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Draft Genome Sequence of *Lactobacillus jensenii* UMB0836, Isolated from the Female Bladder

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ABSTRACT *Lactobacillus jensenii* is a frequent member of both the vaginal and urinary microbiota. Here, we present the draft genome sequence for *L. jensenii* UMB0836, isolated from catheterized urine obtained from a pregnant female. The genome is 1,648,234 bp long, assembled in 40 contigs.

Lactobacillus species, most notably *L. crispatus*, *L. gasseri*, *L. iners*, and *L. jensenii*, inhabit both the vaginal and bladder microbiota of healthy women (1–3). Studies have shown that several of these lactobacilli play a protective role against infection, including limiting the colonization of pathogenic bacteria (4, 5). While *L. gasseri* and *L. crispatus* have been associated with urgency urinary incontinence symptoms and the lack of symptoms, respectively (6), *L. jensenii* has been found in the communities of individuals with and without lower urinary tract symptoms. Here, we present the draft genome of *L. jensenii* UMB0836, isolated from a catheterized urine sample from a pregnant woman.

L. jensenii UMB0836 was isolated as part of a prior institutional review board (IRB)-approved study (7) and cultured using the expanded quantitative urine culture (EQUC) protocol (8). Matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry was used to confirm the genus and species of the isolate, following a protocol previously described (8). The isolate was then stored at –80°C. The strain was streaked on a Columbia nalidixic acid (CNA) agar plate and incubated at 35°C with 5% CO₂ for 24 h. A single colony was then grown in MRS medium supplemented with 1 ml/liter of Tween 80 under the same conditions as described above. DNA was extracted using Qiagen’s DNeasy blood and tissue kit following the manufacturer’s protocol for Gram-positive bacteria with the following exceptions: 230 μl of lysis buffer (180 μl of 20 mM Tris-Cl, 2 mM sodium EDTA, and 1.2% Triton X-100 and 50 μl of lysozyme) was used in step 2, and the incubation time in step 5 was altered to 10 min. DNA was quantified using a Qubit fluorometer. For sequencing, DNA was sent to the Microbial Genome Sequencing Center (MiGS) at the University of Pittsburgh. The Illumina Nextera kit series was used to construct the DNA library, and sequencing was performed using the NextSeq 550 platform. In total, 2,299,084 pairs of 150-bp reads were generated for this isolate. The raw reads were trimmed using Sickle v1.33 (<https://github.com/najoshi/sickle>) and assembled using SPAdes v3.13.0 with the “only-assembler” option for k values of 55, 77, 99, and 127 (9). The genome coverage was calculated using BMap v38.47 (<https://sourceforge.net/projects/bbmap/>). PATRIC v3.6.3 (10) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (11) were used to annotate the genome sequence. Unless previously noted, default parameters were used for each software tool.

The draft genome of *L. jensenii* UMB0836 is 1,648,234 bp long, assembled in 40

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contigs, with a GC content of 34.32%. The genome coverage is 356×, with an N_{50} score of 63,129 bp. PGAP annotation identified 1,458 protein-coding genes, 54 tRNAs, and 7 (3 5S, 3 16S, and 1 23S) rRNA sequences. Both PGAP and PATRIC identified a single CRISPR array. This array includes 20 CRISPR spacer sequences. The draft genome sequence of *L. jensenii* UMB0836 provides data about the genetic content of this important member of the microbiota of the urogenital tract.

Data availability. This whole-genome shotgun project has been deposited in GenBank under the accession no. [JAAUWN000000000](https://ncbi.nlm.nih.gov/ accession/JAAUWN000000000). The version described in this paper is the first version, JAAUWN010000000. The raw sequencing reads have been deposited in SRA under the accession no. [SRR11441036](https://ncbi.nlm.nih.gov/ accession/SRR11441036).

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