32.7; p<0.01). Men with urogenital NG had higher urine Cq values than men without urogenital NG (33.9 vs 32.6;p<0.01). Cq values were higher in urines of HIV positive men compared to HIV negative men (33.9 vs 32.7;p<0.01). In women, Cq-values were higher in oropharyngeal swabs and anorectal swabs compared to vaginal swabs (36.7 and 33.9 vs 30.8;p<0.001). Cq-values were higher in vaginal swabs of HIV positive women compared to HIV negative women (35.1 vs 31.0;p=<0.01).

Conclusion Vaginal swabs and urine samples had much lower Cq values, i.e. higher CT loads, compared to oropharyngeal swabs which could have impact on transmission potential and sequelae. We hypothesize that high risk populations, such as HIV and NG positive patients, likely have repeat CT infections leading to partial immunity and therefore lower CT loads.

Disclosure No significant relationships.

P484 THE IMPACT OF *CHLAMYDIA TRACHOMATIS* NAAT DETECTION PROBABILITY ON TEST-OF-CURE RESULTS

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Background In spite of excellent analytical sensitivity, NAAT assays for *Chlamydia trachomatis* (CT) do not have a 100% detection probability (DP), especially at low concentrations of CT. This might especially impact test results after treatment, when CT concentrations are expected to be very low. The aim of this study was to use repeat testing to investigate the CT DP after treatment.

Methods As part of the FemCure study, women with vaginal or rectal CT infection were followed for 12 weeks after treatment. Single NAAT testing (Cobas 4800 CT/NG) of vaginal and rectal swabs at 1, 2, 4, 6, 8, 10 and 12 weeks after treatment was performed. For this project after initial NAAT, a selection of 63 swabs (29 vaginal and 34 rectal) was tested 4 additional times using again the COBAS 4800 CT/NG assay. DP was defined as the percentage of positive detections/5 repeat tests.

Results A selection of 47 follow-up swabs which tested CT negative with initial NAAT were investigated. Overall, 70% of swabs remained negative in all repeat samples (DP=0%). However, ≥10% of swabs showed a DP ≥60% in spite of the initial negative NAAT. The results were independent of sampling site (vaginal or rectal) and follow-up time-point during the study and included 15 swabs taken at 4–8 weeks (time-points sometimes used for test-of-cure). Additionally, 16 positive swabs prior to subsequent negative testing were also investigated. Results showed a DP of 100% in ~30% of samples confirming initial NAAT, but showed also a DP ≤40% in ~25% of samples.

Conclusion It is important to be aware of limitations in NAAT inherent DP, especially at low CT concentrations found after treatment. Further research will combine current data with CT viability testing which will potentially shed more light on the clinical relevance of NAAT testing below 100% DP.

Disclosure No significant relationships.

P485 PREDICTORS OF LOSS-TO-FOLLOW-UP AMONG HIV INFECTED MSM ON TREATMENT AT A (TRUSTED) COMMUNITY HEALTH CENTRE IN LAGOS, NIGERIA

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Background Antiretroviral Therapy(ART) has been shown to reduce transmission of HIV and HIV-related morbidity and mortality. Despite improved and highly successful coverage with ART, HIV programmes around the world have recorded appreciable rise in the numbers of clients who drop out of care at different points. The objective of this study was to determine the predictors of Lost-To-Follow-Up(LTFU) among HIV infected Men Who Have Sex with Men (MSM) on treatment at a (Trusted) Community Health Centre in Lagos,Nigeria.

Methods A descriptive cross-sectional study was conducted among clients who have been LTFU amongst MSM in HIV care at a (Trusted) Community Health Centre. Active clients on ART were separated from those LTFU, those transferred out and those who died using the PEPFAR software, Retention and Audit Determination Tool(RADET). The clinic folders of the LTFU clients was the source of sociodemographic information (age at start of ART, employment status, occupation etc) as well as clinical information such as staging, last clinic visit date. A semi-structured questionnaire adapted from literature was modified and administered via telephone or in person at any venue of participant's choice to all the selected participants.Data analysis was done using SPSS. Chi-square statistics was used to determine association between variables and binary logistic regression was used to determine the predictors of LTFU. The level of significance was placed at 5%.

Results The mean age of the cohort was 25±5years. Of 150 patients identified, 108(72%) patients were genuinely defined as LTFU as they were not enrolled for treatment anywhere else. Patients with low income, no children, suffered stigma and discrimination among family were at higher risk of LTFU. Travelled out of town, medication side effects were the most common reasons for LTFU.

Conclusion Many MSM on treatment were LTFU. Effective control measures targeting high-risk population should be implemented to improve retention and reduce LTFU.

Disclosure No significant relationships.

