BACTERIAL VAGINOSIS AND HIGH-RISK HUMAN PAPILLOMAVIRUS CO-INFECTION AMONG AFRICAN AMERICAN WOMEN IN THE UNITED STATES

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Background Bacterial vaginosis (BV) increases the risk of many sexually transmitted infections. The co-occurrence of persistent BV and high-risk HPV (HRHPV) 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 Stored vaginal swabs were acquired from a previously completed clinical trial. The kinds of bacteria present in the samples were identified by classifying 16S rRNA gene sequences in each sample using high-throughput pyrosequencing. HPV genotyping was performed using quantitative polymerase chain reaction using TaqMan probes in a customized plate (ThermoFisher 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 were previously treated for BV, 60% were treated five or more times. Douching was reported by 49% of the sample. 55% of TV cases had concurrent BV, while 11.1% of TV cases also had intermediate vaginal flora. There were no associations with prior antibiotic use, hormonal contraception, douching or prior treatment.

Conclusion Young African American women of reproductive age found to have abnormal vaginal flora should be screened for *Trichomonas vaginalis* infection.

Disclosure No significant relationships.

OVERLAP BETWEEN AMSEL’S CRITERIA, NUGENT’S GRAM STAIN SCORE, AND VAGINAL MICROBIOTA COMMUNITY STATE TYPES

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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 was characterized using 16S rDNA 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).

Disclosure No significant relationships.