

also higher among HIV patients, but it only presented a tendency to significance ( $p=0.07$ ). Regarding serum NGAL, no significant difference was observed between the groups ( $p=0.417$ ). There was significant association between urinary NGAL and microalbuminuria ( $r=0.378$ ,  $p=0.003$ ) and MCP-1 ( $r=0.476$ ,  $p<0.001$ ) in all HIV patients.

**Conclusion** HIV patients using cART presents subclinical kidney disease detected through novel biomarkers. KIM-1 may serve as early marker of tenofovir nephrotoxicity, and MCP-1 appears to be related with higher viral load.

### LB1.63 HIGH ACCEPTANCE OF CERVICAL SELF-COLLECTION FOR DETECTION OF HPV, HHV-2 AND HIV-1 IN WOMEN LIVING IN TAPAJÓS REGION, AMAZÔNIA, BRAZIL

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**Introduction** Cervical self-collection is a safe and efficient method for detecting sexually transmitted infections (STIs). The study aims to verify the acceptance of cervical self-collection and the prevalence of HPV, HHV-2 and HIV-1 infection in women living in the Tapajós region, Amazônia, Brazil.

**Methods** Cross-sectional study with women attending in Santarém-Pará. The collection was performed between August 2015 and January 2017. Participants collected cervical scrapings and peripheral blood. Those who accepted, also performed cervical self-collection. Detection of HPV DNA was performed by nested PCR with MY09/11 and GP5/6<sup>+</sup> primers and typing was done by sequencing. Detection of HHV-2 DNA was performed by real-time PCR with Taqman. Identification of anti-HIV-1/2 antibodies was made by Alere Determine Kit.

**Results** A total of 206 specimens were obtained from 112 women. The acceptance of cervical self-collection was 84% (94/112) and HPV DNA was identified in 39.4% (37/94) of the samples. While the prevalence of HPV infection in cervical scraping was 32.1% (36/112). All the women presented Papanicolaou negative for malignancy. The most prevalent types were HPV-16 and HPV-18. The overall prevalence of HHV-2 infection was 8.9%. The concordance rate in the molecular diagnosis between cervical scraping and cervical self-collection was 65% (26/40) for HPV and 50% (4/8) for HHV-2. No woman had HIV-1 reactive serology.

**Conclusion** A high prevalence of HPV infection was found in women without dysplastic lesion. Cervical self-collection had high acceptance, moderate concordance rate in the detection of HPV DNA compared to cervical scraping, and alone it was more efficient in the detection of HPV. This is the first study in women living in Tapajós region and the findings strongly suggest that cervical self-collection may be a useful tool for increasing access to diagnosis of STIs and screening for cervical cancer in women living in the Amazon.

### LB1.64 CD64-MEDIATED PHAGOCYTOSIS OF HUMAN SYPHILITIC SERUM OPSONIZED *TREPONEMA PALLIDUM* BY HUMAN MACROPHAGES REQUIRED IFN-GAMMA

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**Introduction** Syphilis is a multi-stage, sexually transmitted disease caused by the spirochete *Treponema pallidum* (*Tp*). Clinical manifestations result from the treponeme's ability to elicit a robust immune response while at the same time evading host defenses. Syphilitic lesions are comprised of a rich cellular infiltrate, which includes IFN-gamma (IFN $\gamma$ ) producing T cells, NK cells and activated macrophages. We previously, we demonstrated that human syphilitic serum (HSS) promotes efficient uptake of *Tp* by human monocytes and that opsonophagocytosis of *Tp* markedly enhances cytokine production. The purpose of this study is to establish a potential role for macrophages and opsonic Ab in clearance of *Tp* and generation of tissue-based inflammation during human syphilis.

