(STs) previously reported in China (ST1, ST2, ST4, ST9, ST22, ST47), but also eight novel lineages, were detected. Only some quinolone-resistant isolates had amino acid substitutions in ParC (Ser83Leu in UPA) and ParE (Val417Thr in UPA and the novel Thr417Val in UUA), whereas the mechanism (s) for the remaining strains remains unclear. Although several isolates were non-susceptible to macrolides, mutations in 23S rRNA or substitutions in L4/L22 were not detected.
Conclusion This is the first study analysing susceptibility of *Ureaplasma* spp. isolates detected in Switzerland and the clonal distribution outside China. Resistance rates are low compared to other surrounding countries, but the empirical use of quinolones is compromised. We hypothesise that some hyperepidemic STs (e.g., ST4) spread worldwide via sexual intercourse. Large combined microbiological and clinical studies should address this important aspect.

P06 - Genital microbiome

P06.01 WOMEN OF DUTCH ETHNIC ORIGIN HAVE LOWER PREVALENCE OF VAGINAL MICROBIOME DYSBIOSIS THAN WOMEN OF OTHER ETHNIC ORIGIN RESIDING IN AMSTERDAM

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Introduction American women of African or Hispanic ancestry have increased risk of vaginal microbiome dysbiosis compared to women of European or Asian ancestry. However, the association between vaginal microbiome composition and ethnicity within Europe is largely unknown. We investigated this association in Amsterdam, The Netherlands.
Methods Non-pregnant women (18–34 years, n = 564) representing six ethnic origins (Dutch, South-Asian/Indonesian Surinamese, African Surinamese, Ghanaian, Turkish, and Moroccan) were cross-sectionally selected from the ongoing HELIUS multi-ethnic cohort study in Amsterdam for vaginal microbiome analysis. Extracted DNA from self-sampled vaginal swabs was sequenced targeting the V3V4 region of the 16S rRNA gene and using the Illumina MiSeq platform, and sequence reads were clustered using hierarchical clustering.
Results Clustering of 502/564 samples with sufficient read counts resulted in microbiome clusters dominated by *Lactobacillus* crispatus (n = 120), *L. iners* (n = 168), L. jensenii (n = 8), L. gasseri (n = 10), Streptococcus agalactiae (n = 8), Bifidobacteriaceae/Bifidobacterium spp. (n = 10), *Gardnerella vaginalis* (n = 78), and a mixture of anaerobes (n = 100), respectively. Microbiome composition was significantly associated with ethnic origin (P = 0.002). Women of Dutch ethnic origin had the highest prevalence of L.crispatus-dominated microbiome (40% vs 16–26% in the other ethnic groups), the lowest prevalence of *L. iners*-dominated microbiome (28% vs 31–39% in the other groups), and the lowest prevalence of clusters dominated by *G. vaginalis* or a mixture of anaerobes (25% vs 30–45% in other groups). Turkish women and South-Asian/Indonesian Surinamese women had the highest prevalence of *L. iners*-dominated microbiome (38% and 39%, respectively), and women from African descent (African Surinamese and Ghanaian women) the highest prevalence of clusters dominated by *G. vaginalis* or a mixture of anaerobes (48% and 44%, respectively).
Conclusion This large multi-ethnic study shows that dysbiotic vaginal microbiome compositions are significantly increased in women of non-Dutch ethnic origin. Therefore, these women may be at increased risk of STI acquisition and adverse reproductive health outcomes.
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P06.02 LONGITUDINAL CERVICOVAGINAL MICROBIOME MEASUREMENTS OF WOMEN BEFORE AND AFTER HIV-SEROCONVERSION

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Introduction Bacterial vaginosis (BV) by Nugent scoring is associated with enhanced acquisition and cervicovaginal shedding of HIV, but longitudinal molecular studies of these relationships are scarce.
Methods HIV-negative (n = 397) female sex workers in Kigali, Rwanda, were followed for two years. Demographic, behavioural, clinical, HIV, sexually transmitted infection, and cervicovaginal microbiota data were collected at regular intervals. The cervicovaginal microbiota were characterised by Nugent scoring, Amsel criteria (pH >4.5, a positive whiff test and presence of >20% clue cells on wet mount; two or three criteria indicated BV diagnosis), and phylogenetic 16S DNA microarray.
Results During follow-up, 19 women seroconverted for HIV. The associations between BV by Nugent or Amsel criteria and subsequent HIV seroconversion did not reach statistical significance (aOR = 1.56 (95% CI 0.51–4.77) and aOR = 4.85 (95% CI 0.59–39.90), respectively). For 10/19 women, phylogenetic microbiome composition was available before and after seroconversion, with a median of 324 days (range 42–386) before and 196 days (range 121–492) after seroconversion. Before seroconversion, none of the women had a L. crispatus-dominated microbiome, four had a *L. iners*-dominated microbiome, four a moderately dysbiotic microbiome and two severe dysbiosis. The microbiome composition of five women remained stable before and after seroconversion, four shifted to (more severe) dysbiosis, and one shifted from dysbiosis to a *L. iners*-dominated microbiome. After seroconversion, phylogenetic microbiome composition was available for all 19 women. 26% had a *L. iners*-dominated microbiome, 32% moderate dysbiosis, and 42% severe dysbiosis.
Conclusion In this population of high risk women, the association between BV and subsequent HIV seroconversion did not reach statistical significance, but statistical power was limited.