and associations with Amsel criteria may vary between populations. We assessed relationships between vaginal bacteria and Amsel criteria among two distinct cohorts.

Methods Kenyan participants from the placebo arm of the Preventing Vaginal Infections (PVI) trial and participants from a Seattle-based cross-sectional BV study were included. At PVI trial enrollment and bi-monthly follow-up visits and the Seattle study visit, Amsel criteria were recorded, and the vaginal microbiota was characterized using 16S rRNA gene sequencing. For each cohort, logistic regression models were fit to evaluate associations between vaginal bacterial relative abundance and each Amsel criterion (PVI cohort models used generalized estimating equations).

Results Among 84 PVI participants (contributing 496 observations), the prevalence of amine odor was 25%, clue cells 16%, vaginal discharge 10%, elevated vaginal pH 69%, and BV 13%. Among 220 Seattle participants, the prevalence of amine odor was 40%, clue cells 37%, vaginal discharge 52%, elevated vaginal pH 67%, and BV 44%. BV-associated bacterium 1 (BVAB1) was positively associated with each Amsel criterion in both cohorts. *Atopobium vaginae*, *Eggerthella* type 1, *Gardnerella*, *Sneathia amnii*, and *Sneathia sanguinegens* were positively associated with each criterion in the Seattle cohort, and all but discharge in the PVI cohort. *Prevotella amnii* was positively associated with each criterion except discharge in the PVI cohort. *Megasphaera* type 1 and *Prevotella timonensis* were positively associated with each criterion in the Seattle cohort. *Lactobacilli* were negatively associated with individual criteria in both cohorts.

Conclusions A set of core vaginal bacteria were positively associated with Amsel criteria in both cohorts, suggesting their importance in the manifestation of BV signs and symptoms, regardless of population differences. These results may have implications for future BV treatment studies.

Bacterial vaginosis

003.1

BACTERIAL VAGINOSIS AND BEHAVIORAL FACTORS ASSOCIATED WITH INCIDENT PELVIC INFLAMMATORY DISEASE IN THE LONGITUDINAL STUDY OF VAGINAL FLORA

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Background Pelvic inflammatory disease (PID) leads to long-term reproductive consequences for cisgender women. Bacterial vaginosis (BV) and behavioral factors may play a role in PID pathogenesis. We assessed associations between BV, behavioral factors and incident PID in a large prospective cohort.

Methods We analyzed data (n=2,956) from the NIH Longitudinal Study of Vaginal Flora, a cohort of non-pregnant cisgender women followed quarterly for 12 months. PID was defined by at least one of the following: cervical motion

tenderness, uterine tenderness, or adnexal tenderness (160 cases). We tested associations between BV (measured using Nugent's and Amsel's criteria) and PID at the subsequent visit using Cox proportional hazards models. Baseline socio-demographic factors (age, race, highest education level, marital status, monthly household income), time-varying sexual behaviors (condom use frequency, number of sexual partners, sexual partner concurrence), vaginal douching, and Chlamydia trachomatis (CT), untreated at baseline and concurrent with BV, were covariates. Adjusting for the few *Neisseria gonorrhea* and *Trichomonas vaginalis* cases did not alter results.

Results The 2,956 participants contributed a total 2516.2 person-years, with a median 349 days per participant. In multi-variable modeling, Nugent-BV (aHR=1.53, 95% CI:1.05–2.21), symptomatic Amsel-BV (aHR=2.15, 95% CI:1.23–3.75) and vaginal douching (aHR=1.47, 95% CI:1.03–2.09) were associated with greater risk of incident PID. Other factors associated with incident PID included baseline untreated CT, douching, and being married.

Conclusions BV was associated with incident PID in a large prospective cohort, controlling for behavioral factors and sexually transmitted infections (STIs). Larger studies on how BV, STIs, behaviors, and host responses interactively affect PID risk are needed.

003.2

THE SHORT-TERM IMMUNE IMPACT OF BACTERIAL VAGINOSIS TREATMENT IS UNRELATED TO LACTOBACILLUS SPP. ABUNDANCE

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Background Bacterial vaginosis (BV) induces genital inflammation and enhances HIV acquisition risk, while vaginal *Lactobacillus* predominance is associated with mucosal immune quiescence and reduced HIV risk. BV treatment reduces vaginal proinflammatory cytokines, but it is unclear whether this is due to reductions in BV-associated anaerobes or an increase in *Lactobacillus* spp. We investigated the short-term impact of BV treatment on the vaginal immune milieu and microbiome.

Methods Study participants comprised 48 women with BV, all of whom were treated with intravaginal metronidazole for 5 days before enrollment into a clinical trial of the live biotherapeutic LACTIN-V to prevent BV recurrence. Vaginal swabs were collected at baseline and within 48 hours of completing metronidazole treatment, prior to study product administration. Soluble immune factors were assayed from vaginal swabs by multiplex ELISA, relative bacterial abundance was assessed