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 (IC50). 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 PENA 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 ≥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.