

SEXUAL AND CONTRACEPTIVE PRACTICES ARE ASSOCIATED WITH NON-OPTIMAL VAGINAL MICROBIOTA COMPOSITION

Erica L Plummer^{1,2}, Lenka A Vodstrcil^{1,2,3}, Jennifer A Danielewski^{4,5}, Gerald L Murray^{4,5}, Rosie L Latimer^{1,2}, Catriona S Bradshaw^{1,2,3}

¹School of Translational Medicine, Monash University, Melbourne; ²Melbourne Sexual Health Centre, Alfred Health, Carlton; ³Melbourne School of Public Health, University of Melbourne, Parkville; ⁴Centre for Women's Infectious Diseases, Royal Women's Hospital and Murdoch Children's Research Institute, Parkville; ⁵Department of Obstetrics and Gynaecology, University of Melbourne, Parkville

BACKGROUND & AIM

- A non-optimal vaginal microbiota is deficient in lactic acid producing lactobacilli and is associated with genital inflammation, vaginal symptoms and adverse health outcomes.
- Understanding how behavioural and contraceptive practices differentially impact the composition of the vaginal microbiota is important for informing interventions to support optimal reproductive and sexual health.
- Aim:** to determine factors associated with vaginal microbiota composition among symptomatic and asymptomatic women attending a sexual health service.

RESULTS

- Median age was 26 years (interquartile range 23-26)
- Most participants (n=840, 72%) were born outside of Australia, with 38% born in the European WHO region, and 19% born in the Region of the Americas
- Three broad vaginal CST groups were identified:
 - Optimal non-iners *Lactobacillus*-dominated microbiota (CST-I, CST-II, CST-V); n=391
 - Lactobacillus iners* dominated microbiota (CST-III); n=390
 - Non-optimal *Lactobacillus* deficient microbiota (CST-IV); n=425
- Increasing age and increasing numbers of male sexual partners in the past 12 months were associated with increased likelihood of having a non-optimal *Lactobacillus* deficient microbiota (**Table 1**)
- In contrast, consistent condom use and use of a hormonal contraceptive method (excluding hormonal IUD use) were associated with decreased likelihood of having a non-optimal *Lactobacillus*-deficient microbiota
- No characteristics were significantly associated with having an *L. iners* dominated microbiota

Table 1. Multivariable analysis of characteristics associated with vaginal CST group

Characteristic	<i>L. iners</i> dominant microbiota		Non-optimal <i>Lactobacillus</i> deficient microbiota	
	Adj-RRR (95% CI)	P value	Adj-RRR (95% CI)	P value
Age	1.00 (0.97-1.03)	0.930	1.03 (1.00-1.06)	0.034
No. male partners in past 12 mo	1.03 (0.99-1.07)	0.162	1.05 (1.01-1.08)	0.016
STI in the past 6 mo	1.52 (0.97-2.37)	0.066	1.55 (1.00-2.41)	0.052
Contraceptive & condom use				
No contraceptive method & no/inconsistent condom use	ref		ref	
Consistent condom use only	0.79 (0.42-1.50)	0.470	0.46 (0.23-0.92)	0.028
Hormonal (non-IUD)	1.00 (0.72-1.39)	0.994	0.70 (0.50-0.97)	0.034
Levonorgestrel IUD	0.72 (0.43-1.19)	0.201	0.86 (0.54-1.38)	0.539
Copper IUD	1.71 (0.66-4.41)	0.268	2.30 (0.96-5.53)	0.063

Adj-RRR, adjusted relative risk ratio; CI, confidence interval; No., number; mo, months

METHODS

- Cross-sectional analysis of 1206 women attending Melbourne Sexual Health Centre from April 2017-April 2019 who provided a vaginal swab for microbiota analysis
- Data concerning genital symptoms and sexual and contraceptive practices were obtained via questionnaires and medical records
- Vaginal microbiota data obtained using 16S rRNA gene sequencing of V3-V4 regions.
- Multinomial logistic regression assessed the relationship between vaginal community state type (CST) group and participant characteristics
- Associations between bacterial abundance and participant characteristics were assessed using MaAsLin2

- The abundance of several dysbiosis associated (i.e. non-optimal) bacteria was significantly increased with increasing numbers of male sexual partners, including *Gardnerella*, *Sneathia*, *Dialister* and *Prevotella* amplicon sequence variants (ASVs; **Fig 1**)
- Copper IUD use was associated with increased abundance of non-optimal vaginal bacteria, whereas hormonal contraceptive use (excluding hormonal IUDs) was associated with decreased abundance of non-optimal vaginal bacteria

