

HPV ( $p=0.001$ ). Factors that were independently associated with having anal HR-HPV infection included having sex with men only, ever engaging in group sex, living with HIV and practising receptive anal intercourse.

**Conclusion** HR-HPV infections in the anal canal were common among MSM in Cape Town with the highest HR-HPV burden among HIV co-infected MSM, men who have sex with men only and those that practised receptive anal intercourse. Behavioural intervention strategies and targeted HPV vaccination of young MSM are urgently required to address the high prevalence of oncogenic HPV and HIV co-infections among MSM in South Africa.

### P3.73 IDENTIFICATION OF *MYCOPLASMA GENITALIUM* GENOTYPES IN CLINICAL SAMPLES FROM ARGENTINA

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**Introduction:** *Mycoplasma genitalium* (Mg) is a sexually transmitted pathogen associated with non-gonococcal urethritis, cervicitis, pelvic inflammatory disease and infertility. Since Mg is very difficult to culture from clinical samples, typing strains relies on the variability of a 281pb fragment of the *mgpB* gene, encoding the adhesin MgPa. Here we present the analysis of the sequences of 14 Mg strains detected from clinical samples between 2013 and 2016.

**Methods** This was a retrospective study in which we analysed all the Mg positive samples diagnosed in our laboratory in the period 2013–2016. Detection of Mg was performed by in-house PCR assay using primers previously described; the resulting 281pb fragments from Mg positive specimens were sequenced by Sanger method. Sequences were analysed and compared with all currently available clinical sequences.

**Results** A total of 452 genital samples were tested, from which 17 resulted positive for Mg. Of these, only 14 could be successfully sequenced. The analysis of sequenced samples revealed eight different types of sequences. When compared with published data, four sequence types (representing a total of 10 different strains) resulted identical to previously reported genotypes. The relative frequencies of these genotypes were: 29% genotype 1 (4/14), 29% genotype 2 (4/14), 7% genotype 4 (1/14), and 7% genotype 21 (1/14, 7%). The remaining sequences showed between one and four nucleotide differences compared to already existing variants; in three of them this resulted in amino acid changes.

**Conclusion** This is the first study to characterise the molecular types of Mg among clinical strains in our country. Through comparative sequence analysis, eight different *mgpB* region variants were identified, four of which have not been reported in the past. This reveals the presence of new sequence variants in Argentina. Further studies are needed to evaluate the association between these sequence variants and clinical/epidemiological data that could help us to understand the dynamics of Mg infection in the region.

### P3.74 ANTIMICROBIAL SUSCEPTIBILITY PROFILES OF SPECIES OF *UREAPLASMA PARVUM* AND *UREAPLASMA UREALYTICUM* ISOLATED IN BUENOS AIRES, ARGENTINA

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**Introduction:** *Ureaplasma parvum* (Up) and *Ureaplasma urealyticum* (Uu) are small cell wall-lacking bacteria that colonise humans, but can cause disease among pregnant women, neonates, sexually active individuals and immunocompromised. They are naturally resistant to several antibiotics, and treatment relies in fluoroquinolones, tetracyclines, macrolides and chloramphenicol. Acquired resistance has been described in other countries, but data on the antimicrobial susceptibility in Argentina are lacking. We aimed to describe the antimicrobial susceptibility profiles of Up/Uu isolates recovered from clinical samples between 2004 and 2016 in Buenos Aires, Argentina.

**Methods** A total of 89 isolates from clinical samples originally submitted to the STI National Reference Laboratory for diagnosis between 2004 and 2016 were examined. Isolates were grown in conventional culture mediums (broth and agar) and species confirmed by PCR. Antimicrobial susceptibility tests were done by broth microdilution method following CLSI.

