

Phenotypic and Genotypic Diversity of *Gardnerella vaginalis* Isolates from South African Pregnant Women

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ABSTRACT

Background: The diversity of *Gardnerella vaginalis* (*G. vaginalis*), the predominant pathogen responsible for the onset and progression of *bacterial vaginosis* (BV), is yet to be explored in the South African setting. The assessment of diversity is needed for establishing a link between the genotypes and biotypes of this pathogen in association with BV status. This study investigated the phenotypic (biotypes) and genotypic (genotypes) diversity of *G. vaginalis* from South African pregnant women diagnosed as BV positive, BV intermediate and BV negative.

Methods: The study population included 150 pregnant women recruited from a public hospital in Durban, South Africa. The women provided two self-collected vaginal swabs for BV diagnosis by Nugent scoring and culture of *G. vaginalis*. Biotypes were assigned based on β -galactosidase, lipase, and hippurate test profiles. Genotyping of the isolates was achieved using Amplified Ribosomal DNA Restriction Analysis (ARDRA) of the 16S ribosomal RNA gene. Assignment of genotypes was based on restriction fragments obtained with TaqI digestion and further phylogenetic analysis was performed on the sequenced 16S rRNA amplicons.

Results: In this study, 49.3% of the women were BV negative, 28.7% were BV intermediate and 22% were BV positive. There was a significant association ($p=0.025$) between reported symptoms of abnormal vaginal discharge and BV status. Sixteen *G. vaginalis* isolates were cultured from the study population. Among the 16 isolates, four different genotypes were detected with genotype 1 (GT1) being the most dominant. The most prevalent biotype was biotype 3. The most frequent genotype/biotype pairing across the isolates was GT1/biotype 3 which was distributed across the BV negative and intermediate groups. According to the phylogenetic analysis, there was heterogeneity in the gene clusters, i.e. *G. vaginalis* isolates from BV intermediate and positive women clustered together. Similarly, heterogeneity was observed with the clustering of certain biotypes, i.e. *G. vaginalis* isolated from BV intermediate and positive women shared similar biotypes.

Conclusion: This study was the first to have reported on the genotypic and phenotypic diversity of *G. vaginalis* isolates from South African women. Diversity assessments of *G. vaginalis* may aid in a greater understanding of the pathogenesis of this microorganism.

Keywords: *Gardnerella vaginalis*, Diversity, Phenotypic, Genotypic, *Bacterial vaginosis*, Pregnant

Abbreviations: *G. vaginalis*: *Gardnerella Vaginalis*; BV: *Bacterial Vaginosis*; ARDRA: Amplified Ribosomal DNA Restriction Analysis; GT1: Genotype 1

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