more variation in reports of minority taxa and relative abundances. Standardized use of mock communities may improve reproducibility across vaginal microbiota studies.

Disclosure No significant relationships.

**P589 THE INFLUENCE OF PRECONCEPTION VAGINAL MICROBIOTA ON PRETERM BIRTH**

1Kalpana Betha, 2Srinivas Vudathala, 3Saumyadipta Pyne, 1Govind Kushnirwar, 1Pavani Sonjanya, 2PS Reddy, 3Catherine Haggerty, 1SHARE India, Telangana, India; 2PathCare Labs Pvt Ltd., Telangana, India; 3University of Pittsburgh, Pittsburgh, USA; 4University of Pittsburgh, Graduate School of Public Health, Department of Epidemiology, Pittsburgh, USA

Background Preterm birth (PTB) is common worldwide and causes significant neonatal morbidity, Although ascending reproductive tract infection has been implicated in approximately half of spontaneous PTB cases, the microbiologic etiology remains poorly understood and no studies have examined the role of preconception vaginal microbiota in PTB.

Methods We conducted a pilot study comparing bacterial communities among 6 women who experienced a PTB < 34 weeks' gestation and 12 term delivery controls who participated in the Longitudinal Indian Family hEalth (LIFE) study in Telangana, India. Archived preconception vaginal samples were analyzed using broad-range 16S rRNA gene PCR with sequencing. Women with preeclampsia were excluded.

Results Cases had more sequence reads from *Sneathia* spp., *Megaplasma* spp., and *Atopobium vaginae* than controls. Overall, the vaginal microbiota of cases was more diverse than those from controls. Women who delivered at term generally had vaginal microbiota dominated by *Lactobacillus* spp.

Conclusion Our study suggests key differences in preconception vaginal bacterial communities between women who experience a PTB compared to women who deliver at term. Future large scale epidemiologic studies of preconception and prenatal vaginal microbiota and adverse pregnancy outcomes are warranted and may guide PTB interventions.

Disclosure No significant relationships.

**P590 VAGINAL MICROBIOTA AND DOUCHING CESSION: A CROSSOVER PILOT STUDY**

1Sarah Brown, 2Xin He, 3Courtney Robinson, 3Khali Ghanem, 1Jacques Ravel, 1Jonathan Zenilman, 2Rebecca Brotman. 1University of Maryland, Institute for Genome Sciences, Baltimore, USA; 2University of Maryland, College Park, Epidemiology and Biostatistics, College Park, USA; 3Johns Hopkins, Infectious Diseases, Baltimore, USA

Background Observational studies have demonstrated a dose-dependent association between vaginal douching and bacterial vaginosis. We sought to estimate the effect of douching cessation on the vaginal microbiota in a pilot crossover study.

Methods Thirty-two women self-collected vaginal swabs twice-weekly (n=950) during a douching observational phase (“DC”, 4 weeks), followed by douching cessation (“DC”, 12 weeks). Vaginal microbiota were characterized by 16S rRNA gene sequencing (V3-V4) and clustered into community state types (CSTs). A conditional logistic regression model, adjusted for menstruation and sexual behaviors, allowed each woman to serve as her own control. Wilcoxon signed-rank tests were used to evaluate paired changes in microbiota between phases. Broad-range qPCR assays provided estimates of bacterial absolute abundance per swab. A piecewise linear mixed effects model was used to assess differences in rates of change in bacterial absolute abundance before and after douching.

Results There was not a statistically significant change in the odds of *Lactobacillus*-dominated CSTs comparing DC to D (OR 0.54, 95% CI: 0.27–1.11). There were no significant changes for four individual *Lactobacillus* spp. and no meaningful changes in other taxa investigated. The rates of change in bacterial absolute abundance was not significantly different in samples collected 3 days before and after douching (p=0.46). Women who had a *Lactobacillus*-dominated CST at baseline experienced shifts to low-*Lactobacillus* CST in DC, and vice versa for women who had a low-*Lactobacillus* CST at baseline (interaction on entry CST, p-value <0.02), however, these findings were driven by changes occurring in the final weeks.

Conclusion In this pilot study, douching cessation was not associated with major changes in vaginal microbiota. Shifts in *Lactobacillus*-dominance may represent regression to the mean as the shifts occurred late in DC, giving ample time for fluctuations. Disparate findings between this study and prior analyses using Nugent score may be related to low-*Lactobacillus* CSTs receiving low/intermediate Nugent scores.

Disclosure No significant relationships.

