Conclusion A large majority of patients harbour the same ST of *N. gonorrhoeae* at all sites cultured. In a further 2.2% of patients there is minimal variation, which would be consistent with mutation of the *porB* gene during the course of infection. This uniformity is not necessarily due to infection from the same partner, as some STs circulate widely.

This data adds to the understanding of the ecology of *N. gonorrhoeae* in an era where patients positive by nucleic acid amplification tests often receive limited culture for typing and susceptibility testing and assumptions may be made about the strain infecting uncultured sites. This data adds to knowledge of the frequency of mutation of the *porB* locus *in vivo* and the frequency of concurrent gonococcal infections with different strains.

Abstract P3.263 Table 1

Table 1

Paired isolates	Identical ST	ST differing at 1 allele	ST differing at 2 alleles
Urethral/rectal	156 (89.6%)	6 (3.4%)	12 (6.9%)
Urethral/pharyngeal	186 (92.5%)	4 (2%)	11 (5.5%)
Rectal/pharyngeal	104 (90.4%)	6 (5.2%)	5 (4.3%)

P3.264 GENETIC DIVERSITY OF HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 IN DEMOCRATIC REPUBLIC OF CONGO: A REVIEW OF AVAILABLE DATA

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HIV has a genetic diversity that is equal to the complexity of its follow up of the patients. The classification of the different variants has allowed us to understand the virus, the geographical distribution and evolution of the pandemic and to better guide the follow up and the care of patients infected by HIV. Review the specifics of the HIV epidemic in the Democratic Republic of Congo (DRC), in terms of different molecular variants of HIV compared to the published location for the country. The search of the literature and abstracts presented at conferences with the subject of interest to identify different variants of HIV type 1 in the DRC on the websites of research. Online search was based on the following key words: "HIV subtype, DRC", "genotype, HIV, DRC" and "HIV strains in the Democratic Republic of Congo". It was restricted to the published literatures and presented abstracts between 1997 and 2012. According to manuscripts published since 1997, we have noticed a dominating prevalence of group M (100%) and of subtype A at 50.40% [31.2–68.9] for the entire country. In the Eastern part, variants A (44.73%) are dominant on variants C (12.20%), G (11.5%), D (9.12%) and U (7.24%). In the Center, variants A (62.57%) are followed by variants C (10.32%), H (5.02%), U (4.3%) and D (3.9%). In the Western part, variants A (40.91%) are followed by variants G (19.29%), D (10.5%), F (5.65%) and C (4.51%). For the entire country, variants are found in the following order: A (49.40%), G (10.73%), C (9.01%) and D (7.86%). The differences between and within groups are statistically significant for each variants. Several variants of HIV type 1 circulates throughout the DRC. The high number of recombinant forms (CRFs) shows the diversity and dynamics of the virus in this country.

P3.265 DISCORDANT COUPLES IN HIV/AIDS CYCLE

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Objectives A large proportion of new HIV infections in sub-Saharan Africa occur in stable HIV-discordant partnerships. In some couples, the strong desire to conceive a child may lead to risky behaviour despite knowledge of discordant serostatus. Our objective was to compare HIV transmission between discordant couples who did and did not conceive during participation in a clinical trial. Methods: Five hundred and thirty-two HIV-discordant couples were followed for up to 2 years in Kenya Network of Women Living with HIV/AIDS Kenya as part of the Partners in Prevention HSV/HIV Transmission Study. Quarterly HIV-1 antibody and urine pregnancy test results were analysed. Results: Forty-one HIV-1 seroconversions occurred over 888 person-years of follow-up, resulting in an annual incidence of 4.6/100 person-years. Twenty seroconversions occurred among 186 HIV-1-uninfected individuals in partnerships in which pregnancy occurred (10.8% of HIV-1-negative partners in this group seroconverted), in comparison to 21 seroconversions among 353 uninfected individuals in partnerships in which pregnancy did not occur (5.9% of HIV-1-negative partners seroconverted), resulting in a relative risk of 1.8 [95% confidence interval (CI) 1.01–3.26.

Conclusions Pregnancy was associated with an increased risk of HIV sero conversion in discordant couples. These data suggest that the intention to conceive among HIV discordant couples may be contributing to the epidemic. There are an estimated 33 million people in the world infected with HIV, 60% of whom reside in sub-Saharan Africa. Emerging data indicate that a large proportion of new infections in this region occur in stable HIV discordant relationships. Prevention efforts in this population have focused on couples-based HIV testing to equip partners with knowledge of their serostatus in order to motivate behaviour change.

