separately from *G. vaginalis*, *P. bivia*, *L. crispatus* and controls. BVAB induced production of biogenic amines in a species-specific manner. *A. vaginae* and *S. amnii* impacted arginine/citrulline metabolism, leading to pro-inflammatory signaling, and induced production of oxidative stress-related metabolites. In contrast, *G. vaginalis* and *P. bivia* altered epithelial barrier through mucin and collagen degradation and potential ammonia production.

Conclusions We demonstrated the utility of our 3D model to recapitulate the cervicovaginal microenvironment and identified unique and species-specific mechanisms by which BVAB contribute to pathophysiological changes favorable for STIs.

002.2 THE IMPACT OF CONCURRENT PARTNER TREATMENT FOR BACTERIAL VAGINOSIS ON THE GENITAL MICROBIOTA OF HETEROSEXUAL COUPLES: A PILOT STUDY

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Background Approximately 40% of women receiving first-line antibiotics for bacterial vaginosis (BV) experience recurrence within 3-months. Reinfection from an untreated regular sexual partner (RSP) likely contributes to BV-recurrence. We investigated the impact of concurrent partner treatment for BV on the genital microbiota of heterosexual couples.

Methods Women with symptomatic BV (≥ 3 Amsel criteria and Nugent Score[NS]=4–10) were recruited between March 2018–March 2019 with their RSP. Couples received oral metronidazole 400mg BID 7-days, and men additionally applied 2% clindamycin cream topically to penile skin BID for 7-days. Participants self-collected genital samples (women: vaginal; men: cutaneous penile, first-void urine [representing the urethra]) pre-treatment (day-0), post-treatment (day-8) and then 4-weekly until endpoint (week-12 or BV-recurrence). We characterised the genital microbiota using 16S-rRNA gene sequencing. Differential abundance testing was performed using ALDEX2. Changes in microbiota composition post-treatment were assessed using ANOSIM.

Results Data from 29 couples were analysed. Women had a high prevalence of risk factors for BV-recurrence; 79% had a history of BV, 83% had an uncircumcised RSP, all reported condomless sex during the study and 38% had an intrauterine device. Only 4/27 (15%) women completing clinical follow-up experienced BV-recurrence (≥ 3 Amsel criteria, NS=4–10). BV-associated bacteria, including *Atopobium*, *Prevotella* and *Dialister*, significantly decreased in abundance at all three genital sites immediately post-treatment (false discovery rate (FDR)-corrected p-value<0.05). BV-associated bacteria remained decreased at endpoint at all sites, but following FDR-correction this was only significant for the vaginal site. Overall,

partner treatment significantly and immediately changed the composition of the female and male genital microbiota (AON-ISM; p-value=0.001).

Conclusion In a cohort of women at high risk for BV-recurrence, only 15% experienced recurrence within 3-months of concurrent partner treatment. Treatment reduced the abundance of BV-associated bacteria and altered the genital microbiota composition of both partners; although only changes at the vaginal site remained significant at endpoint.

002.3 RECLASSIFICATION OF ATOPOBIUM VAGINAE AS THREE NOVEL FANNYHESSEA SPECIES: IMPLICATIONS FOR UNDERSTANDING THEIR ROLE IN BACTERIAL VAGINOSIS

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Background *Atopobium vaginae* is a prevalent vaginal bacterium associated with bacterial vaginosis (BV). Molecular studies targeting its 16S rRNA gene have shown *A. vaginae* is a useful diagnostic indicator of BV and important secondary colonizer of the vaginal biofilm. Both *A. vaginae* and the vagina's primary biofilm-forming species, *Gardnerella vaginalis*, exhibit extreme genomic heterogeneity. This led to *Gardnerella*'s recent split into approximately nine genomospecies indistinguishable by their 16S genes. The objective of this work was to ascertain whether similar subdivisions should be made for *A. vaginae*.

Methods We performed comparative genomics on publically available *A. vaginae* whole genome sequences. We also genotyped 20 *A. vaginae* isolates from women participating in a BV treatment study and phenotypically characterized select strains to identify their biochemical properties (API/MIC tests) and virulence potential.

Results Three genomospecies were defined by cross-species nucleic acid identity <74%; each shares $\geq 99\%$ 16S rRNA gene identity and belongs to the new genus *Fannyhessea*. Two species previously cultured and sequenced are *Fannyhessea vaginae* (CCUG 38953T, representing 85% of cultured isolates) and *Fannyhessea massiliense* (Marseille-P4126T, PB189–14T). These species differ in alkaline and acid phosphatase activity, as well as leucine arylamidase activity. Novel *Fannyhessea* species type 2 was distinguished by its inability to ferment sucrose or tagatose and its sensitivity to metronidazole. Colony morphology, Gram stain, and lack of detectable catalase, indole, sialidase, proteinase, and hyaluronidase activities were similar for all three species. Functional genomics revealed *F. vaginae* uniquely possesses sialic acid response machinery and several adhesion proteins.

Conclusions Genomic and functional differences support redefining *A. vaginae* as three novel *Fannyhessea* species. More work is needed to re-examine its role in BV in the absence of confounding by the other species, but our findings suggest *F. vaginae* may contribute to treatment failure and interact specifically with the *Gardnerella* biofilm and host epithelium.