women as part of a larger prospective longitudinal cohort study. Bacterial communities were characterized by phylogenetic analysis of 16S rRNA gene sequences. Taxonomic classification was carried out using the Silva 132 classifier for variable region 4, which matches the sequences to the SILVA database. HIV infectivity was measured using an established in vitro model of HIV infectivity, the TZM-bl assay. Descriptive statistics were performed using chi squared test, student's t test and PERMANOVA. Multivariate logistical regression was performed to assess the risk of HIV infectivity related to lactobacillus predominated flora compared to diverse flora after controlling for potential confounders.

RESULTS: The majority of samples (79%) were dominated by one or more species of Lactobacillus that constitute > 50% of all sequences obtained. Such samples were categorized as "lactobacillus predominant," whereas all other samples were categorized as "diverse." Non-lactobacillus predominant populations had a mean Nugent score diagnostic for bacterial vaginosis for both pregnant (9.3 vs. 1.3, p = 0.001) and non-pregnant (9.0 vs. 1.6, p 0.001) patients. In the unadjusted analysis for pregnant patients, the mean HIV inhibition appeared to be lower in the group with diverse flora compared to those with lactobacillus predominated flora, although this difference was not statistically significant (26.5 65.2 vs. 77.4 32.0, p = 0.217). After controlling for potential confounders, there was no difference in risk of HIV infectivity related to lactobacillus predominated flora compared to diverse flora in pregnant (OR 1.03, 95% C.I. 0.97-1.13, p = 0.376) or non-pregnant patients (OR 1.08, 95% C.I. 0.83-1.62, p = 0.595).

CONCLUSION: Further study is necessary to assess the risk of HIV infectivity related to lactobacillus predominated flora compared to diverse flora.

LEARNING OBJECTIVES: Learners will be able to describe characteristics of bacterial communities that may affect HIV infectivity.

9 High viral load in women living with HIV linked to a different dysbiotic vaginal microbiota compared to women without HIV

Chelsea Elwood[1,2], Arianne Y. K. Albert[1,2], Elisabeth McClymont[1], Emily Wagner[2], Daljeet Mahal[1], Keshini Devakandan[1], Bonnie Chaban[3,4], Zahra Pakzad[2], Janet E. Hill[3], Deborah Money[1,2], and the VOGUE Research Group

[1]Department of Obstetrics and Gynecology, University of British Columbia, Vancouver, BC, Canada, [2]Women'sHealth Research Institute, Vancouver, BC, Canada, [3]Department of Veterinary Microbiology, University of Saskatchewan, Saskatoon, SK, Canada, [4]Faculty of Science, Health, Education, and Engineering, University of the Sunshine Coast, Queensland, Australia

OBJECTIVES: To compare the vaginal microbiota of women living with HIV to the vaginal microbiota of women with recurrent bacterial vaginosis and healthy women without HIV to determine if there are differences in the vaginal microbiome between these women, what factors influence these differences, and to characterize HIV clinical parameters including viral load and CD4 count in relation to the vaginal microbiome.

METHODS: Women between the ages of 18-49 years who were premenopausal and not pregnant were recruited into three cohorts: healthy women, women living with HIV, and women with recurrent bacterial vaginosis (BV). Demographic and clinical data were collected via interviews and medical chart reviews. Vaginal swabs were collected for Gram stain assessment and microbiome profiling utilizing the cpn60 barcode sequence. To compare overall community composition differences, we used compositional data analysis methods, then visualized communities with principal components analysis, hierarchical clustering, and Kruskal-Wallis tests where appropriate.

RESULTS: Clinical markers such as odour and abnormal discharge, but not irritation, were associated with higher microbial diversity. WLWH with unsuppressed HIV viral loads are more likely than HIV-negative women with recurrent BV to have non-Gardnerella dominated microbiomes. HIV is associated with higher vaginal microbial diversity and this is related to HIV viral load, with unsuppressed women demonstrating higher relative abundance of Megasphaera, Clostridiales, and Prevotella species.

CONCLUSION: Dysbiosis in these cohorts was clearly defined by metagenomic methods and in women living with HIV, unsuppressed HIV viral loads were associated with a distinct dysbiotic profile consisting of very low levels of Lactobacillus and high levels of anaerobes.

LEARNING OBJECTIVES: identify differences in the vaginal microbiome between women living with HIV, women with recurrent BV and healthy women without HIV or BV.

10 Repeat trichomonas vaginalis infections among pregnant women in the southern United States

O. Van Gerwen[1], K. J. Aaron[1], A. Tamhane[1], K. Shrestha[2], A. Subramaniam[3], C. A. Muzny[1]

[1]Division of Infectious Diseases, Department of Medicine, University of Alabama at Birmingham, [2]School of Medicine, University of Alabama at Birmingham, [3]Division of Maternal-Fetal Medicine, Department of Obstetrics & Gynecology, University of Alabama at Birmingham

OBJECTIVES: The epidemiology of T. vaginalis among pregnant women, including rates of repeat infection, is not well known, particularly in the Deep South. Our objectives were to determine the frequency and predictors of repeat T. vaginalis infection after treatment for an initial episode of infection among pregnant women delivering at a large academic medical center in the Southern United States.

METHODS: Pregnant women with an initial episode of T. vaginalis infection during 2013 were identified from an existing database of women with cervical cancer screening test results within 3 years before delivery. The electronic medical record of these patients was reviewed for socio-demographics, sexual behavior, STI history, diagnostic method of T. vaginalis, treatment of T. vaginalis, and evidence of a repeat positive T. vaginalis test after initial diagnosis (and prior to delivery). The association of clinically significant predictors was then examined using univariate and multivariable logistic regression analyses and expressed as crude and adjusted odds ratios (cORs and aORs), respectively.

RESULTS: Of 3,958 pregnant women with deliveries at our institution during 2013, 2,321 met the eligibility criteria for the cervical cancer screening study and were included in the parent database. Of these 2,321 women, 116 (5.0%) had an initial episode of T. vaginalis infection during their pregnancy and had their medical record abstracted: 59.5% were ≤25 years old, 94.8% were African American, 16.4% currently used illicit drugs, 44.0% reported genital symptoms, and 80.2% were treated with the 2 gram stat dose of metronidazole. Of these 116 women, 8 (6.9%) had evidence of a repeat positive T. vaginalis infection at a median time of 108 days (IQR 55-184 days) after their first positive test. In multivariable analyses, women who were symptomatic at initial T. vaginalis diagnosis (aOR 3.56: 95% CI 0.72, 34.93), who received the 2 gram dose of metronidazole at initial diagnosis (aOR 2.75; 95% CI 0.28,