002.4 RELATIONSHIP BETWEEN THREE NOVEL BACTERIAL VAGINOSIS (BV) ASSOCIATED BACTERIA AND NONGONOCOCCAL URETHRITIS IN MEN WHO HAVE SEX WITH WOMEN

¹K Zinsli*, ²S Srinivasan, ¹J Balkus, ¹L Chambers, ³M Lowens, ³J Morgan, ¹E Rowlinson, ¹T Robinson, ¹S Romano, ²M Munch, ¹L Manhart, ^{2,4}D Fredricks. ¹Department of Epidemiology, University of Washington, Seattle, USA; ²Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center, Seattle, USA; ³Public Health – Seattle and King County, Seattle, USA; ⁴Department of Medicine, University of Washington, Seattle, USA

10.1136/sextrans-2021-sti.59

Background Bacterial vaginosis associated bacteria (BVAB) have been detected among cisgender men who have sex with women (MSW) and may be associated with clinical syndromes in men. We evaluated the frequency and correlates of three BVAB in MSW and their association with nongonococcal urethritis (NGU).

Methods MSW without *Neisseria gonorrhoeae* attending an urban STD clinic from 2014–2018 completed a computer-assisted self-interview, clinical interview and examination. NGU was defined as ≥ 5 polymorphonuclear leukocytes/hpf on a urethral Gram stain plus urethral symptoms or visible discharge. Urine specimens were tested for *Chlamydia trachomatis* and *Mycoplasma genitalium* using Aptima (Hologic, Inc.) and for BVAB2, *Mageeibacillus indolicus*, *Sneathia* spp., *Trichomonas vaginalis*, *Ureaplasma urealyticum*, herpes simplex virus, and adenovirus using quantitative PCR (qPCR). A subset of men contributed serial monthly specimens over 6 months.

Results Of 317 MSW ages 17–71, 67 (21.1%) had *Sneathia* spp., 36 (11.4%) had BVAB2, and 17 (5.4%) had *M. indolicus* at enrollment. Co-colonization with >1 BVAB was observed in 50% (36/71). No demographic and few behavioral characteristics were associated with these BVAB; only having multiple partners (≥ 3 past two months) was more common among men with than without these BVAB (BVAB2: 47% vs. 23%, *M. indolicus*: 53% vs. 24%, *Sneathia* spp: 42% vs. 22%, $p \leq 0.03$ for all). *Sneathia* spp. were associated with lower odds of prevalent NGU (adjusted Odds Ratio [aOR]=0.36, 95% CI=0.13–0.97) whereas neither BVAB2 nor *M. indolicus* were associated with prevalent NGU (aOR=0.62; 95% CI=0.15–2.55; aOR=3.12; 95% CI=0.63–15.54). In 34 men with serial samples, persistence was common and not significantly different between BVAB (median persistence for BVAB2=2 months (range=2–6); *M. indolicus*= 4 months (range=3–5); *Sneathia* spp.=3 months (range=2–8); $p \geq 0.20$ for each comparison).

Conclusions BVAB2, *M. indolicus*, and *Sneathia* spp. were frequently detected in MSW attending an STD clinic, but not associated with increased risk of prevalent NGU.

002.5 SECRETED PROTEOLYTIC ACTIVITY OF BACTERIAL VAGINOSIS-ASSOCIATED BACTERIA

¹K Lithgow*, ¹V Buchholz, ¹S Kenschuh, ^{1,2,3}L Sycuro. ¹Dept of Microbiology, Immunology and Infectious Diseases, University of Calgary, Calgary, Canada; ²Dept of Biochemistry and Molecular Biology, University of Calgary, Calgary, Canada; ³Dept of Obstetrics and Gynaecology, University of Calgary, Calgary, Canada

10.1136/sextrans-2021-sti.60

Bacterial vaginosis (BV) is a prevalent dysbiotic vaginal condition associated with increased risk for acquisition/transmission of sexually transmitted infections (STIs). While the microbes present in women with BV are highly variable, functional features such as increased catabolism of peptides/amino acids are relatively conserved. To date, the bacterial proteases initiating this process and identity of host protein targets remain undefined. We hypothesized that broad-acting proteases are secreted by BV-associated bacteria and modulate host factors relevant to STI acquisition.

Bacterial suspensions and cell-free supernatants from select BV-associated species were evaluated for proteolytic activity using the universal protease substrate, casein, in agar plates and fluorometric assays. Degradation of collagen was explored using zymography or fluorophore-conjugated collagen with or without inhibitors. Fibrinogen/thrombin degradation was explored through clot inhibition assays and protein gel electrophoresis.