**Methods** We used monocyte-derived macrophages to develop an *ex vivo* model for studying spirochete-macrophage interactions. We used macrophage-colony stimulating factor and IFN $\gamma$  for macrophage maturation and evaluated the immunophenotypic modulations by flow cytometry. We assessed *Tp* uptake, in the presence or absence of HSS by confocal microscopy. We also determined the cellular responses initiated by opsonophagocytosis of *Tp* using targeted transcriptional array analysis and cytokine bead array.

**Results** IFN $\gamma$  polarisation of macrophages led to an increase in Fc $\gamma$  receptors (Fc $\gamma$ R) expression, phagocytosis of HSS opsonized *Tp* and cytokine production. Blockade of CD64 significantly diminished spirochetal uptake and pro-inflammatory cytokine secretion by the macrophages.

**Conclusion** Our *ex vivo* studies provide a potential role for macrophages in clearance of *Tp* during human syphilis. These data are the first to demonstrate that CD64 in the primary FcR involved in opsonophagocytosis of *Tp* and IFN $\gamma$  plays a critical role in the macrophages responsiveness following uptake of the spirochete. Moreover, our study results also provide an *ex vivo* surrogate system for use in future syphilis vaccine studies.

### LB1.65 FREQUENCY OF BROADLY NEUTRALISING ANTIBODIES IN HIV-1 CHRONICALLY INFECTED INDIVIDUALS IN UGANDAN CLADES A & D

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**Introduction** The study was aimed at assessing frequencies of neutralising antibodies in individuals affected with the commonest HIV-1 clades A and D in Uganda.

**Methods** This was a cross-sectional study of 83 HIV-1 chronically infected Anti-Retroviral Therapy (ART) naïve adults who were enrolled from Medical Research Council (MRC) cohort and The AIDS Support Organisation (TASO) Clinic in Entebbe. Samples of Plasma were tested for the

neutralisation activity against a panel of 3 clade A and D viruses using the Neutralisation Assays. Neutralisation assays were performed using Env pseudovirus viruses in the TZM-bl cell-based assay. Neutralisation values were obtained as the plasma dilutions at which virus entry was inhibited by 50% compared to that in the absence of plasma (IC<sub>50</sub>). A plasma sample was scored as displaying neutralising activity against a particular virus if at least 50% inhibition of infection was recorded at the lowest plasma dilution tested (1: 20) in at least two independent neutralisation assays.

**Results** Clade A viruses are better neutralised compared to clade D viruses. Individuals whose titers were above 1080 (labelled red required further sample dilution. 51.81% of the participants had their antibody neutralisation titers above 40. There was a significant difference between the proportion of clade A viruses neutralised and those of clade D as obtained statistically using the Mann-Whitney test with a p-value <0.0001. The neutralisation titers obtained for the individual clade A viruses Q23.17, Q769.d22 and Q842.d12 were much higher than those for clade D viruses QA013.H1, Q857.B3 and QD435.5B.

**Conclusion** Generally, the frequency of neutralising antibodies was found to be much higher in Clade A compared to Clade D. This implies that in case of a vaccine design, emphasis should be put on Clade D subtype since it's harder to neutralise naturally.

LB1.66

#### DETECTION OF ZIKA VIRUS AND CYTOMEGALOVIRUS IN CERVICAL CYTOLOGY SAMPLES OF PREGNANT WOMEN FROM GUAYAQUIL, ECUADOR, USING TWO REAL-TIME POLYMERASE CHAIN REACTION (RT-PCR) MOLECULAR ASSAYS

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**Introduction** Zika virus (ZIKV) infection during pregnancy has been linked to severe birth defects. Human Citomegalovirus (CMV) has also been related to important congenital problems when present during pregnancy. The epidemiologic situation of the ZIKV epidemic and the prevalence of the CMV in Ecuador is poorly understood. Given the well-documented effects of ZIKV and CMV in pregnancy, we tested for the presence of both ZIKV and CMV in cervical cytology samples of pregnant women. We report the identification of a population of pregnant women with a high incidence of ZIKV infection and CMV infection in the lower reproductive tract.

