P06.05 DYNAMICS OF VAGINAL IMMUNE CORRELATES AND MICROBIOTA IN WOMEN FROM SUB-SAHARAN AFRICA

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Introduction Alterations in vaginal microbiota (VMB) have been shown to increase HIV acquisition and transmission in women. We carried out a longitudinal characterisation of the VMB, soluble cervicovaginal immune mediators and their determinants in women from Sub-Saharan Africa.

Methods Cervicovaginal lavages from two cohorts of sexually active women from Kenya, South Africa and Rwanda were analysed for IL-1α, IL-1β, IL-6, IL-12(p70), MIP-1β, IP-10, IL-8, GM-CSF, G-CSF, Elafin, SLPI, IL-1RA and total protein. qPCR was used to quantify total *Lactobacillus*, *L. crispatus, L. iners*, L. jensenii, *L. gasseri, L. vaginalis, A. vaginae*, *G. vaginalis*, *P. bivia* and *E. coli* in vaginal swab samples. Cohort A had 40 women with a healthy VMB (Nugent score < 4) at all five bi–weekly visits. Cohort B consisted of 40 women with incident bacterial vaginosis (BV) (Nugent score > 7) in the course of their visits.

Results Cohort A: Individual *Lactobacillus* species were consistently present or absent within each woman over five study visits. Sexual activity was associated with reduced counts of total *Lactobacillus*, *L. iners* and *Prevotella bivia* but increased concentrations of IL-6, IL-12(p70) and IP-10. pH was positively associated with IL-1RA and IL1RA/IL1(α+β) ratio but negatively associated with total protein and SLPI. The amount of total *Lactobacillus* was significantly lower and total soluble immune mediators, MIP-1β and IL-8 higher in 14 women on progesterone-only contraception compared to those with a cycle (20 not on any contraceptives and 6 on combined pill). Cohort B: Total *Lactobacillus*, *L. crispatus*, IP-10, GM-CSF, Elafin, SLPI and total protein were all reduced during the first visit with BV. Conversely, *G. vaginalis*, A. vaginae, E. coli and IL-1β were increased with incident BV.

Conclusion Sexual activity, progesterone, clinical symptoms of pathology and BV alter vaginal mucosal immunity in Sub-Saharan African women potentially increasing their susceptibility to HIV infection.

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P06.06 AZYTHROMYCIN TREATMENT FOR *CHLAMYDIA TRACHOMATIS* IS ASSOCIATED WITH VAGINAL MICROBIOTA LACKING PROTECTIVE *LACTOBACILLUS* SPP

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Introduction Recurrence rate of *Chlamydia trachomatis* genital infection is frustratingly high (~25%). While re-exposure is thought to be the main reason. We hypothesised that after and because of azithromycin treatment, the vaginal microbiota is not optimally restored to a protective *Lactobacillus* spp. dominated state, resulting in enhanced susceptibility to *C. trachomatis* re-infection.

Methods We characterised the composition, structure and metagenome of the vaginal microbiomes in a cohort of 129 *C. trachomatis*-positive (CT+) women followed longitudinally before and after azithromycin treatment. We established *in vitro* susceptibility patterns to azithromycin and doxycycline of vaginal bacteria, including *Lactobacillus* crispatus, *L. iners*, *L. gasseri*, *L. jensenii*, and *Gardnerella vaginalis*.

Results Before treatment, CT+ women harbour communities that comprised either a complex assemblage of strict anaerobes, including *G. vaginalis*, with low proportions of *Lactobacillus* spp. or a high abundance of *L. iners*. After azithromycin treatment, we observed an increased proportion of women with communities dominated by high abundance of *G. vaginalis* and other strict anaerobes, or dominated by *L. iners*. Antibiotic resistance assays showed that certain types of *L. iners* and *G. vaginalis* are highly resistant to azithromycin and to lesser extents to doxycycline. Analysis of *L. iners* genomes reconstructed from vaginal microbial communities metagenomes showed that multiple phylogenetic clades of *L. iners* exist. One of these clades is not associated with CT+ women, and is characterised by low number of phage genes as well as unique secondary metabolites gene clusters, all of which could contribute to their resilience.

Conclusion These findings suggest azithromycin treatment is likely to restore a vaginal microbiota with low protective properties, increasing the risk to *C. trachomatis* re-infection.

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P06.07 THE EFFECTS OF CONTRACEPTION ON THE VAGINAL MICROBIOTA

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Introduction The human microbiota plays important roles in immune system development and resistance to infection.