

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 vs. 65.2 vs. 77.4 vs. 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



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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



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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,

368.60), and who currently reported illicit drug use (aOR 3.45; 95% CI 0.71, 15.05) had a higher odds of repeat *T. vaginalis* infection.

CONCLUSION: Although this study had a small sample size, symptomatic women and those receiving the 2 gram stat dose of metronidazole may be at higher risk for repeat *T. vaginalis* infection during pregnancy. Future studies are needed to elucidate the optimal *T. vaginalis* treatment regimen in pregnant women.

LEARNING OBJECTIVES: Identify the predictors of reinfection with *Trichomonas vaginalis* in pregnant women living in the Southern United States.

11 Patterns and predictors of delayed treatment and tests of reinfection for chlamydia and gonorrhea infections in pregnancy



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OBJECTIVES: To describe the patterns of treatment and tests of reinfection (TOR) for chlamydia and gonorrhea in pregnancy. To investigate factors associated with delayed treatment and TOR.

METHODS: Retrospective cohort study of women who delivered at a single public hospital between July 1, 2016 and June 30, 2018. A positive chlamydia or gonorrhea infection was defined as positive result on nucleic acid amplification testing. Fisher's exact and Kruskal-Wallis H test were used to compare proportions and times to treatment and TOR by STI diagnosis. We used a shared frailty cox proportional hazards model to investigate factors associated with delays in treatment and TOR. An alpha of 0.05 was employed for all tests of significance.

RESULTS: Among 3,349 women, 378 (11.3%) tested positive and 91 (2.7%) were not tested. These 378 positive women contributed 351 unique cases of chlamydia, 51 cases of gonorrhea, and 46 co-infections. Overall, 94.9% of cases received antibiotic treatment, with the proportion treated differing by STI diagnosis (chlamydia = 96.3%, gonorrhea = 88.2%, co-infection = 91.3%, $p = 0.02$). Time to treatment ranged from zero to 221 days with 56% and 19.5% receiving treatment greater than one and four weeks after testing, respectively. Treatment occurred during hospital admission for delivery in 25 cases (5.9%), including the case whose treatment took 221 days to initiate. Time to treatment did not differ significantly by STI diagnosis ($H = 3.60$, $p = 0.17$). A TOR was completed 21 days or more after treatment in 74.8% of cases. TOR was delayed by more than one month in 30.5% of cases. Time to TOR and proportion having a TOR did not differ significantly by STI group ($H = 1.62$, $p = 0.45$; chlamydia = 72.5%, gonorrhea = 82.2%, co-infection = 85.7%, $p = 0.09$). The only demographic or clinical variable that predicted delays in treatment and TOR was increasing gestational age at diagnosis (treatment HR = 1.03, 95% CI = 1.02, 1.04; TOR HR = 1.04, 95% CI = 1.02, 1.05).

CONCLUSION: A substantial proportion of chlamydia and gonorrhea cases experienced delays in treatment and TOR, and a lower proportion of cases involving gonorrhea were treated compared to chlamydia. This may be due in part to the need to report in person for administration of ceftriaxone. Given the impact of treatment on reducing adverse pregnancy outcomes such as preterm birth, point of care testing should be considered in high risk populations in order to expedite treatment.

LEARNING OBJECTIVES: Learners will be able to identify patterns of chlamydia and gonorrhea treatment and tests of reinfection during pregnancy.

12 Mechanisms of 5-nitroimidazole resistance in trichomonas vaginalis: a systematic review of the literature



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OBJECTIVES: *Trichomonas vaginalis* is the most common non-viral STI affecting an estimated 3.7 million men and women in the U.S. and over 200 million worldwide. Currently approved drugs are from the 5-nitroimidazole class (i.e. metronidazole and tinidazole) however resistance rates can range from 5-10%. The objective of our study was to perform a systematic review of the literature on mechanisms of 5-nitroimidazole resistance in *T. vaginalis*.

METHODS: A systematic review of original research focusing on mechanisms of 5-nitroimidazole resistance in *T. vaginalis* over the past 60 years was performed. The PubMed, Science Direct, and EMBASE databases were searched using the keywords: *Trichomonas vaginalis*, trichomoniasis, 5-nitroimidazole, metronidazole, tinidazole, and drug resistance. Foreign language articles and articles not containing *T. vaginalis* resistance testing on the two drugs of interest were excluded.

RESULTS: The search yielded 132 results, of which 103 articles were excluded, leaving 29 results. Drug resistance can arise aerobically or anaerobically. It can also potentially arise through infection of *T. vaginalis* with *Mycoplasma hominis* or *T. vaginalis* virus (TVV). Resistance to 5-nitroimidazoles involves different proteins and enzymes involved in drug activation including pyruvate: ferredoxin reductase, ferredoxin, Nitroreductase, hydrogenases, Thioredoxin reductases, and flavin reductases. Evidence suggests that resistance may depend on intracellular oxygen and iron concentrations as well. There also appears to be a distinguishable difference in the prevalence of drug resistance based on the genetic diversity of *T. vaginalis* and its two population types with higher nitroimidazole resistance seen in type 2 populations as opposed to type 1 populations.

CONCLUSION: Drug resistance to 5-nitroimidazoles is facilitated by the differential expression of enzymes and proteins involved in drug activation, intracellular oxygen and iron concentrations, and genetic mutations in the *T. vaginalis* genome. Resistance prevalence varies depending on the 5-nitroimidazole used to treat trichomoniasis. Resistance to one 5-nitroimidazole can lead to the development of resistance to others within the drug class. Therefore, new alternative methods of treatment outside of the 5-nitroimidazole class, as well as a more complete understanding of the mechanisms behind 5-nitroimidazole drug resistance are needed.

LEARNING OBJECTIVES: Learners will be able to recognize the underlying mechanisms of 5-nitroimidazole resistance.

13 Predictors of trichomoniasis in pregnancy: a retrospective study in a high-risk population in Atlanta, Georgia



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OBJECTIVES: To identify the prevalence and factors associated with trichomoniasis in pregnancy

METHODS: We conducted a retrospective cohort study of women who delivered between 2016 and 2018 at a single institution who were tested for trichomoniasis during pregnancy. Demographic and clinical characteristics were abstracted from the electronic medical