P486 POPULATION STRUCTURE OF LYMPHOGRANULOMA VENEREUM IN BELGIUM: SURVEILLANCE DATA FROM 2010 UNTIL 2017

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Background The number of *Chlamydia trachomatis* (CT) L genotypes/serovars or Lymphogranuloma venereum (LGV) is on the rise in Belgium, however the genetic diversity of the CT L genotypes in Belgium remained unknown. Our aim was

to document the population structure of the LGV cases over the years.
Methods The complete outer membrane protein A gene (*ompA*) of remnant positive LGV samples (previously confirmed by an in-house qPCR; target: *pmpH* gene) was amplified and sequenced using automated DNA sequencing. The obtained aligned sequences were compared with all L-variants described in literature and with all CT ompA sequences using the BLAST search.
Results All samples were from men who have sex with men; mostly HIV positive (82.2%) and from anorectal origin (94.1%). Sequencing of *ompA* (n=118) revealed that, in total, L2 and L2b genotypes were equally found (42.4%) followed by variants of L2 genotypes: L2bV2(6.8%) and L2bV1 (3.4%). Curiously, one strain defined as L2a had one additional mutation (A515C – Lys172Thr) which is also found in L2bV2 (hereafter named L2aV2). Three L1 strains were identified over the years (one in 2016 and two in 2017) but no link between the three could be found. Two strains could not be characterized due to mixed infection with non-L genotypes. Most of infections were symptomatic (80.7%) with proctitis (71.1%) as predominant symptom. Re-infections were common in our population (9.3%) and sequencing showed that individuals could become infected by different strains in a short period of time. No significant association was found between HIV status, presence of symptoms and the L-genotypes.
Conclusion The LGV strains in Belgium are more genetically diverse than initially thought as a total of two L-variants and five L2-genotypes have been identified. No firm conclusions can be made concerning an association between clinical symptoms and specific L-genotypes as asymptomatic infections were found with all L2 variants.
Disclosure No significant relationships.

P487 A NOVEL RAPID REAL-TIME PCR TEST FOR THE DETECTION OF *CHLAMYDIA TRACHOMATIS* IN PATIENT SAMPLES

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Background Point of care (POC) testing for infectious diseases can provide actionable diagnostic information as soon as individuals present to healthcare systems. POC testing for sexually transmitted infections could have a significant impact on sexual health by enabling screening programs, reducing loss to follow-up and enabling immediate and targeted treatment. We have developed a novel rapid real-time PCR assay which can detect *Chlamydia trachomatis* in clinical samples.
Methods DNA was extracted from 122 residual genital swab and urine samples previously tested in the Roche cobas CT/NG assay using the Qiagen DNA mini kit and the DNA extracts were tested for *C. trachomatis* using the rapid real-time PCR assay.
Results Of the 122 samples, forty were negative in both the new rapid real-time PCR assay and the Roche cobas assay; 78 samples were positive in both assays and four samples were positive in the cobas assay but negative in the new novel assay. The specificity of the new novel assay was 100% and its sensitivity was 95.1% respectively. The four samples which were negative in the new assay had high Ct values in the cobas test indicating low levels of chlamydia organisms were present in the samples.
Conclusion The rapid real-time PCR system is rapid, sensitive and specific for the detection of *C. trachomatis* in clinical samples from patients with chlamydia infection. The rapid real-time PCR assay for *C. trachomatis* forms the basis for a low cost, disposable sample to answer diagnostic assay cassette, which will run on the QuantuMDx Q-POC™ platform.
Disclosure No significant relationships.

P488 PUTTING THE U.S. ARMY'S RISING RATES OF CHLAMYDIA AND GONORRHEA IN PERSPECTIVE: A COMPARISON WITH U.S. TRENDS

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Background U.S. chlamydia and gonorrhea rates have increased for four consecutive years, reaching record highs in 2017. Similar trends were reported for the U.S. Army, with Army rates being elevated relative to the general population, due in part to demographic differences. A comparison of standardized rates was needed to put these differences in perspective.
Methods Incidence rates of chlamydia and gonorrhea reported during 2013–2017 among Army active members and U.S. citizens age 15–64 were standardized using the 2015 Army age and sex distribution. The CDC's National Electronic Disease Surveillance System and the Army's Disease Reporting System Internet were used for the analysis.
Results Crude and adjusted chlamydia rates (per 100,000) were over 2-fold higher among Army members (adjusted 2017 rates: 2,160 and 1,005 in the Army and U.S, respectively). Army chlamydia rates were elevated for all age and sex strata. The Army's crude gonorrhea rates (per 100,000) were elevated (annual rate range: 275–373 versus 156 to 266 in the U.S.); however, adjusted U.S. rates surpassed Army rates (2017 rates: 438 in the U.S. versus 360 in the Army). Elevations for chlamydia and gonorrhea were observed in Army women under 25 relative to U.S. women 15–24 (2017 crude rates: 11,132 versus 3,635, respectively, for chlamydia and 1,117 vs 623, respectively, for gonorrhea). Crude gonorrhea rates were higher in U.S. men 25–44 relative to Army peers (2017 rates: 542 vs 269 for men 25–34, and 238 vs 106 for men 35–44, respectively).
Conclusion The Army's incidence of chlamydia was elevated relative to the general population even when demographic differences were taken into account. This may reflect higher individual or sexual network risks or better access to care. The Army's lower adjusted gonorrhea rates may reflect differences in high-risk sub groups such as MSM, differing sexual network risks, or unmeasured confounders.
Disclosure No significant relationships.