P3.266 THE PREVALENCE OF HPV GENOTYPES IN PATIENTS WITH GENITAL WARTS IN SINGAPORE - WILL THE HPV VACCINE BE USEFUL IN THIS POPULATION?

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Introduction Worldwide, 90% of genital warts are caused by HPV types 6 and 11. A HPV vaccine covering HPV 6 and 11 is now available. To evaluate its potential benefits, we aim to characterise the prevalence of the HPV genotypes in genital warts in Singapore.

Methods We utilised a validated commercialised genotyping assay, the HybriBio HPV GenoArray test that is able to identify 21 HPV types including 5 low-risk types (6, 11, 42, 43, and 44). After a prior pilot study of ten patients, a total of 100 patients with genital warts and no prior treatment were recruited into this study. Scrapings from the warts were performed, stored in virus transport medium and DNA was then extracted for analysis. Demographics, sexual history and clinical findings were collected using a self-administered questionnaire.

Results There were 71 male and 29 female patients. The average age of the patients was 32.1 years. The majority (49%) were single and heterosexual. Approximately 50% of the patients had an average of more than five lifetime sexual partners. The majority (69%) had genital warts for the first time. HPV genotypes were characterised in 92% of the patients. Either HPV 6 and/or HPV 11 was detected in 87.0% of the patients. Thirty-four patients had high-risk HPV genotypes detected in their genital warts.

Conclusion A simple scraping methodology from genital warts followed by HPV typing (HybriBio HPV GenoArray test) has been shown

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to be reliable and effective in evaluating HPV genotypes in our population. The majority of the HPV genotypes characterised in all genital warts with readouts were either HPV 6 alone or HPV 11 alone or a combination of the two. This supports the use of a HPV vaccine targeting HPV 6 and 11 in the prevention of genital warts in Singapore.

P3.267 WOMEN COLONISED BY *LACTOBACILLUS CRISPATUS* HAVE A LOWER RISK OF ACQUISITION OF BACTERIAL VAGINOSIS (BV) THAN WOMEN COLONISED BY OTHER LACTOBACILLI

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Objective *L crispatus, L. jensenii, L. gasseri* and *L. iners* are the predominant lactobacilli in the vaginal flora of reproductive aged women. Colonization of the vagina and rectum by lactobacilli has been associated with decreased risk of BV. We evaluated the species-specific role of *Lactobacillus* on the acquisition of BV.

Methods Two hundred forty four healthy asymptomatic women aged 18–40 were followed at 2 month intervals for up to 18 months. At each visit, vaginal and rectal swabs for culture detection of lactobacilli and a vaginal smear for diagnosis of BV using Nugent criteria were collected. Lactobacilli were identified to the species level using repetitive sequence PCR and/or 16S rDNA sequencing. The risk of BV acquisition using *Lactobacillus* colonisation vaginally and/or rectally as a time-varying covariate was evaluated using Cox proportional hazards models.

Results This analysis included 1481 follow-up visits at which 235 women were colonised by *L. crispatus*, *L. jensenii*, *L. gasseri*, or *L. iners*. Of 2734 vaginal and1861 rectal lactobacilli recovered, 1968 were *L. crispatus*, 1024 *L. jensenii*, 909 *L. gasseri*, 410 *L. iners*, and 284 other species. Eighty nine women acquired BV over 220.4 woman-years (WY) for an incidence of 40 per 100 WY. The rate of BV was lowest among women colonised by *L. crispatus* at the prior visit (25 per 100 WY, unadjusted hazards ratio 0.31, 95% confidence interval: 0.16–0.62), compared to a rate of 100 per 100 WY among women having only *L. iners.* Vaginal and/or rectal colonisation by *L. jensenii* or *L. gasseri* was not associated with lower rates of BV acquisition (60 and 76 per 100 WY, respectively ($p > 0.05$)) than the rate observed among women having only *L. iners*.

Conclusions Although there is *Lactobacillus* species diversity in the vaginal microbiome, *L. crispatus* has the greatest protective benefit against acquisition of BV.

