Genome Sequences of 12 Bacterial Isolates Obtained from the Urine of Pregnant Women

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For a commentary on this article, see doi:10.1128/genomeA.00890-16.

The presence of bacteria in urine can pose significant risks during pregnancy. However, there are few reference genome strains for many common urinary bacteria. We isolated 12 urinary strains of *Streptococcus, Staphylococcus, Citrobacter, Gardnerella*, and *Lactobacillus*. These strains and their genomes are now available to the research community.

Received 29 June 2016 Accepted 28 July 2016 Published 29 September 2016

Citation Weimer CM, Deitzler GE, Robinson LS, Park S, Hallsworth-Pepin K, Wollam A, Mitreva M, Lewis WG, Lewis AL. 2016. Genome sequences of 12 bacterial isolates obtained from the urine of pregnant women. Genome Announc 4(5):e00882-16. doi:10.1128/genomeA.00882-16.

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Nearly 8 million urinary tract infections (UTIs) occur each year in the United States alone (1). During pregnancy, dilation of the renal pelvis and ureters makes women more prone to bacterial infection of the kidney. Landmark studies by Mittendorf and coworkers employed a randomized placebo-controlled trial showing that 40% of women with persistent (untreated) asymptomatic bacteriuria (ASB) went on to experience pyelonephritis, while none of the antibiotic-treated women went on experience this outcome (2). Due to the risks posed by pyelonephritis to pregnancy, it is now common practice in the United States to screen and treat pregnant women for asymptomatic bacteriuria.

*Escherichia coli* is the most common and best-studied cause of UTI. However, other less common bacteria are not well studied, despite being responsible for tens of thousands of cases in the United States alone. For example, group B *Streptococcus* (GBS) is a common vaginal bacterium responsible for ~1% of UTIs (1) among young sexually active women (~80,000 cases/year). GBS is also a leading cause of newborn sepsis (3) and commonly causes stillbirth (4) and placental infections in pregnant women (5).

However, little is known about how GBS causes UTIs, and there are few urine isolates with sequenced genomes.

Similarly, there is an emerging understanding that the bladder is home to a surprising variety of bacteria, or at least that the bladder is frequently exposed to bacteria from nearby mucosal reservoirs (6). However, urinary strains from many taxa within these phyla are not readily available.

Here, we isolated and performed genome sequencing for 12 new strains of urinary bacteria. Briefly, clean-catch urine samples were provided by pregnant women as part of the Women and Infants’ Health Specimen Consortium (WIHSC) according to Washington University institutional review board (IRB)-approved protocol 20110382. Samples were sent from the Ob/Gyn clinic to the Barnes Jewish Hospital microbiology laboratory for identification of suspected uropathogens. Species identification was confirmed by full-length 16S rRNA gene sequence analysis. Genomic DNA was obtained using the Wizard purification kit (Promega). Genome assembly and annotation was performed as described more fully in the companion paper published in this issue of Genome Announcements.

### TABLE 1

| Strain identifiers and nucleotide accession numbers |
|---------------------------------------------------|
| **Genus/species** | **Strain** | **BEI catalog no.** | **Nucleotide accession no.** |
|---------------------------------------------------|
| *Streptococcus agalactiae* | PSS7632A | HMS-1244 | LRQM00000000 |
| *Streptococcus agalactiae* | PSS7632B | HMS-1245 | LRQN00000000 |
| *Streptococcus agalactiae* | PSS7625 | HMS-1246 | LRQD00000000 |
| *Streptococcus agalactiae* | PSS7568 | HMS-1247 | LRQH00000000 |
| *Streptococcus agalactiae* | PSS7678 | HMS-1248 | LRQK00000000 |
| *Streptococcus agalactiae* | PSS7722 | HMS-1249 | LRQT00000000 |
| *Streptococcus agalactiae* | PSS7736 | HMS-1250 | LRQO00000000 |
| *Citrobacter koseri* | PSS7778B | HMS-1275 | LRQF00000000 |
| *Gardnerella vaginalis* | PSS7772B | HMS-1276 | LRQG00000000 |
| *Lactobacillus crispatus* | PSS7727C | HMS-1277 | LRQH00000000 |
| *Lactobacillus gasseri* | PSS7772D | HMS-1278 | LRQI00000000 |
| *Staphylococcus aureus* | PSS7673 | HMS-1279 | LRQJ00000000 |
issue (“Genome sequences of 11 human vaginal Actinobacteria”). Briefly, genomes were assembled de novo using the One Button Velvet assembly pipeline (version 1.1.06) (7). Gene products were predicted/annotated using GeneMark, Glimmer3 (8, 9), NCBI’s nonredundant bacterial (NR) database, and Pfam (10), tRNAscan-SE (11), Rfammer (12), and Rfam (13).

**Accession number(s).** These whole-genome shotgun projects have been deposited in GenBank under the accession numbers listed in Table 1. The sequences described in this paper are the first versions. To facilitate future research in this field, we have also made the strains available to the research community by depositing them with the Biodefense and Emerging Infections (BEI) Research Resource Repository (see BEI numbers in Table 1).

**ACKNOWLEDGMENTS**

We thank Deborah Frank for editorial assistance, the Women and Infants Health Specimen Consortium (WIHSC) for consenting and collecting specimens from patients, the Barnes Jewish Microbiology lab for providing isolates, and BEI Resources for providing the isolates to other investigators. We also gratefully acknowledge the patients who provided urine samples.

This work was funded in part by NIDDK DK092586-01A1 (A.L.L.), P50 DK064540-11 (A.L.L., project II), the Children’s Discovery Institute (W.G.L. and A.L.L.), and the Human Microbiome Project 5U54HG00496804. A summer stipend was provided by the Planning Center for Research in Benign Urology Summer Research Program P20DK097798 (G.E.D.).

**FUNDING INFORMATION**

This work, including the efforts of Amanda L. Lewis and Warren G. Lewis, was funded by Children’s Discovery Institute (CDI).

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