CHARACTERIZATION OF THE VAGINAL MICROBIOTA AMONG SEXUAL RISK BEHAVIOR GROUPS OF WOMEN WITH BACTERIAL VAGINOSIS

Christina A. Muzny 1, Imran R. Sunesara 1,2, Ranjit Kumar 3, Leandro A. Mena 4, Michael E. Griswold 2, David H. Martin 5, Elliot J. Lefkowitz 3,6, Jane R. Schwebke 1, Ed Swiatlo 4

1 Division of Infectious Diseases, University of Alabama at Birmingham
2 Center of Biostatistics and Bioinformatics, University of Mississippi Medical Center
3 Biomedical Informatics, Center for Clinical and Translational Sciences, University of Alabama at Birmingham
4 Division of Infectious Diseases, University of Mississippi Medical Center
5 Division of Infectious Diseases, Louisiana State University Health Sciences Center
6 Department of Microbiology, University of Alabama at Birmingham

BACKGROUND: The pathogenesis of bacterial vaginosis (BV) remains elusive. BV may be more common among women who have sex with women (WSW). The objective of this study was to use 454 pyrosequencing to investigate the vaginal microbiome of WSW, women who have sex with women and men (WSWM), and women who have sex with men (WSM) with BV to determine if there are differences in organism composition between groups that may inform new hypotheses regarding the pathogenesis of BV.

METHODS: Vaginal swab specimens from eligible women with BV at the Mississippi State Department of Health STD Clinic were used. After DNA extraction, 454 pyrosequencing of PCR-amplified 16S rRNA gene sequences was performed. Sequence data was classified using the Ribosomal Database Program classifier. Complete linkage clustering analysis was performed to compare bacterial community composition among samples. Differences in operational taxonomic units with an abundance of ≥2% between risk behavior groups were determined. Alpha and beta diversity were measured using Shannon’s Index implemented in QIIME and Unifrac analysis, respectively.

RESULTS: 33 WSW, 35 WSWM, and 44 WSM were included. The vaginal bacterial communities of all women clustered into four taxonomic groups with the dominant taxonomic group in each being Lactobacillus, Lachnospiraceae, Prevotella, and Sneathia. Regarding differences in organism composition between risk behavior groups, the abundance of Atopobium (relative ratio (RR)=0.24; 95% CI 0.11-0.54) and Parvimonas (RR=0.33; 95% CI 0.11-0.93) were significantly lower in WSW than WSWM, and the abundance of Prevotella was significantly higher in WSW than WSM (RR=1.77; 95% CI 1.10-2.86), and the abundance of Atopobium (RR=0.41; 95% CI 0.18-0.88) was significantly lower in WSWM than WSM. Overall, WSM had the highest diversity of bacterial taxa.

CONCLUSION: The microbiology of BV among women in different risk behavior groups is heterogeneous. WSM in this study had the highest diversity of bacterial taxa. Additional studies are needed to better understand these differences.