**Methods** In late 2016, a case control study was performed to determine the incidence of ZIKV infection and CMV infection among low-income, pregnant women at risk for preterm delivery compared to matched controls. Cervical cytology specimens were tested for ZIKV by rRT-PCR using a lab developed, clinically validated assay (ZCD assay) and for CMV using a commercial RT-PCR assay (CMV DiaPro).

**Results** Fifty-nine pregnant women were enrolled. The incidence of ZIKV was 45.7% (27/59) overall: 15/31 (48.3%) in cases and 12/28 (42.8%) in controls. The general incidence of CMV was 37.2% (22/59): 12/31 (38.7) in cases and 10/28 (35.7) in controls. Overall, outcomes for neonates born to

ZIKV-positive and ZIKV-negative mothers were similar. There were no significant differences in the outcomes of neonates born to CMV positive and CMV-negative mothers. However, two neonates were born with microencephaly to case mothers who were ZIKV-positive.

**Conclusion** We report a high incidence of ZIKV infection (45.7%) and CMV infection (37.2) in a distinctive population in Guayaquil, Ecuador. We identify ZIKV and CMV in cervical samples. These data raise concerns regarding the breadth of the ZIKV epidemic in Ecuador and the importance of CMV infection in pregnant women. Our findings add to the body of evidence of female-male sexual transmission of ZIKV. This data demonstrate the utility of cervical cytology specimens for ZIKV and CMV testing.

LB1.67

#### REDUCED SUSCEPTIBILITY TO CEFTRIAXONE IN *NEISSERIA GONORRHOEAE* IN THE NETHERLANDS RECENTLY PREDOMINANTLY FOUND IN ASSOCIATION WITH AN A501V/T MUTATION IN THE *PEN A* GENE

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**Introduction** *Neisseria gonorrhoeae* (NG) resistance to ceftriaxone interferes with effective treatment of gonorrhoea. Ceftriaxone-resistant NG isolates have not yet been isolated in the Netherlands, but strains with reduced susceptibility to ceftriaxone (CTR-RS) have been cultured.

**Methods** We compared 141 CTR-RS NG strains (MIC  $\geq 0.064$  mg/L) isolated between 2009 and September 2015 with 142 susceptible control strains (MIC <0.032 mg/L), frequency matched for year of isolation and sexual background. NG-MAST, MLVA and *penA* sequencing was performed for all strains. MLVA was also done for 25 additional CTR-RS strains isolated up to September 2016.

**Results** CTR-RS strains originated more frequently from tonsils (23%) in comparison to controls (6%). CTR-RS strains had more often a mosaic *penA* gene (n=63, 45%), an A501V/T mutation (n=65, 46%) or a P551S mutation (n=8, 6%, not including 12 strains with double mutations at A501 and P551). These characteristics were found in only 6 (4%), 6 (4%) and 0 controls, respectively. Using MLVA, CTR-RS strains were more frequently found in clusters than controls (60% vs 23%). Eleven clusters were identified, of which 3 only and 5 mainly included CTR-RS strains. Three clusters consisted of controls only. Of the 3 largest CTR-RS clusters, 2 consisted of strains with a mosaic *penA* gene (almost all isolated before 2013), and 1 of strains with an A501T mutation (often isolated since 2013). Predominant NG-MAST genogroups among CTR-RS strains were G1407 (n=47, 37%) and G2400 (n=37, 27%). Of the 25 CTR-RS strains isolated after September 2015, only 1 clustered with mosaic *penA* strains, 14 grouped in other clusters, including 3, which clustered with previously isolated controls. Ten strains did not cluster.

**Conclusion** CTR-RS strains isolated before 2013 mainly contained the *penA* mosaic gene. More recently, a A501V/T mutation is often found. CTR-RS strains can appear in clusters of susceptible strains, illustrating that genetic antimicrobial resistance development can occur independently of divergence of the background genome.