

Associations between vaginal microbiota, bacterial vaginosis and urinary tract infections in a premenopausal population

Authors:

Wild N^{1,2}, Plummer EL^{1,2}, Matthews LG^{1,2}, Htaik K^{1,2}, Vodstrcil LA^{1,2,3}, Bradshaw CS^{1,2,3}

¹School of Translational Medicine, Monash University, Melbourne, Australia,

²Melbourne Sexual Health Centre, Alfred Health, Melbourne, Australia, ³Melbourne School of Population and Global Health, The University of Melbourne, Melbourne, Australia

Background:

Epidemiological data and anecdotal reports suggest bacterial vaginosis (BV) may increase the risk of urinary tract infection (UTI). *In-vitro* studies and research in peri- and post-menopausal populations indicate a protective role of vaginal lactobacilli against UTIs. However, the influence of BV and the vaginal microbiome on UTI risk in pre-menopausal populations is understudied.

Methods:

This case-control study utilised epidemiological, clinical, and 16S rRNA gene-sequenced vaginal microbiota data from pre-menopausal people with a vagina enrolled in the OMG study between 2017 and 2019 at the Melbourne Sexual Health Centre. Three case groups were defined; participants with i) urinary symptoms (dysuria and/or frequency, n=544), ii) UTI-positivity (positive urine dipstick and/or microscopy, n=127), and iii) uropathogen-positivity (UTI-positive with a uropathogenic isolate on culture, n=55). We investigated factors associated with each case group compared to an asymptomatic control group (n=180) in multivariable models (including variables with p<0.2 in univariable analyses). Differential abundance analyses were performed to identify under/overrepresented bacterial species in each case group relative to controls.

Results:

BV was significantly associated with urinary symptoms (adjusted-odds-ratio[AOR]=2.70, 95%CI=1.58-4.59, p<0.001) and diagnosis of a UTI (AOR=2.29, 95%CI=1.08-4.85, p=0.030) compared to controls. In cases with urinary symptoms, the relative abundance of *Gardnerella vaginalis* was also significantly greater than in controls (FDR-adjusted p-value=0.025). Conversely, an optimal vaginal microbiome composition was negatively associated with urinary symptoms (AOR=0.66, 95%CI=0.46-0.94, p=0.027) and diagnosis of a UTI (AOR=0.46, 95%CI=0.26-0.80, p=0.006). The relative abundance of *Lactobacillus crispatus* was significantly lower in all three case groups compared with controls (FDR-adjusted p-value [urinary symptoms=0.001; UTI-positivity=0.011; uropathogen-positivity=0.056]).

Conclusion:

Our results suggest *L.crispatus* and an optimal vaginal microbiome are protective against UTIs in our pre-menopausal population. Furthermore, we report a positive association between BV and urinary symptoms and UTIs. These findings may support BV testing and treatment as an important facet of UTI prevention and management.

Disclosure of Interest Statement:

The authors have no conflicts of interest to declare.