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

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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).

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.

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

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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 young African American 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).

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) increases the risk of many sexually transmitted infections. The co-occurrence of persistent BV and high-risk HPV (HR-HPV) increases the risk of developing cervical cancer. This study aims to investigate the co-occurrence of HR-HPV and BV among young women in the U.S.

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, 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% 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. 35% 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.