

SEXUAL BEHAVIOURS IMPACT THE VAGINAL MICROBIOTA OF WOMEN WHO HAVE SEX WITH WOMEN

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Introduction:

We investigated the impact of sexual behaviours on the vaginal microbiota of women participating in the WOW Health study, a two-year cohort study of Australian women-who-have-sex-with-women (WSW) designed to examine epidemiological and microbiological factors associated with incident bacterial vaginosis (BV).

Methods:

Women self-collected high vaginal swabs and completed a behavioural questionnaire every three months for 24 months or until incident BV. We characterised the vaginal microbiota using 16S-rRNA gene sequencing of the V3V4 region. Community state types (CSTs) were identified using hierarchical clustering. Bacterial diversity was calculated using the Shannon diversity index and instability of the vaginal microbiota was assessed using both change of CST and Bray-Curtis dissimilarity between consecutive longitudinal specimens. The impact of behaviours on the diversity and instability of the vaginal microbiota was determined using multivariate regression models. Linear discriminant analysis (LDA) effect size was used to identify bacteria associated with exposure to a new sexual partner.

Results:

A total of 370 specimens from 100 women were included in analyses. The vaginal microbiota clustered into five CSTs: three dominated by *Lactobacillus* spp. (CST1 *L. crispatus*; CST2 *L. crispatus*/*L. iners*; CST3 *L. iners*), one abundant in *Gardnerella vaginalis* (CST4) and one of mixed bacteria (CST5). Exposure to a new sexual partner increased the bacterial diversity (Adjusted coefficient=0.22,95%CI:0.01,0.44; p=0.042) and instability of the vaginal microbiota, both in terms of change of CST

(adjusted odds ratio=2.76,95%CI:1.36,5.60; p=0.005) and increased Bray-Curtis dissimilarity (Adjusted coefficient=0.21,95%CI:0.1,0.32; p<0.001). Sex with a new partner was associated with increased abundance of key bacteria often detected in vaginal dysbiosis including *G. vaginalis*, *Megasphaera* and BVAB1 (p<0.05, LDA score<-3). Conversely, no sex/sex in established ongoing relationships was associated with a favourable microbiota.

Conclusion:

Sex with a new partner reshapes the vaginal microbiota of WSW by increasing the diversity and abundance of potentially dysbiotic bacteria.

Disclosure of Interest Statement:

No conflict of interest for any listed authors.