Bacterial Vaginosis and High-Risk Human Papillomavirus Coinfection Among African American Women in the United States

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Purnima Madhivanan*, 1Maikella Coudray, 2Daniel Ruiz-Perez, 3Brett Colbert, 4Karl Krupp, 5Hansi Kumar, 6Kaiji Mathee, 7Giri Narasimhan, 8Florida International University, College of Arts and Sciences, Miami, USA; 2Florida International University, Bioinformatics Research Group, Miami, USA; 3Florida International University, Department of Biological Sciences, College of Arts and Sciences, Miami, USA; 4Florida International University, Department of Health Promotion and Disease Prevention, Robert Stempel College of Public Health, Miami, USA; 5Florida International University, Biomolecular Sciences Institute, Miami, USA

Background: While the etiology of bacterial vaginosis (BV) is still not known, it is described as a polymicrobial condition that lacks lactic-acid producing Lactobacillus species with an overgrowth of anaerobic bacteria and elevated vaginal pH. This study aims to evaluate the relationship between BV assessed by Nugent scoring of vaginal Gram stain and Trichomonas vaginalis infection among African American women in the U.S.

Methods: Stored vaginal swabs from a previously completed clinical trial were acquired for this study. The kinds of bacteria present in the samples were identified by classifying 16S rRNA gene sequences using high-throughput pyrosequencing. Vaginal smears were also categorized by the Nugent Gram stain score (0–3, normal; 4–6, intermediate state; 7–10, BV). TV genotyping was performed using quantitative polymerase chain reaction, performed using TaqMan probes in a customized plate (Thermo Fisher Scientific; Waltham, Massachusetts). BV was classified using Nugent Scores of Gram stain.

Results: Eighty reproductive age African American (AA) women were included in the analysis. The point prevalence of HrHPV was 48.1% (95% CI: 37–59%). The mean age of the participants was 21.4 years (SD: 2.11). 81.2% graduated high school. Prior antibiotic use was low (3.8%), and 75% were not treated for BV during their lifetime. Among those who had been treated previously for BV, most women were treated ≥ five times (60%). According to Nugent Scores, 70% had BV, 13.7% had intermediate flora and 16.3% were healthy. Among HrHPV positive women, 66.7% were infected with single HrHPV genotype, 33.3% with multiple HrHPV genotypes. Concurrent HrHPV and BV infection was found among 33.3% of the sample. However, there was no significant difference between the prevalence of HrHPV among women with and without BV.

Conclusion: Co-occurrence of HrHPV and BV among this group of young African American women was relatively high. Considering that these conditions are very common among women worldwide, further research in this field is imperative. More studies are needed to accurately evaluate temporal sequence of acquisition of both conditions in any attempt to establish a causal relationship.

 Disclosure: No significant relationships.

Co-Occurrence of Bacterial Vaginosis and Trichomonas Vaginalis Among Young African American Women

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Purnima Madhivanan*, 1Maikella Coudray, 2Daniel Ruiz-Perez, 3Brett Colbert, 4Karl Krupp, 5Hansi Kumar, 6Giri Narasimhan, 7Kaiji Mathee, 8Florida International University, College of Arts and Sciences, Miami, USA; 2Florida International University, Bioinformatics Research Group, Miami, USA; 3Florida International University, Department of Biological Sciences, College of Arts and Sciences, Miami, USA; 4Florida International University, Department of Health Promotion and Disease Prevention, Robert Stempel College of Public Health, Miami, USA; 5Florida International University, Biomolecular Sciences Institute, Miami, USA

Background: Bacterial vaginosis (BV) increases the risk of many sexually transmitted infections. The co-occurrence of persistent HrHPV and BV increases the risk of developing cervical cancer. This study aims to investigate the co-occurrence of HrHPV and BV among young women in the US.

Methods: Single HrHPV genotype, 33.3% with multiple HrHPV genotypes. Concurrent HrHPV and BV infection was found among 33.3% of the sample. However, there was no significant difference between the prevalence of HrHPV among women with and without BV.

Conclusion: Co-occurrence of HrHPV and BV among young women in the US.

Disclosure: No significant relationships.

Overlap Between Amsel’s Criteria, Nugent’s Gram Stain Score, and Vaginal Microbiota Community State Types

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Antonio Salas, 1Khail Ghanem, 2Rebecca Brotman, 2Jacques Ravel, 1Susan Tuddenham. 1Johns Hopkins University School of Medicine, Baltimore, USA; 2University of Maryland, Institute of Genome Sciences, Baltimore, USA

Background: Bacterial vaginosis (BV) is characterized by low-Lactobacilli and increased anaerobes. BV can be determined by clinical assessment (Amsel’s criteria) or microscopy (Nugent scoring); molecular methods are also under study. We investigated concordance between Amsel-BV, Nugent-BV and low-Lactobacillus vaginal microbiota identified via 16S rRNA gene sequencing.

Methods: Vaginal swabs and clinical data were collected from women enrolled in a longitudinal study. Amsel’s criteria were determined clinically and Nugent scoring (Nugent-BV = 7–10, intermediate=4–6) was determined by microscopy. Vaginal microbiota were characterized using 16S rRNA gene sequencing and categorized into 7 community state types (CSTs): 4 dominated by Lactobacillus spp. (CST I, II, III and V), and 3 by Streptococcus spp. (CST VI), Bifidobacterium spp. (CST VII), or a variety of anaerobes (CST IV).