

P372 BACTERIAL VAGINOSIS AND HIGH-RISK HUMAN PAPILLOMAVIRUS COINFECTION 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 had been treated previously for BV, most women were treated \geq 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.

P373 CO-OCCURRENCE OF BACTERIAL VAGINOSIS AND TRICHOMONAS VAGINALIS AMONG YOUNG AFRICAN AMERICAN WOMEN

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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 young 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). Descriptive statistics were conducted to determine the odds of TV infection among women with BV.

Results This study included 80 African American reproductive age women with a mean age of 21.4 years (SD: 2.11 years). Most (81.2%) women had graduated high school. 70% (95% CI: 37–59%) had BV, 13.7% had intermediate and 16.3% had healthy vaginal flora. TV was diagnosed among 11.1% (95% CI: 4–8%) of the women. Prior antibiotic use was low (3.8%), and 75% of women had not been treated for BV during their lifetime. Among those who were previously treated for BV, 60% were treated five or more time. 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 association 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.

P374 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 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).