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

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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., *Megasphaera* 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 CESSATION: A CROSSOVER PILOT STUDY

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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 ("D", 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 (aOR 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

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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 into 7 community state types (CSTs): 4 dominated by *Lactobacillus* spp, and 3 by *Streptococcus* spp (CST VI), *Bifidobacterium* spp (CST VII), or a variety of anaerobes (CST IV). 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