



5-14-2020

## Draft Genome Sequence of *Lactobacillus jensenii* UMB0847, Isolated from the Female Urinary Tract

Ella West-Pelak  
*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 Putonti  
*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

West-Pelak, Ella; Miller-Ensminger, Taylor; Voukadinova, Adelina; Wolfe, Alan J.; and Putonti, Catherine. Draft Genome Sequence of *Lactobacillus jensenii* UMB0847, 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.00395-20>

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 International License](#).  
© West-Pelak et al., 2020.



# Draft Genome Sequence of *Lactobacillus jensenii* UMB0847, Isolated from the Female Urinary Tract

Ella West-Pelak,<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** *Lactobacillus jensenii* is a protective bacterium native to the female urinary tract. Here, we present the 1.6-Mbp draft genome for *Lactobacillus jensenii* UMB0847, isolated from a catheterized urine sample obtained from a pregnant female.

*Lactobacillus jensenii*, along with *L. crispatus*, *L. gasseri*, and *L. iners*, is frequently found within the microbiota of the female urogenital tract (1, 2). It is believed to be involved in maintaining a healthy urogenital tract (1–4). Many strains of *L. jensenii* produce hydrogen peroxide, which can be toxic to other organisms (5). Previous studies have shown that many lactobacilli, including *L. jensenii*, are effective in displacing or inhibiting the growth of urogenital pathogens, including *Escherichia coli* (6, 7), *Enterococcus faecalis* (8), and *Neisseria gonorrhoeae* (9). Analysis of *L. jensenii* genomes from the vaginal microbiota has yielded evidence of adaptation to this particular environment (3). Recently, we began sequencing *L. jensenii* representatives of the urinary microbiome (10). Here, we introduce the draft genome of another *L. jensenii* strain from the urinary tract, *L. jensenii* UMB0847, which was isolated from a pregnant female.

*L. jensenii* UMB0847 was isolated from a prior institutional review board (IRB)-approved study (11) using the expanded quantitative urinary culture (EQUC) protocol (12). The genus and species were confirmed by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry, as previously described (12), and then stored at  $-80^{\circ}\text{C}$  until sequencing. We streaked the *L. jensenii* isolate onto a Columbia nalidixic acid (CNA) agar plate and incubated it at  $35^{\circ}\text{C}$  in 5%  $\text{CO}_2$  for 24 h. A colony was selected to grow in liquid brain heart infusion (BHI) medium at  $35^{\circ}\text{C}$  in 5%  $\text{CO}_2$  for 24 h. DNA was extracted using the Qiagen DNeasy blood and tissue kit following the manufacturer's protocol for Gram-positive bacteria with the following exceptions: 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. The extracted DNA was quantified using a Qubit fluorometer and sent to the Microbial Genomic Sequencing Center at the University of Pittsburgh for sequencing. DNA libraries were constructed using the Nextera XT kit. The DNA was sequenced using the Illumina NextSeq 550 platform, producing 3,260,770 pairs of 150-bp reads. These raw reads were trimmed using Sickle v1.33 (<https://github.com/najoshi/sickle>). We used SPAdes v3.13.0 (13) with the “only-assembler” option for k values of 55, 77, 100, and 127. We used PATRIC v3.6.3 (14) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (15) to annotate the genome. Genome coverage was calculated using BMap v38.47 (<https://sourceforge.net/projects/bbmap/>). Unless specifically noted, all software tools used default parameters.

**Citation** West-Pelak E, Miller-Ensminger T, Voukadinova A, Wolfe AJ, Putonti C. 2020. Draft genome sequence of *Lactobacillus jensenii* UMB0847, isolated from the female urinary tract. Microbiol Resour Announc 9:e00395-20. <https://doi.org/10.1128/MRA.00395-20>.

**Editor** J. Cameron Thrash, University of Southern California

**Copyright** © 2020 West-Pelak 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** 12 April 2020

**Accepted** 20 April 2020

**Published** 14 May 2020

The *L. jensenii* draft genome has a length of 1,644,700 bp and consists of 44 contigs with a GC content of 34%, genome coverage of 485×, and an  $N_{50}$  score of 57,991 bp. The PATRIC annotation identified 1,044 genes that produce functional proteins, 54 tRNAs, and 6 rRNAs (3 5S, 2 16S, and 1 23S). Furthermore, 1 CRISPR array containing 12 spacer sequences was detected. Continued investigation of *L. jensenii* from the urinary microbiota will increase our knowledge of the genetic diversity of this beneficial member of the female urogenital tract microbiota.

