implementation of a 2 hour point-of-care (POC) STI care model for clinical trial participants.

Methods As part of a Phase I/IIa vaccine study, CAPRISA implemented POC STI testing for chlamydia, gonorrhoea (Xpert CT/NG, 90 min) and trichomonas (OSOM, 15 min) at a site laboratory of a research clinic in Durban, South Africa, in July 2015. Since then, the POC model has been adopted by 5 other prevention studies, becoming the main STI testing model at CAPRISA.

Results A total of 1426 Xpert CT/NG assays were run on two 4-module Genexpert machines between July 2015 and November 2016. Chlamydia was detected in 206 (14.4%), gonorrhoea in 79 (5.5%) samples, and 52 (3.6%) samples showed both infections. No infection was detected in 1070 (75.0%) samples. 143 (8.6%) samples showed either an error message (5.0%), an invalid result (3.0%) or no result (0.6%) requiring repeat testing, either on the same or next convenient visit. Trichomonas testing was conducted simultaneously on all female participants (n=1093, prevalence 2.7%). Gram staining to diagnose bacterial vaginosis and candida infection was performed on-site in one of the studies. Implementation of this model allowed early detection of screen failures for Phase I/IIa vaccine studies. During follow-up, participants with STIs received enhanced risk reduction counselling and immediate treatment on the day of sample collection. This resulted in improved care, early partner notification, and cost-savings by avoiding unnecessary screening procedures and repeat visits.

Conclusion A 2 hour POC STI testing model can streamline screening and follow-up of participants in HIV prevention studies, and should be considered for implementation by other research sites.

Support: Cepheid loaned two 4-module Genexpert machines to the study team free-of-charge, but did not contribute to the preparation of this abstract

Introduction Understanding patterns of chlamydia incidence and prevalence is important for addressing inequalities, planning cost-effective control programmes and defining performance indicators. Population-based surveys are costly; the best data for England come from the Natsal surveys which are only available once per decade, and are nationally representative but not powered to compare localities. Estimates at finer spatial and temporal scales are required.

Methods We present a method for estimating local incidence and prevalence by modelling the infection, testing and treatment processes. Parameters describing natural history and treatment-seeking behaviour are informed by the literature or calibrated using national prevalence estimates. By combining them with local-level surveillance data on numbers of chlamydia tests and diagnoses in England, we estimate local screening rates, incidence and prevalence.

Results There is substantial local-level variation in infection burden. Highest infection rates are in the most-deprived areas – but deprivation is a poor predictor of prevalence, with large variation within each deprivation quintile. Importantly, positivity is not a reliable proxy for prevalence. Most localities that meet the current performance target of 2300 annual diagnoses per 1 00 000 population have higher incidence and prevalence than most that do not, and the target may be unrealistic for many localities.

Conclusion Our approach provides local estimates of chlamydia incidence and prevalence from surveillance data, which can be used to inform analysis of local variation and assess local control programmes. Many localities are unlikely to be able to meet the current annual diagnosis rate target, and successful prevention interventions like condom promotion make the target harder to reach. A better performance indicator could be the proportion of incident infections that are treated, as estimated by our model, since a higher value is always better for public health and other prevention activities make a higher value easier to achieve.

Introduction Current CDC guidelines recommend screening "at least annually" for *Chlamydia trachomatis* (CT) and *Neisseria gonorrhoeae* (GC) at sites of exposure using nucleic acid amplification tests (NAAT) in HIV-infected MSM. National screening rates remain suboptimal in this high-risk population, particularly at extra-genital sites.

Methods We enrolled HIV-infected MSM from a routine care visit at the 1917 HIV clinic in Birmingham, Alabama. Inclusion criteria included age >18, receptive anal intercourse in the past 30 days and lack of antibiotic exposure. Participants provided four self-collected rectal swabs and a urine sample. A pharyngeal sample was provider-collected. Samples from the rectal and genital sites were run on four testing platforms with the composite infection standard ($\geq$2 NAAT positive) defining a positive result. Pharyngeal samples were run on two platforms and the patient infection standard (2 NAAT positive) was used to define positivity.

Results A total of 175 unique HIV-infected MSM were enrolled between December 2014 and November 2016. Overall, 34 men (19.4%) had CT or GC infection detected. CT infection rates by site were: 13.1% rectal, 3.4% urogenital, 0% pharyngeal. GC infection rates by site were: 8.6% rectal, 3.4% urogenital and 2.3% pharyngeal. In addition, 5.7% of men had co-infection with CT and GC at the rectal site and 1.7% had simultaneous CT or GC infection at genital and rectal sites. Most infections (79.4%) would have been missed by genital screening alone.

Conclusion Sexually active, HIV-infected MSM in Birmingham, Alabama have high prevalence rates of CT and GC infection, particularly at the rectal site. This has public health implications since CT/GC coinfection may increase HIV transmission rates. Clinics that provide care for HIV-infected MSM should streamline extragenital testing; this may include the incorporation of patient-collected rectal swabs into routine care.

