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GENOME SEQUENCES

Draft Genome Sequence of *Lactobacillus crispatus* UMB1163, Isolated from the Female Urinary Tract

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ABSTRACT *Lactobacillus crispatus* is a Gram-positive bacterium shown to protect against urinary and vaginal infections. Here, we report the draft genome sequence of *L. crispatus* UMB1163, isolated from the female urinary tract.

Lactobacillus crispatus is a nonpathogenic bacterium native to the healthy female urogenital tract (1, 2). *L. crispatus* is critical in preventing common bacterial infections (3–5), such as bacterial vaginosis and vulvovaginal atrophy (VVA), by preserving low pH and producing hydrogen peroxide (4). *L. crispatus* creates a biofilm in the vaginal epithelium, providing protection against pathogens that cause sexually transmitted diseases and urinary tract infections. Due to its ability to limit pathogens in the urogenital system, *L. crispatus* strains are being explored for use as a probiotic to prevent urinary tract infections (UTI) in women (6). Here, we present the draft genome sequence of *L. crispatus* UMB1163, isolated from the bladder of a female with a UTI.

The urine specimen was collected via a transurethral catheter from a woman seeking clinical care at Loyola University Medical Center's Female Pelvic Medicine and Reconstructive Surgery Center (Maywood, IL, USA) as part of a prior institutional review board (IRB)-approved study (Loyola University Chicago, IRB approval no. 206469) (7). *L. crispatus* was isolated from this urine specimen using the expanded quantitative urinary culture (EQUC) method (8). The genus and species of the bacterium were determined using matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (8) prior to storage at −80°C. *L. crispatus* UMB1163 was streaked onto a Columbia nalidixic acid (CNA) agar plate and incubated for 24 h at 35°C with 5% CO_2. A single colony was selected and incubated in De Man, Rogosa, and Sharpe (MRS) liquid medium supplemented with newborn calf serum (50 ml/liter) and incubated for 24 h at 35°C with 5% CO_2. DNA was extracted using the Qiagen DNeasy blood and tissue kit with a Gram-positive protocol modified as follows: 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 were used in step 2, and the incubation time in step 5 was reduced to 10 min. The DNA was quantified using a Qubit fluorometer. Sequencing was done at the University of Pittsburgh Microbial Genomic Sequencing Center (MiGS) on the Illumina NextSeq 550 platform. MiGS created the libraries using the Illumina Nextera kit. Sequencing produced 1,781,766 pairs of 150-bp reads. Sickle v1.33 (https://github.com/najoshi/sickle) was used to trim the raw reads, which were then assembled using SPAdes v3.13.0 with the "only-assemble" option for k values of 55, 77, 99, and 127 (9). Genome coverage was calculated using BBMap v38.4 (https://sourceforge.net/projects/bbmap/). We used PATRIC v3.6.3 to annotate the genome (10). The publicly available genome was annotated with the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v4.11 (11). Unless otherwise stated, default parameters were used for each software tool.

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The *L. crispatus* UMB1163 draft genome sequence is 2,384,113 bp long assembled into 151 contigs with an N_{50} score of 26,484 bp, genome coverage of 177×, and GC content of 36.6%. The *L. crispatus* assembly has 66 tRNAs and 5 complete rRNAs (3 5S, 1 16S, and 1 23S). PGAP identified 2,353 protein-coding genes. PATRIC identified 1 CRISPR array, with 7 spacer sequences. While numerous genomes of *L. crispatus* strains from the vaginal microbiome are available, a greater representation of the genetic diversity of this species within the urinary tract is needed. Sequencing isolates from the urinary tract will provide insight into the role that *L. crispatus* plays in the female urinary tract.

Data availability. This whole-genome shotgun project has been deposited in GenBank under the accession no. JAAUWJ000000000. The raw sequence reads were deposited in the SRA under the accession no. SRR11441017.

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