

THE CONTRIBUTION OF THE VAGINAL MICROBIOTA TO BACTERIAL VAGINOSIS RECURRENCE FOLLOWING FIRST-LINE ANTIBIOTICS

Authors:

Plummer EL^{1,2*}, Sfameni AM^{1,2*}, Vodstrcil LA^{1,2,3}, Danielewski JA^{4,5,6}, Murray GL^{4,5,6}, Fehler G², Fairley CK^{1,2}, Garland SM^{4,5,6}, Chow EPF^{1,2,3}, Hocking JS³, Bradshaw CS^{1,2,3}

¹Central Clinical School, Monash University, Melbourne, Victoria, ²Melbourne Sexual Health Centre, Alfred Hospital, Carlton, Victoria, ³Melbourne School of Population and Global Health, The University of Melbourne, Parkville, Victoria, ⁴Murdoch Children's Research Institute, Parkville, Australia, ⁵Women's Centre for Infectious Diseases, The Royal Women's Hospital, Parkville, Australia, ⁶Department of Obstetrics and Gynaecology, The University of Melbourne, Parkville, Australia

*joint first authors

Background:

Bacterial vaginosis (BV) is a common vaginal dysbiosis that often recurs following first-line antibiotics. Studies exploring the contribution of the vaginal microbiota to recurrence are limited and conflicting. We investigated if the vaginal microbiota composition pre-treatment or immediately post-treatment was associated with BV recurrence within one-month of treatment.

Methods:

We analysed samples and data from 121 women who participated in three published trials evaluating novel interventions for improving BV cure, including concurrent antibiotic treatment of regular sexual partners (RSP). Women attending the Melbourne Sexual Health Centre who were diagnosed with BV received first-line antibiotics, and self-collected vaginal swabs pre-treatment and the day after finishing antibiotics (immediately post-treatment). 16S-rRNA gene sequencing was used to characterise the vaginal microbiota. Logistic regression, adjusted for confounders, was performed to examine the association between BV recurrence and 1) bacterial diversity and 2) centre-log ratio transformed abundance of individual bacterial taxa pre- and post-treatment.

Results:

Sixteen women (16/121; 13%; 95%CI:8-21%) experienced BV recurrence within one-month of enrolment. Women with an untreated RSP were more likely to experience recurrence than women with no RSP (9/28 vs 3/44; P=0.008) or women with a male RSP who received concurrent partner treatment (4/49; P=0.011). The diversity of the vaginal microbiota did not differ pre-treatment (adjusted odds ratio [AOR]=1.99, 95%CI:0.77–6.71, p=0.203) or immediately post-treatment (AOR 1.37, 95%CI:0.60–2.97, p=0.435) between recurrence and cure cases. However, a higher abundance of *Prevotella* spp. pre-treatment (AOR=1.35, 95%CI:1.05-1.91, p=0.041) and *Gardnerella* spp. immediately post-treatment (AOR=1.23, 95%CI:1.03-1.49, p=0.026) were both associated with increased odds of BV recurrence after adjusting for partner type and treatment status.

Conclusion:

Our findings suggest that specific taxa may play a role in the high rates of treatment failure following recommended BV therapy. Further work should prioritise understanding the contribution of *Prevotella* and *Gardnerella* species to BV recurrence.

Disclosure of Interest Statement:

The authors report no conflict of interest.