P3.112 | USE OF SOCIAL APPS AMONG YOUNG MEN WHO HAVE SEX WITH MEN (YMSM) BETWEEN THE AGES 18 TO 24 AT THE WESTERN REGION OF PUERTO RICO: EVALUATION OF PROTECTIVE AND RISK FACTORS

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Introduction Increasing new cases of HIV among Men who have Sex with Men (MSM) has been observed in Puerto Rico (PR). According to the HIV Surveillance System, 23% of the HIV/AIDS cases are among MSM. Adoption and proliferation of digital platforms have become a new venue for MSM to meet new sexual partners. Researchers have studied these new venues without getting any consensus if the use of social apps are a protective or risk factor for HIV infection. This study aims to understand the use of social apps among young MSM (18–24 years), practices with those who they met online and perceived risk of infection.
Methods Data collected from the needs assessment of the Youth Prevention Program between March and September 2016, was used. A convenience sampling of 183 MSM were recruited in the Western region of PR. Descriptive analysis was used to portray selected characteristics and use of social apps.
Results More than half (80%) of the participants reported the use of any social apps for meeting sexual partners in their lifetime. Among those who use apps, 65% reported was for hook-up. The average number of lifetime sexual partners met by these apps were 5.7±4.7 partners. Inconsistent condom use was reported among 40%, which indicated have not used condom while having sex with partners they met online. The most common app used was Grindr (66%), followed by Facebook (55%). When asked their perceived risk of HIV, only 16% reported they considered to be at high risk of contracting with HIV when meet their sexual partners online. Of further note, 24% sent photos of their bare buttock, 31% of their penis and 48% display their chests.
Conclusion The study intends in the future to demonstrate if there is any association from using these social apps and HIV infection. This preliminary analysis showed that apps are becoming a frequent to meet sexual partners but they don't consider these apps as risk venues for contracting HIV. This study will help strengthen prevention programs and prevention initiatives for high risk populations in the island.

P3.113 | HIV-1 DRUG RESISTANCE MUTATIONS IN INFECTED CHILDREN AND ADOLESCENTS FAILING THERAPY: IMPACT IN THE SUSCEPTIBILITY OF DRUGS USED IN SALVAGE THERAPIES

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Introduction Paediatric HIV-1 infection remains an important public health issue in resource-limited settings. In Brazil, the access to combined antiretroviral therapy (cART) and the HIV-1 genotyping test are available for all infected children and adolescents. However, mainly due to low patient adherence, multidrug-resistant (MDR) viruses have been increasing over the last years. This study estimate the resistance associated to the new generation protease inhibitors (PIs) and non-nucleoside reverse transcriptase inhibitors (NNRTIs) and the possible use in rescue strategies for children and adolescents failing cART.
Methods Between 2008 and 2014, blood samples from 246 HIV-1-infected children and adolescents failing different cART regimens, were collected in the Rio de Janeiro State, Brazil. The profiles of HIV-1 resistance mutations were evaluated in the Stanford website and subtype confirmed by phylogeny.
Results The majority of genotyped samples were classified as HIV-1 subtype B (75.6%), followed by subtype F1 (15.4%), BF recombinants (4.1%), subtype C (3.3%) and subtype A1, CRF_02AG and the recombinant A1B in one subject each. A total of 31.2% of patients showed resistance associated to first line therapy, 45.3% for the second line and 23.4% to third line. MDR mutations were detected in only 3% of the children. The prevalence of PI-associated mutations was low (3.6%), except for the M46I/L mutation (24.4%) associated to the majority of PIs. The resistance to PIs used in the rescue therapies, were 2.8% for the darunavir and 3.6% for the tipranavir. High prevalence of thimidine associated mutations (TAMs) and to lamivudine, were observed (>80%). But, mutations to the nucleotide reverse transcriptase inhibitor (NRTI) Tenofovir, showed low prevalence (5.3%). In addition, resistance mutations associated to the decrease of a virological response to etravirine were 5.4% and 3.8% to rilpivirine.
Conclusion Low prevalence of drug resistance mutations associated to the new generation of PIs and NNRTIs was observed in our genotyping database. The impact of resistance mutations under darunavir seems lower than for tipranavir in children failing other PI-based regimens. Although prior failure to other PIs or NNRTI might produce cross-resistance, the results show that all of these drugs used in the therapy rescue, could be effective and constitute a good option for children who failure other regimens.

P3.114 | ANALYSIS OF NOTIFICATION`S CASES OF CONGENITAL SYPHILIS IN AN UNIVERSITY HOSPITAL FROM NITEROI, 2008–2015

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Introduction Congenital syphilis (CS) is a serious public health problem in Brazil, being the cause of fetal death and other perinatal complications, besides it is a good indicator of prenatal quality. The objective of this study is knowing the frequency of CS notification at Antonio Pedro University Hospital of Federal Fluminense University (HUAP), Niterói, Rio de Janeiro, and analyse several data from the compulsory notification sheets (CNS) of this disease.
Methods Retrospective temporal study about the frequency of CS's notification in HUAP (Epidemiological Surveillance Department) in the period from 2008–2015.
Results We found 56 CNS. We analysed data on diagnosis, treatment, signs and symptoms of CS, among others. We exclude four sheets (4/56/7.14%) because they do not contain minimum data for analysis. So, we worked with 52 CNS of