

## RESEARCH BASED TEMPLATE

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### **Sexual and contraceptive practices are associated with non-optimal vaginal microbiota composition**

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**Background:** The vaginal microbiota has a key role in supporting optimal reproductive and sexual health outcomes. We aimed to determine factors associated with vaginal microbiota composition among women attending a sexual health service in urban Australia.

**Methods:** Between April 2017-April 2019 1,318 women were recruited to a cross-sectional study at Melbourne Sexual Health Centre. Women completed a questionnaire asking about genital symptoms and sexual practices. Data concerning contraceptive practices was obtained from medical records. Women self-collected a vaginal swab for microbiota characterisation using 16S rRNA gene sequencing. We assessed the association between vaginal microbiota community state types (CSTs) and behavioural and contraceptive factors using multinomial regression. Differential abundance analysis was used to examine factors associated with bacterial abundance.

**Results:** The vaginal microbiota of 1,206 women was categorised into three broad CSTs: optimal *Lactobacillus*-dominant microbiota (primarily *Lactobacillus crispatus* dominant communities; present in n=391/1,206 women; 32.4%), *Lactobacillus iners*-dominant microbiota (n=390/1,206; 32.3%), and non-optimal *Lactobacillus*-deficient microbiota (n=425/1,206; 35.2%). Relative to optimal *Lactobacillus*-dominated microbiota, *L. iners*-dominant microbiota and *Lactobacillus*-deficient microbiota were both associated with increasing numbers of male sexual partners (adjusted-relative-risk-ratio[aRRR]=1.04, 95%CI:1.00-1.08 and aRRR=1.06, 95%CI:1.02-1.10, respectively). *Lactobacillus*-deficient microbiota was associated with having a copper intrauterine device (copper-IUD) *in situ* (aRRR=2.74, 95%CI:1.13-6.62). The abundance of bacteria commonly associated with vaginal dysbiosis (including *Sneathia*, *Prevotella* and *Atopobium*) increased significantly with increasing numbers of male sexual partners. Compared to women using no contraception,

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women reporting hormonal contraceptive use (excluding IUDs) had decreased abundance of dysbiosis-associated bacteria (including *Gardnerella*, *Dialister* and *Prevotella*). In contrast, women using a copper-IUD had increased abundance of dysbiosis-associated bacteria.

**Conclusion:** The composition of the vaginal microbiota was significantly associated with sexual and contraceptive practices. Notably, copper-IUD use was associated with *Lactobacillus*-deficient microbiota and increased abundance of dysbiosis-associated bacteria, whereas hormonal contraceptive use was associated with lower abundance of dysbiosis-associated bacteria.

### **Disclosure of Interest Statement:**

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