCM.02876-13>.
- 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>.
- Brettin T, Davis JJ, Disz T, Edwards RA, Gerdes S, Olsen GJ, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Thomason JA, Stevens R, Vonstein V, Wattam AR, Xia F. 2015. RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. *Sci Rep* 5:8365. <https://doi.org/10.1038/srep08365>.
- 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>.