**Results** Of the 89 isolates analysed, two showed resistance to levofloxacin (MIC 4 ug/ml) and one was resistant to tetracycline (MIC 4 ug/ml), giving a prevalence of resistance of 2.2% (CI 0.6%–7.8%) and 1.1% (CI 0.2%–6.1%), respectively. All isolates were susceptible to erythromycin and azithromycin. MIC<sub>50</sub>, MIC<sub>90</sub> and MIC ranges were 1, 2, 0.25–4 for levofloxacin; 0.5, 1, 0.06–4 for tetracycline; 2, 4, 0.25–4 for erythromycin; and 2, 4, 0.25–8 for azithromycin. Levofloxacin and tetracycline MIC values were higher for Uu (n=18, 20%) than for Up (n=71, 80%), but no differences were observed among macrolides. No MICs differences were observed between 2004–2009 strains (n=49, 55%) and 2010–2016 (n=40, 45%) isolates. Finally, no coresistant strains were identified.

**Conclusion** To our knowledge, this is the first study analysing the susceptibility patterns of species of ureaplasma in Argentina following CLSI recommendations. We found low resistance rates to levofloxacin and tetracycline, and no resistance to macrolides, but continue surveillance is needed to detect the emergence of resistant strains and to characterise the molecular determinants of these findings.

### P3.75 VIRAL SUPPRESSION IN LATE PRESENTING HIV-INFECTED PREGNANT WOMEN

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**Introduction** The maternal HIV viral load (VL) is a major predictor of mother to child transmission (MTCT). Therefore, it is necessary a rapid decrease of VL among late-presenting (LP) (after 28 weeks) pregnant women living with HIV (PWLH) aiming viral suppression (VS). We aimed to identify the

population of LP-PWLH and compare the VS to the group who had earlier access (EA) to prenatal care.

**Methods** A retrospective cohort carried out at the major HIV reference centre in Bahia, Brazil. Medical records of PWLH attended at prenatal care were reviewed from January 2011 to December 2013. HIV VL and TCD4+ count data were obtained from the national database. Statistical analyses were performed with SPSS 20.0.

**Results** A total of 235 PWLH enrolled in the study, of which 29.4% were LP. Among the latter, the mean age was 28.3 ( $\pm 6.9$ ) years, similar to the EA group. Thirty four percent of the LP had <8 schooling years ( $p=0.16$ ), 40.7% were single ( $p=0.64$ ), 24.6% reported alcohol use ( $p=0.15$ ), 1.6% drug use ( $p=0.44$ ) and only 16.7% regular condom use ( $p=0.92$ ). The majority of LP (62.9%) had partners with unknown serological status, 25.7% had seroconcordant and 11.4% had serodiscordant partners ( $p<0.01$ ). LP predominantly had HIV diagnosis during pregnancy (60.9%;  $p<0.01$ ) and were ARV naïve (78.3%;  $p<0.01$ ), while only 14.5% were on ART at conception ( $p<0.01$ ). As for the initial ART regimen during pregnancy, 89.9% of LP were using a protease inhibitor based regimen and 11.6% had had regimen changes during pregnancy ( $p=0.36$ ). LP had a higher initial VL ( $\log_{10}$  3.4;  $p<0.01$ ) and those with recent diagnosis also had higher VL ( $\log_{10}$  3.8;  $p=0.02$ ). LP were more likely to not have a second VL during pregnancy or early peripartum (33.3%;  $p<0.01$ ). VS was less achieved (34.8% vs 71.8%;  $p<0.01$ ; OR 4.7, CI95% 2.36–9.66) by the LP group.

**Conclusion** LP showed an increased risk of MTCT, with recent HIV diagnosis, higher VL at prenatal onset and a lower rate of VS. Thus, the use of integrase inhibitors would be a better choice for this population, since it promotes a quickly decrease of VL.