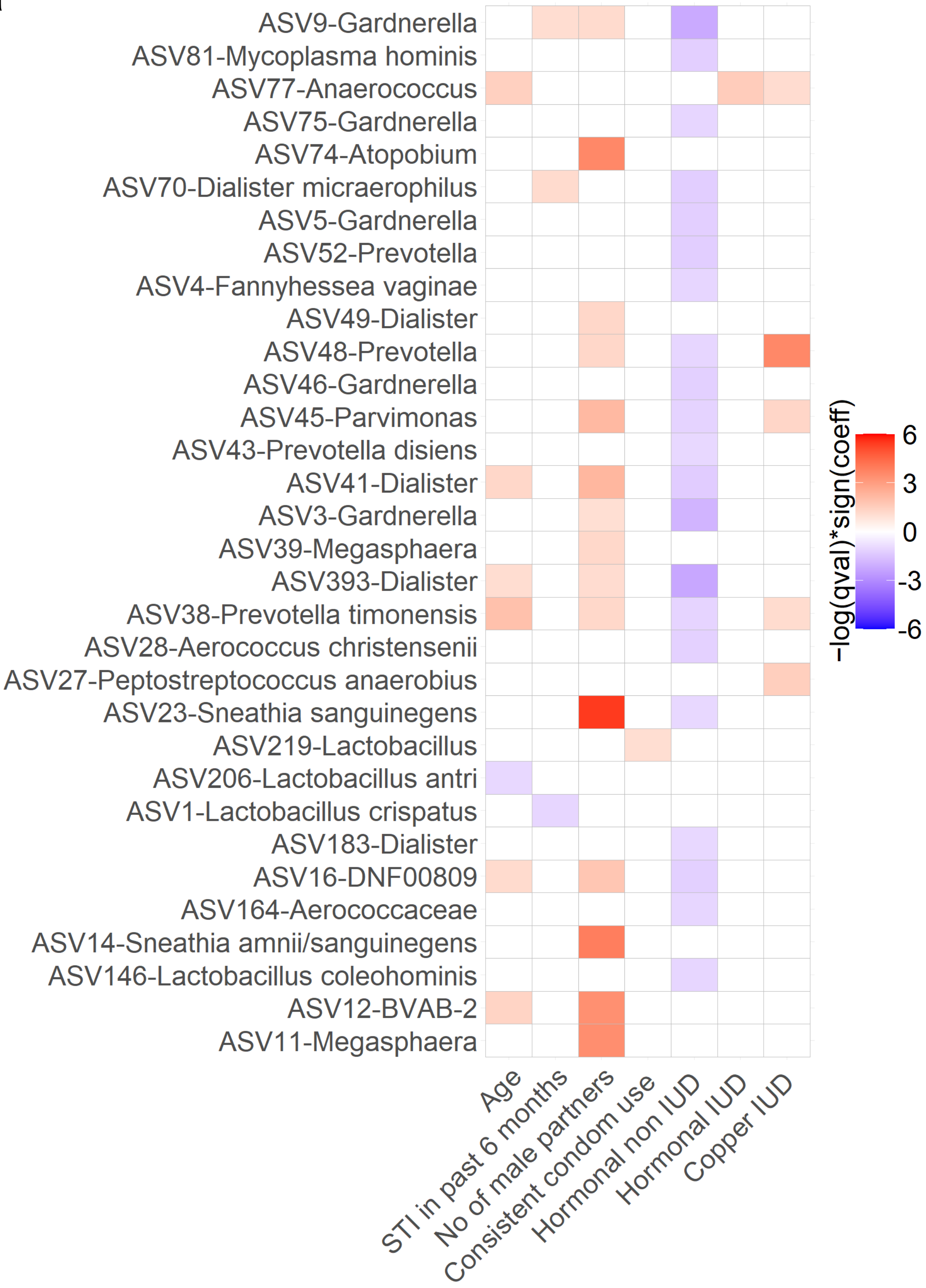


Fig 1. Heatmap of significant associations (q-value<0.01) between bacterial abundance and participant characteristics. Red boxes reflect increased abundance of the ASV in individuals with the specific characteristic, and blue boxes reflect decreased abundance.

CONCLUSION

The composition of the vaginal microbiota was significantly associated with sexual and contraceptive practices. Notably, contraceptive practices were differentially associated with vaginal microbiota composition, with hormonal contraceptive practices associated with optimal vaginal microbiota characteristics and copper IUD use associated with non-optimal vaginal microbiota characteristics.