



6-4-2020

## Draft Genome Sequence of Escherichia coli UMB1353, Isolated from the Female Urinary Tract

Tanea Crawford  
*Loyola University Chicago*

Taylor Miller-Ensminger  
*Loyola University Chicago*

Adelina Voukadinova  
*Loyola University Chicago*

Alan J. Wolfe  
*Loyola University Chicago*, [awolfe@luc.edu](mailto:awolfe@luc.edu)

Catherine Putoni  
*Loyola University Chicago*, [cputonti@luc.edu](mailto:cputonti@luc.edu)

Follow this and additional works at: [https://ecommons.luc.edu/bioinformatics\\_facpub](https://ecommons.luc.edu/bioinformatics_facpub)



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

### Recommended Citation

Crawford, Tanea; Miller-Ensminger, Taylor; Voukadinova, Adelina; Wolfe, Alan J.; and Putoni, Catherine. Draft Genome Sequence of Escherichia coli UMB1353, Isolated from the Female Urinary Tract. *Microbiology Resource Announcements*, 9, : , 2020. Retrieved from Loyola eCommons, Bioinformatics Faculty Publications, <http://dx.doi.org/10.1128/MRA.00416-20>


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](mailto:ecommons@luc.edu).



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



# Draft Genome Sequence of *Escherichia coli* UMB1353, Isolated from the Female Urinary Tract

Tanea Crawford,<sup>a</sup> Taylor Miller-Ensminger,<sup>b</sup> Adelina Voukadinova,<sup>b</sup> Alan J. Wolfe,<sup>c</sup>  Catherine Putonti<sup>b,c,d,e</sup>

<sup>a</sup>Neuroscience Program, Loyola University Chicago, Chicago, Illinois, USA

<sup>b</sup>Bioinformatics Program, Loyola University Chicago, Chicago, Illinois, USA

<sup>c</sup>Department of Microbiology and Immunology, Stritch School of Medicine, Loyola University Chicago, Maywood, Illinois, USA

<sup>d</sup>Department of Biology, Loyola University Chicago, Chicago, Illinois, USA

<sup>e</sup>Department of Computer Science, Loyola University Chicago, Chicago, Illinois, USA

**ABSTRACT** Here, we present the draft genome sequence of *Escherichia coli* UMB1353, isolated from a patient with a urinary tract infection. The sequence of this antibiotic-resistant *E. coli* strain contains one intact P2-like phage.

*Escherichia coli* is a Gram-negative, rod-shaped, facultative, anaerobic bacterium commonly found in the human gastrointestinal tract (1). While often a commensal species in this niche, it can cause meningitis, gastrointestinal symptoms and disorders, and urinary tract infections (UTIs) (2). UTI is one of the most common human infections (3, 4), and *E. coli* is the leading cause of UTIs (5). Despite many genome-sequencing projects of commensal and uropathogenic *E. coli*, the distinction between the two has yet to be determined (6). Here, we present the draft genome sequence of *E. coli* UMB1353, a strain isolated from a transurethral catheter urine sample obtained from a woman with a UTI.

Using the expanded quantitative urine culture (EQUC) method (7), *E. coli* UMB1353 was isolated as part of a prior institutional review board (IRB)-approved study (8). This urine specimen was collected from a woman seeking clinical care at Loyola University Medical Center's Female Pelvic Medicine and Reconstructive Surgery Center (Maywood, IL, USA) from June 2014 to August 2015. The genus and species were identified using matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry before being stored at  $-80^{\circ}\text{C}$ . *E. coli* UMB1353 was streaked onto a Columbia nalidixic acid (CNA) plate and incubated at  $35^{\circ}\text{C}$  with 5%  $\text{CO}_2$ . A single flat colony was recovered and placed in LB broth and incubated at  $37^{\circ}\text{C}$  with shaking for 24 h. The DNA was extracted with the Qiagen DNeasy blood and tissue kit using the protocol for Gram-positive bacteria with the following modifications: we used  $230\ \mu\text{l}$  of lysis buffer (including  $50\ \mu\text{l}$  of lysozyme) in step 2 and incubated for 10 min at  $56^{\circ}\text{C}$  in step 5. Extracted DNA was quantified with a Qubit fluorometer. Library preparation and sequencing were done at the Microbial Genome Sequencing Center at the University of Pittsburgh. First, the DNA was enzymatically fragmented using an Illumina tagmentation enzyme. Indices were attached using PCR, and then the library was sequenced on the Illumina NextSeq 550 platform. Sequencing produced a total of 2,302,396 pairs of 150-bp reads. Raw reads were trimmed using Sickle v1.33 (<https://github.com/najoshi/sickle>). The trimmed reads were assembled using SPAdes v3.13.0 with the “only-assembler” option for k values of 55, 77, 99, and 127 (9). Genome coverage was calculated using BBMap v38.47 (<https://sourceforge.net/projects/bbmap/>). Annotations were produced using PATRIC v3.6.3 (10), but the publicly available genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (11). Unless previously noted, default parameters were used for each software tool.

