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 report 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_{50}, MIC_{90} and MICranges 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