

Methods TV positive samples (by NAAT) were collected from two Public Health Laboratories in the Netherlands, from 2012 to 2016. TV was typed using multi-locus sequence typing (MLST) of 7 household genes. MLST profiles were put into a minimum spanning tree together with reference strains and so allocated a genotype. TVV RNA was detected using nested reverse-transcriptase PCR with newly designed primers and visualised on gel.

Results We included 157 clinical samples from 151 clients (most were female; n=133, 87%). In total, 120 samples were genotyped for TV; TV genotype I was most common (n=65; 54%). Over half of these samples were found positive for TVV RNA (n=65; 54%). Most TVV infections were found in TV genotype I (n=49; 75%). The amplified products for TVV1, TVV2 and TVV3 were respectively 97 bp, 290 bp and 156 bp and sequencing showed high identity with TVV genomes; TVV1-C344 (93%), TVV2-OC3 (89%) and TVV3-UR1 (85%), supporting specificity of the primers for these targets. TVV1 was most prevalent (n=45; 41%), followed by TVV3 (n=34; 31%) and finally TVV2 (n=31; 28%). Co-infections occurred in 60% of TVV positive samples. TVV4 was not found at all. Sensitivity for TVV detection still needs to be established using TV samples with a known TVV (genotype) status.

Conclusion TVV detection can be performed directly on clinical samples using nested RT-PCR. TVV infection occurs most frequently in TV type I parasites as in agreement with previous findings. This opens the way for molecular epidemiological studies to gain insight into the role of TVV in TV pathogenicity.

P3.40 SOCIO DEMOGRAPHIC AND SEXUAL BEHAVIOURAL CORRELATES OF HERPES SIMPLEX VIRUS TYPE 2 INFECTION AMONG PREGNANT WOMEN IN SOUTHWESTERN NIGERIA

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Introduction Herpes Simplex Virus type 2 (HSV 2) is the most common cause of genital ulcer disease and facilitates the acquisition of Human Immunodeficiency Virus (HIV). It leads to lifelong latent infection and this raises concerns among women of reproductive age, considering the risk of neonatal transmission. This study aims to determine HSV-2 seroprevalence among pregnant women, identify the correlation with socio-demographic characteristics, sexual behaviour, pregnancy outcomes and co-infection with HIV.

Methods A total of 270 pregnant women attending antenatal clinic of the University College Hospital Ibadan were enrolled in this cross-sectional study. Their serum samples were tested for HSV-2 IgG using type specific third generation ELISA and HIV1, using Uni-Gold Recombigen and ALERE determine. Pretested questionnaire were used to obtain bio-data on socio-demographic characteristics, sexual behaviour and obstetrics history of the participants. Data analyses was done using SPSS version 20.

Results The seroprevalence of HSV 2 type specific IgG was 33.3% (90/270) and a HIV/HSV 2 co-infection rate of 39% (35/90) was observed. Logistic regression analysis showed that polygamy, low educational level, positive HIV status, previous

sexually transmitted infections (STIs), early age at sexual debut and multiple sexual partners were independent risk factors for HSV-2 infection. Obstetrics complications such as intrauterine foetal death, congenital malformations and spontaneous abortion were predictors of HSV-2 infection.

Conclusion The seroprevalence of HSV-2 in this pregnant population is lower than what is observed in some other Sub-Saharan African countries; however, co-infection with HIV is high and majority of the women are still susceptible to primary HSV-2 infection in pregnancy. The demographic, sexual behaviour and bad obstetrics histories found to be predictors of HSV 2 infection in this study may be important in selecting candidates for screening tests, developing strategies towards effective health promotion campaign and reducing risk of HIV transmission.

P3.41 PREVALENCE, SOCIO-DEMOGRAPHIC AND SEXUAL BEHAVIOURAL RISK FACTORS FOR HEPATITIS B VIRUS INFECTION AMONG PREGNANT WOMEN IN SOUTHWESTERN NIGERIA

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Introduction In endemic countries, Hepatitis B virus (HBV) infection occurs mainly during infancy and early childhood, with vertical transmission from an infected mother being a major route of infection. This study aimed at identifying the prevalence and sexual behavioural risk factors for HBV infection among pregnant women in Ibadan, Nigeria.

Methods A cross-sectional study was done at the antenatal clinic of the University College Hospital Ibadan. One hundred and eighty pregnant women were recruited over a six month period, and their serum was tested for Hepatitis B surface antigen (HBsAg) (BIORAD FRANCE) using third generation ELISA and HIV-1 and 2, using Uni-Gold Recombigen and ALERE determine. Positive HBsAg samples were tested for Hepatitis B envelope antigen (HBeAg), antibody (HBeAb) and Hepatitis B core antibody (HBcAb) (DIAPRO Italy) while serum HBV DNA was detected using PCR. Data were obtained using questionnaires and analysed using SPSS-20

Results The seroprevalence of HBsAg was 8.3% out of which 26.7% were positive for HBeAg, 53.3% had HBeAb, 20% had neither HBeAg nor HBeAb, 100% had total HBcAb and 86.7% had HBV DNA in their serum. A co-infection rate (HBV/HIV) of 26.7% was observed. The mean age was 32.1 years, the highest HBV infection rate occurred in 25–29 year age group. Multiple sexual partners (OR= 3.987, P- value=0.026), early age at sexual debut (OR =11.996, P- value=0.022) were independent risk factors for HBV infection.

Conclusion The result of this study brings to light the high prevalence and high infectivity rate of chronic HBV virus infection among women of child bearing age in Nigeria. Thus, there is a dire need for routine screening for all pregnant women during antenatal care, immunoprophylaxis for exposed newborns and surveillance for those with chronic infection. The socio-demographic and risky sexual behavioural characteristics found to be predictors of HBV infection should be considered when developing strategies towards effective sexual