The molecular microbiome analysis showed that high levels of L. crispatus may protect against HIV acquisition and that recently acquired HIV infection may make women more prone to dysbiosis. More research is needed to confirm these relationships and determine causality.

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P06.03 INCREASED *G. VAGINALIS* CLADE DIVERSITY IS ASSOCIATED WITH PENILE VAGINAL SEX AND BACTERIAL VAGINOSIS

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Introduction While BV is considered to be polymicrobial, some investigators consider *Gardnerella vaginalis* to be integral to its pathogenesis. *G. vaginalis* is however, also detected in women without BV. Recent evidence indicates different *G. vaginalis* clades exist, but it is unclear how these may be associated with the pathogenesis of BV.

Methods Established qPCR and multiplex assays were used to determine the association between *G. vaginalis* load and 4 clades of *G. vaginalis* with onset of penile-vaginal sex and BV in two distinct study populations. The WOW study investigated incident BV in women having sex with women (WSW); 378 longitudinal samples were selected from 51 WSW who developed incident BV and 51 who did not. 178 samples were selected from 42 17–21 year old female students without BV from the FUSS study: 15 women had no prior sexual experience with others, 15 had only engaged in non-coital activities and 12 had engaged in penile-vaginal sex.

Results *G. vaginalis* load was higher in women with BV [n = 37; $\log_{10}$ median load = 6.2 (IQR = 6.5)] compared to those without BV (n = 156; $\log_{10}$ median load = 3.2 (IQR = 4.8); p = 0.0001) in the WOW population. No difference in *G. vaginalis* load was found between women with no history of penile-vaginal sex [n = 40; $\log_{10}$ median load = 4.1 (IQR = 3.3)] compared to women engaging in penile-vaginal sex [n = 35; $\log_{10}$ median load = 4.1 (IQR = 4.8); p = 0.548] in the FUSS population. WOW participants with BV were more likely to have multiple *G. vaginalis* clades (88.6%; 95% CI = 0.74–0.95) compared to participants without BV (60.3%; 95% CI = 0.52–0.68, p = 0.0013). Multiple clades of *G. vaginalis* were also more common in FUSS participants who engaged in penile-vaginal sex (64.5%; 95% CI = 0.47–0.79) compared who had not (34.5%; 95% CI = 0.20–0.53, p = 0.0379).

Conclusion Penile-vaginal sex was associated with increased *G. vaginalis* clade diversity in young women without BV. Increased *G. vaginalis* loads and increased clade diversity were associated with BV in WSW.

Disclosure of interest statement No pharmaceutical grants were received in the development of this study.

P06.04 *GARDNERELLA VAGINALIS* PRESENCE IN VAGINAL DYSBIOSIS: A SECONDARY ANALYSIS

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Introduction It has been hypothesised that *Gardnerella vaginalis* (GV) is necessary for the development of bacterial vaginosis (BV), and BV is associated with an increase of GV abundance and/or biofilm formation. We conducted a secondary analysis using data from multiple studies to investigate the first two hypotheses.

Methods Gram-stained Nugent scores and log-transformed bacterial counts obtained by in-house quantitative PCR for selected *Lactobacillus* species, GV and *Atopobium vaginae* (AV) counts were available for 1577 samples of women from Belgium (n = 469), Tanzania (n = 204), South Africa (n = 439), Kenya (n = 369), and Rwanda (n = 96). We determined the presence and median bacteria counts by Nugent score category using univariate analysis stratified by country.

Results Using Nugent scores, 1054(67%), 125(8%), and 398 (25%) samples had normal, intermediate and BV microbiota, respectively. GV presence was associated with BV in all countries (Chi^2: $p < 0.001$). The median GV counts were higher for samples with intermediate-score (Kruskal-Wallis: $p < 0.001$) and BV-score ($p = 0.001$) compared to samples with normal-score, with no difference between samples with intermediate-score and BV-score ($p = 0.459$). Only 25(6%) of the 398 samples with BV-score were negative for GV by PCR compared to 30(24%) with intermediate-score, and 663(63%) with normal-score. Of the 25 samples with BV and no presence of GV, AV was detected in 13 (52%). The AV presence and counts in the 25 samples were lower compared to BV-positive-GV-positive samples (88%) (Chi^2: $p < 0.001$; Kruskal-Wallis: $p < 0.001$) whereas AV presence and counts were higher compared to BV-negative samples (20%) (Chi^2: $p < 0.001$; Kruskal-Wallis: $p < 0.001$).

Conclusion We confirm that GV presence and higher GV loads are strongly correlated with BV by Nugent score. Half of the samples of women with GV-negative dysbiosis had AV present. Future research is needed to investigate the role of GV and/or AV-associated biofilm in BV and to evaluate the role of threshold of GV and AV for potential PCR based diagnostic testing for BV.

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