Our investigations reveal that BV-associated bacteria including *Prevotella amnii*, *Prevotella bivia*, *Porphyromonas asaccharolytica*, *Porphyromonas uenonis*, *Sneathia amnii*, *Sneathia sanguinegens*, *Gardnerella vaginalis*, and *Gardnerella piotti* produce secreted proteases with broad substrate specificity. However, only select species degrade specific host protein polymers, namely collagen. Further investigation of *Porphyromonas* enzymes revealed that metallo- and cysteine proteases coordinate broad activity. Both species secrete three collagenases, which were fully abrogated by metalloprotease inhibitors in *P. uenonis*, but not *P. asaccharolytica*. Finally, both species degrade fibrinogen and thrombin to abrogate blood clotting.

These studies reveal proteolytic activity is conserved among numerous vaginal bacteria with important roles in BV pathogenesis. However, modulation of specific host targets is more variable. Vaginal *Prevotella* and *Porphyromonas* species increase risk of HIV acquisition and our findings show *Porphyromonas* species exhibit proteolytic activities through diverse and redundant enzymes. These activities could induce barrier disruption and microhemorrhage in the cervicovaginal niche, thereby increasing the risk of STI acquisition. Further characterization of secreted proteases and their targets could identify new therapeutics for BV and STIs.

002.6 ASSOCIATIONS BETWEEN VAGINAL BACTERIA AND BACTERIAL VAGINOSIS SIGNS AND SYMPTOMS: A COMPARATIVE STUDY OF KENYAN AND AMERICAN CISGENDER WOMEN

¹K Carter*, ^{1,2}J Balkus, ³O Anzala, ⁴J Kimani, ⁵N Hoffman, ²T Fiedler, ⁶V Mochache, ^{2,7}D Fredricks, ^{1,4,7,8}R McClelland, ²S Srinivasan. ¹Department of Epidemiology, University of Washington, Seattle, USA; ²Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center, Seattle, USA; ³Department of Medical Microbiology, University of Nairobi, Nairobi, Kenya; ⁴Institute for Tropical and Infectious Diseases, University of Nairobi, Nairobi, Kenya; ⁵Department of Laboratory Medicine and Pathology, University of Washington, Seattle, USA; ⁶Centre for Public Health Research, Kenya Medical Research Institute, Nairobi, Kenya; ⁷Department of Medicine, University of Washington, Seattle, USA; ⁸Department of Global Health, University of Washington, Seattle, USA

10.1136/sextrans-2021-sti.61

Background Vaginal colonization with specific bacterial vaginosis (BV)-associated bacteria has been associated with individual BV signs and symptoms (Amsel criteria). Bacterial colonization

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

¹R Turpin*, ²S Tuddenham, ¹X He, ³M Klebanoff, ⁴K Ghanem, ⁵R Brotman. ¹University of Maryland, College Park, College Park, USA; ²Division of Infectious Diseases, Johns Hopkins University School of Medicine, Baltimore, USA; ³Center for Perinatal Research, Nationwide Children's Hospital, Columbus, USA; ⁴Department of Epidemiology and Public Health, University of Maryland School of Medicine, Baltimore, USA; ⁵Institute for Genome Sciences, University of Maryland School of Medicine, Department of Epidemiology and Public Health, Baltimore, USA

10.1136/sextrans-2021-sti.62

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

¹E Armstrong*, ²A Hemmerling, ³S Miller, ⁴K Burke, ²S Newmann, ⁵S Morris, ⁶H Reno, ⁷S Huibner, ⁸M Kulikova, ⁹E Crawford, ¹⁰G Castañeda, ^{11,12}B Coburn, ²C Cohen, ^{1,7,13}R Kaul. ¹University of Toronto, Institute of Medical Science, Department of Medicine, Toronto, Canada; ²University of California, San Francisco, Department of Obstetrics, Gynecology and Reproductive Sciences, San Francisco, USA; ³University of California, San Francisco, Department of Laboratory Medicine, San Francisco, USA; ⁴Ruth M. Rothstein CORE Centre and Stroger Hospital of Cook County Health, Chicago, USA; ⁵University of California, San Diego, Department of Family Medicine and Public Health, San Diego, USA; ⁶Washington University, Division of Infectious Diseases, Department of Medicine, St. Louis, USA; ⁷University of Toronto, Department of Medicine, Toronto, Canada; ⁸University Health Network, Toronto General Hospital Research Institute, Toronto, Canada; ⁹University of California, San Francisco, Department of Microbiology and Immunology, San Francisco, USA; ¹⁰Chan Zuckerberg Biohub, San Francisco, USA; ¹¹University of Toronto, Department of Laboratory Medicine and Pathobiology, Toronto, Canada; ¹²University of Toronto, Department of Immunology, Toronto, Canada; ¹³University Health Network, Toronto General Hospital, Immunodeficiency Clinic, Toronto, Canada

10.1136/sextrans-2021-sti.63

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