**Data availability.** This whole-genome shotgun project has been deposited in GenBank under accession no. [JAAUWK000000000](https://www.ncbi.nlm.nih.gov/GenBank/JAAUWK000000000). The version described in this paper is the first version, JAAUWK010000000. The raw sequencing reads have been deposited in the SRA under accession no. [SRR11441018](https://www.ncbi.nlm.nih.gov/SRA/SRR11441018).

## ACKNOWLEDGMENTS

This work was conducted as part of the Bacterial Genomics course at the Loyola University of Chicago's Department of Biology.

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

- Pearce MM, Hilt EE, Rosenfeld AB, Zilliox MJ, Thomas-White K, Fok C, Kliethermes S, Schreckenberger PC, Brubaker L, Gai X, Wolfe AJ. 2014. The female urinary microbiome: a comparison of women with and without urgency urinary incontinence. *mBio* 5:e01283-14. <https://doi.org/10.1128/mBio.01283-14>.
- Ravel J, Gajer P, Abdo Z, Schneider GM, Koenig SSK, McCulle SL, Karlebach S, Gorle R, Russel J, Tacket CO, Brotman RM, Davis CC, Ault K, Peralta L, Forney LJ. 2011. Vaginal microbiome of reproductive-age women. *Proc Natl Acad Sci U S A* 108:4680–4687. <https://doi.org/10.1073/pnas.1002611107>.
- Mendes-Soares H, Suzuki H, Hickey RJ, Forney LJ. 2014. Comparative functional genomics of *Lactobacillus* spp. reveals possible mechanisms for specialization of vaginal lactobacilli to their environment. *J Bacteriol* 196:1458–1470. <https://doi.org/10.1128/JB.01439-13>.
- Lepargneur J-P. 2016. *Lactobacillus crispatus* as biomarker of the healthy vaginal tract. *Ann Biol Clin (Paris)* 74:421–427. (In French.) <https://doi.org/10.1684/abc.2016.1169>.
- Eschenbach DA, Davick PR, Williams BL, Klebanoff SJ, Young-Smith K, Critchlow CM, Holmes KK. 1989. Prevalence of hydrogen peroxide-producing *Lactobacillus* species in normal women and women with bacterial vaginosis. *J Clin Microbiol* 27:251–256. <https://doi.org/10.1128/JCM.27.2.251-256.1989>.
- Boris S, Suárez JE, Vázquez F, Barbés C. 1998. Adherence of human vaginal lactobacilli to vaginal epithelial cells and interaction with uropathogens. *Infect Immun* 66:1985–1989. <https://doi.org/10.1128/IAI.66.5.1985-1989.1998>.
- Hudson PL, Hung KJ, Bergerat A, Mitchell C. 2020. Effect of vaginal *Lactobacillus* species on *Escherichia coli* growth. *Female Pelvic Med Reconstr Surg* 26:146–151. <https://doi.org/10.1097/SPV.0000000000000827>.
- Stoyancheva G, Marzotto M, Dellaglio F, Torriani S. 2014. Bacteriocin production and gene sequencing analysis from vaginal *Lactobacillus* strains. *Arch Microbiol* 196:645–653. <https://doi.org/10.1007/s00203-014-1003-1>.
- Spurbeck RR, Arvidson CG. 2010. *Lactobacillus jensenii* surface-associated proteins inhibit *Neisseria gonorrhoeae* adherence to epithelial cells. *Infect Immun* 78:3103–3111. <https://doi.org/10.1128/IAI.01200-09>.
- Putonti C, Ahmad A, Baddoo G, Diaz J, Do M, Gallian N, Lorentzen C, Mohammed H, Murphy J, Olu-Ajeigbe A, Yang T, Miller-Ensminger T, Stark N, Maskeri L, Van Dusen J, Wolfe AJ. 2019. Draft genome sequences of 11 *Lactobacillus jensenii* strains isolated from the female bladder. *Microbiol Resour Announc* 8:e00970-19. <https://doi.org/10.1128/MRA.00970-19>.
- Jacobs KM, Thomas-White KJ, Hilt EE, Wolfe AJ, Waters TP. 2017. Microorganisms identified in the maternal bladder: discovery of the maternal bladder microbiota. *AJP Rep* 7:e188–e196. <https://doi.org/10.1055/s-0037-1606860>.
- 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>.
- 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, III, 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, Chetvertnin 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>.