P3.268 A PILOT STUDY OF GENOTYPING EXTRARECTAL LYMPHOGRANULOMA VENEREUM STRAINS

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Background The first case of LGV in Barcelona was diagnosed in 2005 and since then around 200 cases have been notified up to 2012. All cases have been diagnosed among MSM, 80% of them coinfected with HIV and 97% of the cases had proctitis. Since 2008 some cases have appeared with extrarectal manifestations.

Objective To compare the molecular epidemiology profiles of extrarectal LGV cases diagnosed in Barcelona with profiles reported in rectal cases.

Methods A convenient 14 samples from 9 confirmed LGV cases in 2012 with extrarectal involvement were selected for LGV typing. DNA was extracted from samples using a semi automated system and kept al –80° C. The strains were further analysed by genotyping using a multilocus sequence typing (MLST) based on 5 highly variable gene regions, in addition the ompA gene was sequenced.

Results DNA quality for MLST was suboptimal in some samples. The genotyping pattern showed one single MLST-5 profile (27, 13, 17, 13, 28) among all the samples. In ompA there were two variants (22 and 28), in the 2 cases with ompA variant 22 the samples were obtained from inguinal ganglia.

Discussion The MLST-5 profile in LGV cases from Barcelona is the same as the predominating sequence type found in rectal cases. This is in line with the spread of a single clone, without specific tissue tropism. In ompA the 2 cases with variant 22 were identical to ompA in the reference strain L2/434/Bu, but differed from the currently predominating variant L2b among MSM. Considering the difference in ompA is minor it is more probable that L2b is a classical L2 isolate that has been circulating for a long time but showing now a new spectrum of manifestations. Our study does not support any difference in LGV strains obtained from extrarectal sites or from rectum.

P3.269 ASSOCIATION OF *NEISSERIA GONORRHOEAE* NG-MAST STRAIN TYPES AND SPECIFIC MUTATION PATTERN COMBINATIONS IN *PENA, MTRR* AND *PORB*

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Background Antimicrobial resistance to third generation cephalosporins, penicillin and tetracycline in *Neisseria gonorrhoeae* isolates can be associated with particular strain types (STs) as well as specific mutation patterns in *penA, mtrR or porB*. With a view to developing molecular diagnostics for antimicrobial susceptibility, we investigated whether antibiotic resistant and susceptible *N. gonorrhoeae* isolates from Saskatchewan Canada were associated with specific STs and combined mutation patterns in *penA, mtrR or porB*.

Methods DNA sequences of *penA, mtrR* and *porB* for 146 *N. gonorrhoeae* isolates were compared to "wild type" *penA* (GenBank#M32091), *mtrR* (GenBank#Z25796) and *porB* (GenBank#M21289) sequences. Mutation pattern numbers for *penA* were assigned as described by others. STs were ascertained by NG-MAST. Isolates were selected based on antimicrobial susceptibility phenotypes to 7 antibiotics.

Results Strains were classified into 51 NG-MAST STs; 6 STs (86/146; 59%) comprised ≥ 5 isolates, 10 STs included 2–4 isolates, and 35 STs contained 1 isolate. Isolates with ST 25 (33/36, 92%) were associated ($P < 0.0001$) with *penA/mtrR/porB* pattern I/WT/WT and with antibiotic susceptibility. ST 3654 was associated ($P < 0.0001$) with *penA/mtrR/porB* pattern IX/G45D/G120K,A121D (n = 13/17) and CMRNG (n = 7) or CMTR (n = 6) isolates. Isolates with chromosomal resistance to tetracycline were significantly associated ($P < 0.0001$) with several STs and *penA/mtrR/porB* patterns including: ST 3655 (XXII/A-,G45D/G120N,A121N - n = 8/12), ST 921 (pattern IX/G45D/G120D,A121N - n = 6/9), ST 508 (XXII/G45D/G120D,A121N - n = /6), and ST 3656 (pattern XXII/A-,G45D/G120D,A121N - n = 5/6). 24 isolates had higher cefixime MICs (0.03–0.06 mg/L) and included 17 STs with *penA* pattern IX (n = 17) and *mtrR* G45D (n = 16) and *porB* G120K,A121D (n = 12) mutations. Seven of these isolates were associated ($P < 0.0001$) with ST 3654 (pattern IX/G45D/G120K,A121D).

Conclusions We identified significant associations between particular mutation pattern combinations in *penA*, *mtrR* and *porB* and specific STs. This indicates that certain combined mutation patterns may be predictive of antimicrobial susceptibility and useful for molecular diagnosis.

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