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