**Citation** Crawford T, Miller-Ensminger T, Voukadinova A, Wolfe AJ, Putonti C. 2020. Draft genome sequence of *Escherichia coli* UMB1353, isolated from the female urinary tract. *Microbiol Resour Announc* 9:e00416-20. <https://doi.org/10.1128/MRA.00416-20>.

**Editor** David Rasko, University of Maryland School of Medicine

**Copyright** © 2020 Crawford 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](mailto:cputonti@luc.edu).

**Received** 14 April 2020

**Accepted** 17 May 2020

**Published** 4 June 2020

The assembled draft genome is 5,282,250 bp long with a GC content of 50.25%, genome coverage of 82×, and  $N_{50}$  score of 89,083 bp. The genome is composed of 195 contigs encoding 4,867 protein-coding genes per the PGAP annotation. PATRIC identified several transporter genes, drug target genes, and antibiotic resistance genes. Further investigation of the antibiotic resistance genes using ResFinder v3.2 (12) identified those for beta-lactams, macrolides, and tetracycline. PHASTER (13) identified one intact phage, similar to *Enterobacteria* phage P2. This was confirmed by querying the predicted prophage nucleotide sequence against the nonredundant nucleotide (nr/nt) database via MegaBLAST (GenBank accession no. [LR595869.1](https://doi.org/10.1128/JCM.02876-13); query coverage, 81%; percent identity, 97.62%). Analysis of this genome builds on previous research of uropathogenic *E. coli* and has clinical relevance by contributing to research for developing new UTI treatments.

**Data availability.** This whole-genome shotgun project has been deposited in GenBank under the accession no. [JAAUWE000000000](https://doi.org/10.1128/JCM.00044-16). The version described in this paper is the first version, JAAUWE010000000. The raw sequencing reads have been deposited in the SRA under the accession no. [SRR11441035](https://doi.org/10.1128/JCM.00044-16).

## ACKNOWLEDGMENTS

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

## REFERENCES

- Gill SR, Pop M, Deboy RT, Eckburg PB, Turnbaugh PJ, Samuel BS, Gordon JI, Relman DA, Fraser-Liggett CM, Nelson KE. 2006. Metagenomic analysis of the human distal gut microbiome. *Science* 312:1355–1359. <https://doi.org/10.1126/science.1124234>.
- Kaper JB, Nataro JP, Mobley HL. 2004. Pathogenic *Escherichia coli*. *Nat Rev Microbiol* 2:123–140. <https://doi.org/10.1038/nrmicro818>.
- Keating KN, Perfetto EM, Subedi P. 2005. Economic burden of uncomplicated urinary tract infections: direct, indirect and intangible costs. *Expert Rev Pharmacoecon Outcomes Res* 5:457–466. <https://doi.org/10.1586/14737167.5.4.457>.
- Schappert SM, Rechtsteiner EA. 2011. Ambulatory medical care utilization estimates for 2007. *Vital Health Stat* 13:1–38.
- Terlizzi ME, Gribaudo G, Maffei ME. 2017. UroPathogenic *Escherichia coli* (UPEC) infections: virulence factors, bladder responses, antibiotic, and non-antibiotic antimicrobial strategies. *Front Microbiol* 8:1566. <https://doi.org/10.3389/fmicb.2017.01566>.
- Schreiber HL, Conover MS, Chou W-C, Hibbing ME, Manson AL, Dodson KW, Hannan TJ, Roberts PL, Stapleton AE, Hooton TM, Livny J, Earl AM, Hultgren SJ. 2017. Bacterial virulence phenotypes of *Escherichia coli* and host susceptibility determine risk for urinary tract infections. *Sci Transl Med* 9:eaaf1283. <https://doi.org/10.1126/scitranslmed.aaf1283>.
- 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 resident bacterial flora in the adult female bladder. *J Clin Microbiol* 52:871–876. <https://doi.org/10.1128/JCM.02876-13>.
- 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>.
- 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>.
- 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>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvermin 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>.
- 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>.
- Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. *Nucleic Acids Res* 44:W16–W21. <https://doi.org/10.1093/nar/gkw387>.