

Draft Genome Sequence of a Metronidazole-Resistant *Gardnerella vaginalis* Isolate

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We report the draft genome sequence of a *Gardnerella vaginalis* strain (3549624) isolated from a vaginal specimen. *G. vaginalis* is associated with bacterial vaginosis, the most common cause of vaginal discharge, which is often treated with metronidazole. This isolate is highly resistant to metronidazole (MIC, 500 $\mu\text{g}/\text{ml}$) and may be useful for comparative genomic studies to determine the molecular basis of metronidazole resistance in this species.

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Gardnerella vaginalis was the first organism (1) associated with bacterial vaginosis (BV), the most common gynecological infection in the United States, affecting 29% of women (2). The antibiotic metronidazole is a first-line therapy for BV (3), but treatment failure (4) and recurrent disease are common (5). Metronidazole resistance is observed in clinical *G. vaginalis* isolates (6–8), although it has not been definitively linked to BV treatment failure or recurrent disease. An MIC of $\geq 32 \mu\text{g}/\text{ml}$ has been used in prior studies to define resistance (8). To facilitate a greater understanding of metronidazole resistance in this species, we sequenced the genome of *G. vaginalis* strain 3549624, an isolate highly resistant to metronidazole (MIC, 500 $\mu\text{g}/\text{ml}$).

This strain was isolated from a discarded cervicovaginal swab cultured onto human blood Tween (HBT) bilayer medium (Becton Dickson). Gram staining and PCR amplification and sequencing of 16s rDNA were used to confirm the isolate as *Gardnerella vaginalis*. The metronidazole MIC was determined using a metronidazole Etest strip (bioMérieux). Genomic DNA was isolated using a Genra PureGene kit (Qiagen). Genomic DNA was sequenced using the 454-GS Junior System (Roche) following the manufacturer's instructions. Genome assembly was performed using the GS *de novo* assembler version 3.0. Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok).

We generated 111,275 reads totaling 44,322,233 nucleotides. These reads were assembled into a draft genome of 1,732,251 nucleotides at 26-fold coverage. The genome encodes 1,399 genes, 5 rRNA operons, 45 tRNA genes, 67 pseudogenes, 1 noncoding RNA (ncRNA), and 1 clustered regularly interspaced short palindromic repeat (CRISPR) array. *G. vaginalis* strains can be categorized by biotype, based on beta-galactosidase, lipase, and hippurate hydrolase activity (9). Based on the presence of annotated genes encoding enzymes with these three activities (KMT46314.1, KMT46323.1, and KMT46748.1, respectively), we conclude that strain 3549624 is a biotype 1 isolate. *G. vaginalis* has a population structure that consists of four clades (10). The presence of genes encoding alpha-L-fucosidase

(KMT46494.1) and galactokinase (KMT46262.1) indicates that this strain belongs to clade 1 (11). Comparison of this genome using GS Reference Mapper version 3.0 to that of ATCC 14019 (GenBank accession number NC_014644.1), another biotype 1 and clade 1 isolate, found 20,333 high-confidence differences (i.e., nucleotide polymorphisms) as well as structural variants, including 48 deletions, 19 duplications, 18 insertions, and 32 inversions, indicating that there is substantial genetic diversity even within the same *G. vaginalis* biotype and clade. Further analysis of this genome in comparison to other sequenced *G. vaginalis* genomes may provide insight into the molecular basis of metronidazole resistance in this species.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under the accession number [LFWD00000000](https://www.ncbi.nlm.nih.gov/nuclseq/LFWD00000000). The version described in this paper is the first version, LFWD00000000.1.

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