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Genome Sequences of 15 *Gardnerella vaginalis* Strains Isolated from the Vaginas of Women with and without Bacterial Vaginosis

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***Gardnerella vaginalis* is a predominant species in bacterial vaginosis, a dysbiosis of the vagina that is associated with adverse health outcomes, including preterm birth. Here, we present the draft genome sequences of 15 *Gardnerella vaginalis* strains (now available through BEI Resources) isolated from women with and without bacterial vaginosis.**

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Bacterial vaginosis (BV) is a common condition characterized by low levels of “healthy” vaginal lactobacilli and overgrowth of diverse anaerobes (1, 2). Women with BV have higher risks of many adverse health outcomes, including HIV transmission, intrauterine infections, and preterm birth (3–7). Unfortunately, the condition is highly recurrent; most women experience another episode of BV within months of treatment (8, 9). *Gardnerella vaginalis* is a facultative anaerobe in the family *Bifidobacteriaceae* and is one of the dominant species in BV (10). Recent studies demonstrated that *G. vaginalis* (strain JCP8151B) was sufficient to cause several features of BV in a mouse vaginal infection model (11, 12). To support further studies aimed at understanding the role of *G. vaginalis* in BV, we sequenced the genomes of 15 *G. vaginalis* strains (including JCP8151B) that were isolated from the vaginal swabs from 12 women enrolled in the institutional review board (IRB)-approved Washington University Contraceptive CHOICE Project (13).

Strains were isolated by plating vaginal swabs on *Gardnerella* semiselective medium, as described previously (12). After 24 to 48 h of growth at 37°C in an anaerobic chamber, pinpoint colonies were subcultured and tested by PCR using *Gardnerella*-specific primers (14). Full-length 16S rRNA gene sequences confirmed their identity. All strains were derived from different women, with the exception of three strain pairs sharing the same numerical identifier (i.e., JCP8151A and JCP8151B, JCP8017A and JCP8017B, and JCP8481A and JCP8481B).

For genome sequencing, strains were grown overnight in NYCIII broth, and DNA was isolated with the Wizard genomic DNA purification kit (Promega). Shotgun libraries were generated and sequenced with Illumina sequencing technology. Contigs were assembled with Velvet 1.1.06. GeneMark and Glimmer3 (15, 16) were used to predict coding regions, and the remaining sequences were examined for homology to sequences in the NCBI

nonredundant protein database. Putative protein functions were predicted with a suite of programs, including KEGG (17), PSORTb (18), and InterProScan (19). tRNAscan-SE was used to identify tRNAs (20), and additional noncoding RNA genes were determined with RNAmmer (21) and Rfam (22).

The average genome coverage of the sequenced strains was 150×. The average genome size was 1.6 Mbp. The strains contain, on average, 2,800 protein-coding genes, 15 rRNA genes, and 92 tRNA genes, and have a G+C content of 42.5%.

Accession number(s). The draft genome sequences for the 15 *G. vaginalis* strains have been deposited in GenBank under the accession numbers listed in Table 1. The sequences described in this paper are the first versions. We have also made 14 of these

TABLE 1 GenBank and BEI accession numbers of the sequenced *G. vaginalis* strains

| Strain/BEI no. | BEI accession no. | Nucleotide accession no. |
|----------------|-------------------|--------------------------|
| JCP7275 | HM-1105 | ATJS00000000 |
| JCP7276 | HM-1106 | ATJR00000000 |
| JCP7659 | HM-1107 | ATJQ00000000 |
| JCP7672 | HM-1108 | ATJP00000000 |
| JCP7719 | HM-1109 | ATJO00000000 |
| JCP8017A | HM-1110 | ATJN00000000 |
| JCP8017B | HM-1111 | ATJM00000000 |
| JCP8066 | HM-1112 | ATJL00000000 |
| JCP8070 | HM-1113 | ATJK00000000 |
| JCP8108 | HM-1114 | ATJJ00000000 |
| JCP8151A | HM-1115 | ATJI00000000 |
| JCP8151B | HM-1116 | ATJH00000000 |
| JCP8481A | NA ^a | ATJG00000000 |
| JCP8481B | HM-1118 | ATJF00000000 |
| JCP8522 | HM-1119 | ATJE00000000 |

^a NA, not available.

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).

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