Methods Using data from the Provincial Laboratory and STI clinic, an anonymized dataset with the last HIV Ab (HIVGO1/2, Abbott, AxSYM +/- Western Blot) (STI clinic patients) or first syphilis Ab+ (Architect, Abbott +/- RPR & InnoLi) was constructed with: (1) All patients: age, gender, date of testing, N. gonorrhoea (NG) and C. trachomatis co-infection within 30 days of HIV/syphilis test, infectious syphilis stage, and HIV testing as of Dec 2010 and (2) STI clinic patients only: syphilis test results within 30 days of their HIV Ab- test. Patients remaining HIV Ab- > 180 days after the sample receipt date were excluded from HIV pNAT. The remaining samples were divided into SyphAb+ and SyphAb-subsets. Pools of 25 samples were tested using the Roche COBAS AmpliPrep/COBAS Taq-Man HIV-1 Test (pNAT). Positive pools were broken down to identify positive individuals. Percentage calculations were based on patients with pNAT.

Results 7954 HIV Ab- patients were eligible. Of these, 2237 were retested and were HIV Ab- > 180 days; 216 (10%) of this subset were SyphAb+, 5441 (95%) of the remaining patients had samples available for pNAT. 5001 were SyphAb-, 531 were SyphAb+, and 109 had no syphilis testing. Four SyphAb+ patients (0.07% of all, 1.2% of SyphAb+), all seen at STI clinic, had detectable HIV RNA using pNAT; one patient had Early Latent Syphilis and positive NG culture.

Conclusions pNAT testing can be used to identify acute HIV infections in high risk populations. Patients with positive syphilis serology may be an important subset for this approach.

P3.251 SYPHILIS AND HIV CO-INFECTION IN PATIENTS ATTENDING AN AIDS OUTPATIENT CLINIC IN VITORIA, BRAZIL


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Background HIV-positive patients should be regularly screened for syphilis. Detection and treatment of syphilis can help to reduce HIV transmission.

Objective Our goal was to determine the prevalence of and associated factors with syphilis in HIV patients attending an AIDS outpatient clinic in Vitoria, Brazil.

Methods Cross-sectional study was conducted in HIV/AIDS patients. They were interviewed for demographic, behavioural and clinical characteristics and had blood collected (venipuncture and fingertip) for VDRL and treponemal tests (rapid test) after signing an informed consent.

Results A total of 438 patients were included in the study. Over half (55%) of the sample was male; mean age was 48 years (SD±11 years), and mean years of schooling was 8.1 (SD±4.2 years). The prevalence of syphilis was 5.5%(CI 95%: 3.3%–7.3%). The treponemal test was positive in 18.9% of patients. Over one third (37.8%) of the male patients reported a history of sex with men (MSM). No women reported homosexual behaviour. More than two-thirds (70%) of the participants reported consistent condom use in the last year; 6.4% were sexworkers and 25.8% were illicit drug users. A total of 72.4% reported having had one sexual partner in the last year In multivariate analysis, syphilis was associated with male gender [OR = 4.57(CI95%:1.03–20.0)], men who have sex with men [OR = 1.78(IC95%:1.64–4.14)], not on antiretroviral therapy [OR = 0.18(CI 95% 0.06–0.59)], and history of previously treated syphilis infection [OR 5.54 (CI95%:1.95–15.76).

Conclusions Our finding highlights the importance of preventing and promptly treating syphilis in people living with HIV/AIDS. Patients with HIV/AIDS must be screened and monitored annually for early detection of syphilis, to provide early treatment and follow-up to avoid reinfections.
donors in comparison to male donors. TTIs prevalence was highest among blood donors in the age group 21 to 30 years (P = < 0.05). HIV was reported to be more prevalent among replacement donors (0.33%) than volunteer donors (0.12%). Other TTIs were insignificantly more prevalent among volunteer donor than replacement donors.

Conclusions Screening of donated blood should be done with highly sensitive and specific tests so as not to transfuse infected blood. It is also important to strengthen donor counselling before donation.

**P3.254** THE SPATIAL AND TEMPORAL ASSOCIATIONS BETWEEN NEIGHBOURHOOD DRUG MARKETS AND RATES OF SEXUALLY TRANSMITTED INFECTIONS IN AN URBAN SETTING

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**Background** This study examined temporal and spatial relationships between neighbourhood drug markets and gonorrhoea among census block groups from 2002 to 2005. Our central hypothesis was that drug markets through their drug and sex economies set up dense sexual networks among a high STI prevalence group which creates conditions that are necessary and sufficient for STI transmission.

**Methods** The study design was a spatial, longitudinal ecologic study. The primary outcome of interest was age and sex standardised gonorrhoea counts from 2002 to 2005. The primary exposure of interest was drug markets defined as illicit drug dealing within a specific geographic area and measured using drug market arrest data. Poisson regression was utilised with adjustment in final models for socioeconomic status, stability and vacant housing.

