

P3.190 HIGH RATE OF REPEAT SEXUALLY TRANSMITTED INFECTIONS AMONG MEN WHO HAVE SEX WITH MEN IN SOUTH AFRICA

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Introduction Men who have sex with men (MSM) are considered an important key population in South Africa. Insight in the dynamics of sexually transmitted infections (STI) is of paramount importance to address the burden of infection. We aim to characterise incident STI among South African MSM.

Methods This prospective cohort study was conducted at two primary healthcare clinics that specifically target MSM in Johannesburg City Centre and Soweto, South Africa. We recruited MSM presenting with urethral discharge and provided standard syndromic management. Participants were requested to return for follow-up testing after six weeks, or earlier in case of symptoms. A urine specimen and rectal swab were collected for molecular microbiological investigations at both visits.

Results We recruited 78 MSM of whom 69% identified as gay; 43% was HIV-infected. *Neisseria gonorrhoeae* was the main cause of discharge in 46 men (59%), followed by *Chlamydia trachomatis* in 9 (12%), *Mycoplasma genitalium* in 1 (1.3%) and *Trichomonas vaginalis* in 3 (3.8%). Rectal swabs were positive for *N. gonorrhoeae* (28%), *C. trachomatis* (13%) and *T. vaginalis* (3.8%). Sixty-one (78%) men came for follow-up visit. Twenty-three men (38%) had a total of 34 STI diagnosed at follow-up, including 20 urethral and 14 rectal infections. The majority of these infections (68%) were considered newly acquired STI based on microorganism detected and anatomic site involved. This includes all infections with *C. trachomatis* (n=5), *M. genitalium* (n=3) and *T. vaginalis* (n=9). Seventeen MSM tested positive for *N. gonorrhoeae* at follow-up; six of which were new infections.

Conclusion We demonstrate a high rate of repeat STI in this unique cohort of South African MSM and show that most of these infections are newly acquired. This supports the effectiveness of syndromic management for most STI, but also highlights that strengthening of prevention efforts is highly warranted. The observation of repeat *N. gonorrhoeae* infections is concerning and molecular typing for further analysis of these strains is underway.

P3.191 HIV IN INDIGENOUS MSM IN GUATEMALA: A HIDDEN PROBLEM

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Introduction In Guatemala, data regarding HIV epidemics doesn't show much data about indigenous population, although nearly 50% of the population in Guatemala are indigenous. In metropolitan area, MSM HIV prevalence is around 9%. But there is not data about HIV prevalence in indigenous MSM. This data is the first report in this important group.

Methods Cross-sectional data analysis from October 2015 to July 2016. MSM were recruited as part of the implementation

of Global Fund projects. Activities were implemented in three department of the Guatemalan highlands: Sololá, Totonicapán and Chimaltenango. Recruitment was performed by peers, by face-to-face or using social networks. Rapid HIV testing was performed in-site and confirmation in reference laboratory, STI were evaluated by syndromic management. Data was analysed using Stata 13.

Results 1196 MSM were tested for HIV and 293 had STI evaluation. 42% lived in Chimaltenango and 19% in Sololá. Median age was 22 years old (IQR 19–26); 40.3% of them self-reported as indigenous, 11% of them K'iche' and 10% kakchiquel. 60% of them had high school or higher education, 58 HIV cases were diagnosed, for a global HIV prevalence of 4.8%. In indigenous MSM HIV prevalence was higher (5.1 vs 4.9, no difference). In K'iche' MSM (N:156) HIV prevalence was higher (4.2%) than in kakchiquel (3.9%), but no difference. 18% had an STI, the most prevalent were anal warts (13%).

Conclusion HIV prevalence in indigenous MSM is lower than reported in Guatemala city, however is a major public health problem not previously reported in Guatemala. Population representative studies in the highlands are needed to assess HIV prevalence in MSM, as well to improve current interventions.

P3.192 HUMAN PARVOVIRUS B19 AMONG BRAZILIAN PATIENTS INFECTED WITH HIV

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Introduction Human Parvovirus B19 (B19V) infection may cause red cell aplasia in patients infected with human immunodeficiency virus (HIV). The introduction of highly active antiretroviral therapy (HAART) has improved the immune function of these patients, modifying the course of B19V infection. To better understand the importance of B19V infection in the HAART era, a follow-up study of a cohort of HIV-infected individuals was conducted during an eight-year period (2001–2008) at the Infectious Diseases Department of Antonio Pedro University Hospital (HUAP) at the Fluminense Federal University (Niterói, RJ, Brazil).

Methods Blood samples were collected from 313 HIV-infected individuals who attended the general medical outpatient clinic for routine care. IgG and IgM antibodies against B19V were detected in serum samples using a commercial enzyme immunoassay (Biotrin). B19V viraemia was evaluated by the detection of B19V-DNA by polymerase chain reaction (PCR). To genotype B19V strains PCR products were subjected to direct sequencing and phylogenetic analysis.

Results The seropositivity to B19V IgG antibodies was 72% (225/313). Approximately 30% (28/88) of anti-B19V IgG negative patients seroconverted. Most seroconversions occurred during incidence peaks of a B19V infection in Niterói (2005–2006). No clinical manifestations of B19V infection were detected during the seroconversion period. B19V-DNA was detected in 5/88 patients, four of whom also exhibited seroconversion. Four of the patients were infected with subgenotype 1a strains and the remaining patient was infected with a subgenotype 3b. Anaemia was detected in 8/88 patients, but