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Clinical

Abstract Title

The impact of hygiene behaviours and sexual practices on the vaginal microbiome

Background

The common vaginal condition, bacterial vaginosis (BV), is associated with poor reproductive health outcomes, increased risk for STIs, and characterized by a dysbiotic microbiome. There is a lack of knowledge of whether some hygiene behaviours or sexual practices can change the vaginal microbiome, promoting BV occurrence.

Objective

The objective of the study is to determine if an increased frequency in hygiene behaviours and sexual practices is associated with a non-optimal microbiome.

Methods

Information from "The Study of Host-bacterial Relationships and Immune function in different Vaginal Environments" (THRIVE) BV, a prospective observational study, which took place in Manitoba from 2018-2022 was used. Baseline cervicovaginal specimens from 40 BV positive and 26 BV negative participants were compared to baseline behavioural data and demographics. Primary analysis was performed with the Chi-square test, Fisher's Exact test, and Mann-Whitney-Wilcoxon test. Further analyses were performed with the Mann-Whitney-Wilcoxon test corrected through multiple comparisons.

Results

We observed trending differences in the bacterial taxa for 8 hygiene and sexual behaviours (p<0.05). We also observed trending differences in the bacterial functions for 13 hygiene and sexual behaviours. With the use of anti-itch cream, we observed a significant (p.adj = 0.03) increase in the bacterial function of cysteine and methionine metabolism. Gardnerella was observed to play the most prominent role in this bacterial function change, with both lactate dehydrogenase and branched chain aminotransferase proteins significantly increased with the use of anti-itch cream.

Conclusion

We had power to assess 13 hygiene practices and sexual behaviours, which all had trending differences in the microbiome, however we only observed significant bacterial functional changes with the use of anti-itch cream. The clinical relevance of this functional change needs to be investigated further, as it has been shown to play a role in pre-term birth(1)

Citation: 1] Zhang J, Li L, Zhang M, et al. Distinct vaginal microbiome and metabolome profiles in women with preterm delivery following cervical cerclage. Front Cell Infect Microbiol 2025;15. https://doi.org/10.3389/fcimb.2025.1444028 .	

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