**Results** Increased drug market arrests in a focal neighbourhood were significantly associated with a 15% increase gonorrhoea (Adjusted RR 1.15; 95% CI 1.09, 1.20). Increased drug market arrests in adjacent neighbourhoods were significantly associated with a 32% increase in gonorrhoea (ARR 1.32; 95% CI 1.22, 1.42), independent of focal neighbourhood drug markets. Increased drug market arrests in the previous year in the focal neighbourhood were not associated with increases in gonorrhoea (ARR 1.00; 95% CI 0.95, 1.06), adjusting for focal and adjacent neighbourhood drug markets.

**Conclusions** While the temporal lag of one year was not supported, our findings support an associative link between drug markets and gonorrhoea. The findings suggest that drug markets and their associated sexual networks may extend beyond local neighbourhood boundaries indicating the importance of including spatial lag effects in regression models investigating these associations.

**P3.255** TRICHOMONAS VAGINALIS AND ASSOCIATED FACTORS AMONG WOMEN LIVING WITH HIV/AIDS IN AMAZONAS, BRAZIL

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**Background** STIs facilitate HIV transmission through direct and biological mechanisms. Early detection and treatment of STI can be an addition to the HIV prevention strategies.

**Objectives** Our goal was to determine the prevalence of Trichomonas vaginalis (TV) and its associated factors among HIV/AIDS women attending an AIDS clinic in Manaus, Amazonas, Brazil.

**Methods** Cross-sectional study. Women attending an AIDS clinic in Manaus between March and December 2010 for gynaecological examination were invited to participate. Enrolled patients answered a face-to-face interview including demographic, behavioural and clinical data. They also underwent a gynaecological evaluation and cervical scrape samples were collected for wet mount, Gram stain, culture and cytological analysis. A blood sample was obtained to determine TCD4+ lymphocytes and viral load.

**Results** A total of 341(91.2%) women participated in the study. The prevalence of TV was 4.1%(CI95%:2.0%–6.2%). Median age was 32 (interquartile range (IQR): 27–38) and median of education was 9.0 (IQR 4–11) years of schooling. A total of 165 (53.2%) HIV women were classified as patients with AIDS. In multivariate analyses, squamous intraepithelial lesions in cytology [OR = 2.46 (CI95%:1.31–4.63, p = 0.005)] and reporting anal sex [OR = 3.62 (CI95%:1.08–12.19, p = 0.037)], were associated with TV.

**Conclusions** These results highlight HIV-infected women should be screened for TV. The control of this infection may have an impact on preventing reproductive complications among these women.

**P3.256** TRANSMITTED RESISTANCE AMONG INDIVIDUALS RECENTLY DIAGNOSED WITH HIV/AIDS IN THE METROPOLITAN REGION OF RECIFE, NORTHEAST OF BRAZIL

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**Background** The highly active anti-retroviral therapy (HAART) has increased survival of patients with HIV/AIDS. However, some individuals may present therapeutic failure due to a variety of factors, including transmitted antiretroviral resistance. Thus, the objective of the study was investigate frequency of primary resistance and recent infection among HIV-1 seropositive individuals at five Voluntary Counseling and Testing Centers (VCT) at Metropolitan Region of Recife in Northeast of Brazil.

**Methods** For RNA transcription to cDNA and PCR amplification with genetic sequencing of the product was carried out using the TRUENE® HIV-1 Genotyping Assay. The sequences were analysed using the software OpenGene® DNA Sequencing System and ARV resistance mutations and subtypes were submitted to the Stanford HIV Drug Resistance Database and further confirmed by SIMPL0T v2. The BED Calypso® assay was carried out for detection of recent HIV infection.

**Results** A total of 130 samples were analysed. Most participants were males (56%) and aged 31–50 years. Median T CD4+ lymphocyte was 408 cells/mm² and viral load was 3,683 copies/ml. Primary resistance rate was 4.6%. Recent infection rate was 23%. Mutations associated with resistance to NNRTI, NRTI and PIs occurred in 5.84%, 1.55% and 0.77%, respectively.

**Conclusions** The present study showed that 4.6% of the strains had transmitted antiretroviral resistance mutations, which coincides with the low resistance rates that have been found in Brazil. Despite a high prevalence of recent infection, there were no significant differences in the prevalence of mutations between the recent and chronic infection groups (p = 0.327).

**P3.257** DISTINCT BUT ALSO HIGHLY SIMILAR CHLAMYDIA TRACHOMATIS STRAINS IN NANNING, CHINA AND IN AMSTERDAM, THE NETHERLANDS

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**Background** This study examined the genetic diversity of C. trachomatis strains isolated from women in Nanjing, China and from Amsterdam, The Netherlands.

**Methods** A total of 63 C. trachomatis strains were isolated from 61 women in Nanjing, China and 28 strains from 26 women in Amsterdam, The Netherlands. The isolates were genotyped by using multiplex PCR for five major multilocus genotypes and by sequencing the ompA and 16S rRNA genes.

**Results** Genotyping results revealed 15 distinct genotypes, which were distributed as follows: 10 genotypes were isolated in both areas, while 5 genotypes were only isolated in Nanjing, China. Sequencing of the ompA and 16S rRNA genes showed that all strains were highly similar, with only minor differences in the nucleotide sequence.