P3.76

#### HTLV-1/2 SEROLOGY IN THE TESTS BATTERY FOR FOLLOWING UP PATIENTS WITH VIRAL HEPATITIS IN BRAZIL

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**Introduction** Brazil is endemic for HIV-1, HTLV-1 and HTLV-2, these retrovirus share routes of transmission with HCV and HBV, thus coinfections can occur. Several studies tried to evaluate the impact of human retroviruses on the course of HCV infection, and association of HTLV-1 with spontaneous clearance of HCV, mostly in HIV coinfecting patients, and less hepatic injury were detected. In contrast, an increase in HCV viral load in HIV and/or HTLV-2 coinfecting individuals was described. Concerning HBV infection, one study showed higher rate of HBV antigenemia in HIV/HTLV-1 coinfecting patients. Thus, searches for HTLV infections in HCV and HBV infected patients have prognostic value.

**Methods** Plasma samples from 1244 individuals sent to Instituto Adolfo Lutz for measuring HCV and HBV viral load: 622 HCV+ (G1=343 male, 279 female), and 622 HBV+ (G2=327 male, 295 female) were evaluated for HTLV-1/2 infection by enzyme immunoassay (EIA, HTLV-I/II, Gold ELISA, REM), and confirmed by line immunoassay (INNO-LIA HTLV-I/II, Fujirebio). HIV infection was detected by

immunochromatographic assay (Rapid Check HIV 1+2, UFES).

**Results** On screening test 44 plasma samples reacted, and HTLV-1 was confirmed in 25 samples [20(G1), 5(G2)]. HTLV-2 was detected in 16 samples [13(G1), 3(G2)]. Two samples were indeterminate, and one negative (G2). The overall prevalence of HTLV in HCV+ was 5.3% (3.2% HTLV-1% and 2.1% HTLV-2), and HBV +1.3% (0.8% HTLV-1% and 0.5% HTLV-2). No difference in the median age of patients was detected between HCV-infected and HCV/HTLV coinfecting (50.7 vs. 50.6 years), also in HBV and HTLV/HBV coinfecting (45.8 vs. 53.5 years). In HCV/HTLV coinfecting patients 30.3% were HIV+, while in HBV/HTLV coinfecting patients, all except one were HIV+.

**Conclusion** The results emphasise the need for searching HTLV infections mostly in patients with HCV. Thus, we suggest to include the serology for HTLV in the tests battery for following up the hepatitis virus infected patients in Brazil, regardless of your HIV status.

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P3.77

#### MOTHER-TO-CHILD TRANSMISSION OF HIV IN SOUTHERN SANTA CATARINA, BETWEEN 2005 AND 2015: ASSESSMENT OF SEROCONVERSION

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**Introduction** In Brazil, 92,210 HIV-infected pregnant women were notified from 2000 through June 2015, most of whom living in the Southeast (40.5%) and South (30.8%). Detection rates of pregnant women living with HIV in Brazil have increased in the last ten years. In 2005, rates of seropositivity for newborns were as high as 2.0 cases per 1000 live births, which increased to 2.6 in 2014, indicating a 30.0% rise. The aim of this study was to analyse the frequency of seroconversion among newborns to HIV-positive mothers living in southern Santa Catarina, Brazil, from 2005 through 2015.

**Methods** A cross-sectional study was conducted to collect secondary data. All the newborns that were exposed to HIV by vertical transmission, and attended the municipal healthcare centre between 2005–2015 participated in the study. The study included all infants between 0 and 18 months of age, exposed to HIV vertically, who attended the healthcare centre that serves 18 municipalities in southern Santa Catarina, Brazil, over the 2005–2015 period.

**Results** During the study period, there were 93 exposures to HIV, of which 3 (3.2%) seroconversions were confirmed and 2 (2.1%) died of AIDS during the follow-up period. Seroconversion was associated with breastfeeding (PR=29.3; 95% CI=9.6–89.2;  $p=0.002$ ) and the lack of antiretroviral therapy during pregnancy (PR=21.0; 95% CI=2.4–184.5;  $p=0.006$ ).

**Conclusion** The results from this study allowed us to conclude that seroconversion among newborns was 5.4%, resulting in a rate of 3.4 cases per 1000 live births, which was higher than the national average. Seroconversion was associated with