

Antimicrobial Resistance Patterns in *Gardnerella vaginalis* Isolates from a Pregnant South African Population

Kayla Pillay*

University of KwaZulu-Natal, South Africa.

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ABSTRACT

Bacterial vaginosis treatment includes broad-spectrum antibiotics, metronidazole, and clindamycin. However, in clinical settings, increasing antimicrobial resistance has resulted in recurrent BV. This study aimed to determine susceptibility patterns of *G. vaginalis* isolates to various antibiotics. Additionally, the genetic diversity of isolates (*G. vaginalis* clades) was investigated and linked to antimicrobial resistance.

Methods: In total, n=150 enrolled pregnant women, 18 years and older, were provided two self-collected vaginal swabs, used for BV diagnosis and *G. vaginalis* culture. Genetic diversity assessments of isolates were based on genetic differences in the *tuf* gene using clade-specific primers in a quantitative polymerase chain reaction (PCR). Antimicrobial susceptibility profiles were generated using the Sensititre™ Anaerobe MIC Plate (ThermoFisher Scientific, United States).

Results: In this study, 49.3% of the women were BV negative, 28.7% were intermediate and, 22% were positive. Sixteen *G. vaginalis* isolates were successfully cultured from this population. The genotyping/clade PCR detected three clades with frequencies of 100% for clade 1, 37.5% for clade 2 and 43.8% for clade 4. Multiple clades were found in 62.5% of isolates. Only fourteen isolates were viable for susceptibility testing, of which, 8/14 (57.1%) were susceptible to metronidazole (MIC of $\leq 8\mu\text{g/ml}$) and 6/14 (42.9%) were resistant (MIC of $\geq 32\mu\text{g/ml}$).

Conclusion: This study reported on the resistance patterns of clinical *G. vaginalis* isolates, with high levels of metronidazole resistance observed. Obtaining approvals for clindamycin and vancomycin for future treatment of BV should be considered in our current setting.

Keywords: *Gardnerella vaginalis*, Antimicrobial resistance, Clindamycin, Genetic diversity

Corresponding author: Kayla Pillay, University of KwaZulu-Natal, South Africa, E-mail: kaylapillay7@gmail.com

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