**P591 THE EFFECT OF HORMONAL CONTRACEPTION ON THE VAGINAL MICROBIOTA OVER 2 YEARS**

1Susan Tuddenham, 1Khali Ghanem, 2Pawel Gajer, 3Courtney Robinson, 1Jacques Ravel, 2Rebecca Brotman. 1Johns Hopkins, Infectious Diseases, Baltimore, USA; 2University of Maryland, Institute of Genome Sciences, Baltimore, USA

Background Despite widespread use, the effect of hormonal contraception (HC) on the vaginal microbiota (VMB) is understudied. We compared VMB in a longitudinal observational study of women during intervals on and off HC.

Methods Women stopping and starting any form of HC and women off HC (controls) collected vaginal swabs twice-weekly for 2 weeks prior to 7 study visits over 2 years. 16S rRNA gene sequencing was conducted, and the VMB was categorized for 2 weeks prior to 7 study visits over 2 years. 16S rRNA gene sequencing was conducted, and the VMB was categorized into 7 community state types (CSTs): 4 dominated by *Lactobacillus* spp. and 3 by *Streptococcus* spp (CST VI). Mixed effects logistic regression models assessed differences in CST proportions. Bayesian double exponential random effects models estimated differences between stability indices within HC and control subjects (measured by median Jensen-Shannon distance [MJSD] from the subject’s own centroid and from the centroid of CST I [L. crispatus-dominated]).

Results 4185 samples from 105 women (73 HC, 32 controls) were available for analysis. The VMB was more stable in women on HC as compared to controls (MJSD 0.16 vs 0.22, p<0.01) and in oral contraceptive pill users versus controls (MJSD 0.14 vs 0.22, p<0.01). Women had increased stability after being on HC for ≥3 months as compared to <3 months (MJSD difference 0.43, p<0.01). Women on HC for ≥3 months were more likely to be in CST I (51.3% vs 37.3%, p<0.01) and less likely to be in CST IV (11.4% vs 22.5%, p=0.01) than controls. Women on HC ≥3 months maintained
MICROBIOTA CONCORDANCE BETWEEN MID-VAGINAL SWABS AND BOTH CLEAN- AND RANDOM-CATCH URINE SAMPLES

1Courtney Robinson*, 1Johanna Holm, 2Sarah Brown, 1Jacques Ravel, 3Khalil Ghanem, 4Rebecca Brotman*; 1University of Maryland, Institute for Genome Sciences, Baltimore, USA; 2University of Maryland, Institute of Genome Sciences, Baltimore, USA; 3Johns Hopkins, Infectious Diseases, Baltimore, USA; 4University of Maryland, Institute of Genome Sciences, Baltimore, USA

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Background While urine has successfully been used for STI testing, it has not been routinely used in urogenital microbiota studies. This work explores whether random-catch and/or clean-catch urine could be a proxy for assessing the vaginal microbiota.

Methods In two studies, urinary and vaginal microbiota from women ages 17–45 were compared for (1) 91 participants with paired mid-vaginal swabs and random catch urine samples and (2) 99 participants with paired mid-vaginal swabs and clean catch urine samples. Microbiota composition was characterized by amplicon sequencing of the V3-V4 regions of the 16S rRNA gene. Taxonomic classification was assigned based on SILVA and SpeciateIt. Community State Types (CST) were assigned using an algorithm trained on 13,000 well-characterized samples. CST I, II, III, and V were dominated by: Lactobacillus crispatus, L. gasseri, L. iners, and L. jensenii, respectively. CST IV-A, IV-B, and IV-C represented low-Lactobacillus states. Similarity of paired urine and vaginal samples was measured at the CST-level by kappa statistics and the population-level with the Yue-Clayton theta indices.

Results We obtained 12 and 7.8 million sequences from urine and vaginal samples, respectively. At the CST-level, random-catch and clean-catch urines were 82.4% and 81.8% concordant with paired mid-vaginal swabs, respectively. Substantial agreement was observed between urine and paired vaginal specimen (K_{random-catch}= 0.770 and K_{clean-catch}=0.743). At a population-level, average similarity of random- and clean-catch samples to paired vaginal samples indicated a high degree of similarity (θ=0.7496 and 0.7565, respectively). Comparison of the distributions of random-catch and clean-catch θ similarity scores showed no differences (p=0.86).

Conclusion Bacterial compositions of random catch and clean catch urine samples showed substantial agreement to paired mid-vaginal samples assessed by CST- and community-level analyses. Random and clean catch urine samples could potentially be used as a proxy for vaginal microbiota in studies assessing the urogenital microbiota. 

Disclosure No significant relationships.