

Abstract O1-S05.01 Table 1 Associations between prevalence of BV candidate organisms and lifetime sexual partners

Candidate organism	<i>Megasphaera spp.</i> detected (prevalence %)	<i>Sneathia spp.</i> prevalence detected (prevalence %)	<i>Leptotrichia spp.</i> detected (prevalence %)	<i>L. crispatus</i> prevalence detected (prevalence %)	<i>G vaginalis</i> prevalence detected (prevalence %)	BVAB1 prevalence detected (prevalence %)	BVAB2 prevalence detected (prevalence %)	BVAB3 prevalence detected (prevalence %)	<i>A. vaginae</i> prevalence detected (prevalence %)
Women with normal flora									
Lifetime sexual partners									
0	2/79 (3)	3/79 (4)	3/79 (4)	45/79 (57)	24/79 (30)	0/79	0/79 (0)	0/79	53/79 (67)
1–10	1/82 (1)	4/82 (5)	3/82 (4)	60/82 (73)	41/82 (50)	0/82	6/82 (7)	0/82	56/82 (68)
>10	6/72 (8)	10/72 (14)	12/72 (17)	59/72 (82)	49/72 (68)	0/72	6/72 (8)	2/72 (3)	34/72 (48)
p for trend	0.1	0.03	0.006	0.001	<0.001	Undefined	0.2	0.2	0.02
Women with BV									
Lifetime sexual partners									
0	1/3 (33)	1/3 (33)	1/3 (33)	1/3 (33)	3/3 (100)	0/3 (0)	0/3 (0)	0/3 (0)	2/3 (67)
1–10	12/33 (36)	17/33 (52)	16/33 (49)	11/33 (33)	31/33 (94)	1/33 (3)	18/33 (55)	4/33 (12)	33/33 (100)
>10	12/69 (17)	60/69 (87)	59/69 (86)	35/69 (51)	69/69 (100)	6/69 (9)	54/69 (78)	13/69 (19)	67/69 (100)
p for trend	0.07	<0.001	<0.001	0.2	0.3	0.3	0.004	0.3	0.04

were scored by the Nugent method. Three-hundred-and-thirty-nine samples from women with normal flora and BV were selected for analysis using quantitative PCR assays (qPCR) targeting the specific 16S rRNA gene sequences of eight published COs (*G vaginalis*, *A. vaginae*, *Megasphaera spp.*, *Sneathia spp.*, BVAB1, BVAB2, BVAB3, and *Leptotrichia spp.*) and *L. crispatus*. Detection of COs and *L. crispatus* and their total bacterial loads were compared between women with BV and normal flora. The associations between prevalence of COs and specific sexual behavioural practices were examined by univariate and multivariate analysis.

Results Analysis found all COs were strongly associated with BV compared with normal flora and *L. crispatus* was negatively associated. *G vaginalis* and *A. vaginae* were relatively common in sexually inexperienced women: however other COs were absent in a truly virginal population. When women with normal flora and BV were analysed separately, *Sneathia spp.*, BVAB1, BVAB2, BVAB3, *Leptotrichia spp.* and *G vaginalis* all demonstrated a progressive increase in prevalence with increasing sexual experienced and increasing numbers of vaginal sexual partners see Abstract O1-S05.01 table 1. *Megasphaera spp.* however differed from other COs, with a higher prevalence being strongly associated with increasing oral sex frequency and oral sex partner number.

Conclusions These data provide compelling evidence for sexual transmission of several COs—with absence of COs in virginal women and increasing prevalence with increasing sexual exposure. Interestingly the COs *Sneathia spp.*, BVAB1, BVAB2, BVAB3, *Leptotrichia spp.* and *G vaginalis* are significantly associated with vaginal sex while the epidemiological association of *Megasphaera spp.* differed from the other COs being significantly associated with oral sex.

O1-S05.02 BIOLOGICAL EVIDENCE OF SEMEN EXPOSURE IS ASSOCIATED WITH INCIDENT BACTERIAL VAGINOSIS

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Objectives (1) To identify correlates of incident *Bacterial vaginosis* (BV) among high-risk women and (2) to identify predictors of discordance between self-reported lack of semen exposure in the past 6 months and the detection of spermatozoa on Gram stain, which provides biological evidence of recent exposure.

Methods Analyses were based on among 871 HIV-infected and 439 HIV-uninfected women participating in HIV Epidemiology

Research Study (HERS) which was conducted in 4 sites in the US. Participants completed study visits conducted at baseline and at 6-month intervals thereafter. We conducted both cohort and case-crossover analyses, stratified by HIV infection status, to evaluate potential correlates of incident BV. We also used logistic regression to identify predictors of discordance between self-reported lack of exposure to semen and the detection of spermatozoa on Gram stain. **Results** BV incidence was 21% among HIV-infected women and 19% among HIV-uninfected women. We found fewer correlates of incident BV when assessed with a case-crossover design than with a cohort design. Reporting frequent coitus (regardless of consistency of condom use) was correlated with incident BV in the cohort analyses but not in the case-crossover analyses. The sole correlate that emerged in both the cohort and case-crossover analyses among HIV-infected and -uninfected women was the detection of spermatozoa on Gram stain. Seven factors were associated with discordance between self-reported semen exposure and spermatozoa detection in the multivariable analysis. Discordance differed by study site and race/ethnicity and was more common among younger women. The following infections or conditions also were predictive of discordance: HIV (adjusted OR [aOR], 2.8; 95% CI, 1.7% to 4.6%), BV (aOR, 1.9; 95% CI, 1.5% to 2.5%), and human papillomavirus (aOR, 1.3; 95% CI, 1.0% to 1.8%). Finally, reporting current injection drug use (aOR, 0.6; 95% CI, 0.4% to 0.9%) was inversely related to discordance.

Conclusions The inconsistent association between condom use and BV found in prior studies could be the result of participant reporting bias. The present study found evidence of a relationship between semen exposure and incident BV. Also, given the number and range of correlates of discordance between self-reported and biological evidence of semen exposure, inaccuracies in the reporting of sexual behaviours cannot be assumed to be distributed randomly across a study population.

O1-S05.03 BEHAVIOURAL FACTORS ASSOCIATED WITH BACTERIAL VAGINOSIS (BV) IN WOMEN WHO HAVE SEX WITH WOMEN (WSW): THE WOMEN ON WOMEN'S (WOW) HEALTH STUDY

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Background We are conducting a national 2 year cohort study in 400 Australian WSW to determine the behavioural and microbiological