Bacterial vaginosis (BV) increases the risk of many sexually transmitted infections. The co-occurrence of persistent 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 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). 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.

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

P374

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).