

main age group was 20–24 with speed=106 cases/year, ($p=0.045$).

Conclusion There was a decreasing trend of AIDS cases and growth in HIV+, with expressive speed among young MSM. This analysis points to the need for discussions of unprotected sexual practices, combined prevention and other actions aimed to controlling the epidemic in greater vulnerability groups.

P3.152 PREVALENCE OF BACTERIAL VAGINOSIS INFECTION AND ASSOCIATED FACTORS IN WOMEN WHO HAVE SEX WITH WOMEN

MTC Duarte, MAO Ignacio, J Andrade, APF Freitas, MG Silva. *São Paulo State University, Brazil*

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Introduction The present research aims to fill a gap in the national and international literature concerning prevalences and factors related to Bacterial vaginosis (VB) in Women who Have Sex with Women (WSW).

Methods It is a cross sectional, analytical and non-randomized study with 128 WSW from Botucatu - SP and surrounding regions who answered the call from social media, mass communication means, health services and friends or acquaintances from January to November, 2015. Data was obtained by the researchers involved in the main study, through interviews and gynaecological exam. The diagnostic of VB was obtained through gram staining. Associations were estimated by multiple regression.

Results The prevalence of BV was 41.1% and factors associated were vaginal douching [OR=3.29 (IC:95%: 1.26–8.59) $p=0.014$] and sex toys use [OR=2.34 (IC:95%: 1.00–5.50); $p=0.049$].

Conclusion Considered as whole, these data lead to conclusion that the individuals of this study presented high vulnerability to STI/AIDS, as shown by the high prevalence of VB. This study clearly shows the need for a specific health assistance to these women, promoting prevention and education in a holistic approach.

P3.153 SPATIAL AND TEMPORAL ASSOCIATIONS BETWEEN CONGENITAL SYPHILIS CASES AND EPIDEMIOLOGICAL CHARACTERISTICS OF INFECTIOUS SYPHILIS IN ENGLAND

Martina Furegato, Helen Fifer, Hamish Mohammed, Ian Simms, Louise Logan, Noel Gill, Andre Charlett, Gwenda Hughes. *Public Health England, London, UK*

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Introduction There has been a rapid rise in infectious syphilis (IS) diagnoses in England since 2011 but congenital syphilis (CS) is rare. In 2016, 3 CS cases were diagnosed in geographically dispersed areas of England. Unusually, their mothers had tested negative at first trimester antenatal screen (screen-negative), indicating syphilis acquisition during pregnancy. Simulation modelling using historical CS cases indicated an event probability of 3%. We investigated the spatial and temporal relationship between screen-negative CS cases and IS epidemiology in the affected areas.

Methods Data from 01/2011–06/2016 were obtained from GUMCADv2, the national electronic surveillance system.

England was divided into 3 syphilis epidemiological areas (SEAs): wider incident areas (WIAs; the 3 affected and immediate surrounding counties); endemic areas (with established epidemics in men who have sex with men-MSM) and non-incident non-endemic areas (NINEAs). Time-series analysis (TSA) was used to estimate IS outliers by gender, sexual orientation and SEA. Associations between IS characteristics and SEA (WIAs vs. NINEAs) were assessed using Pearson's chi-square and Kruskal-Wallis tests. Mothers of CS cases were excluded from analyses.

Results In 2011–2016, IS rates/100,000 in WIAs rose in heterosexual women (1.3–3.0) and MSM (8.9–13.9) but fell in heterosexual men (3.7–3.0). In NINEAs, rates rose in heterosexual women (1.6–1.9), MSM (5.0–10.8) and heterosexual men (2.7–3.2). On TSA, IS cases significantly exceeded expected bounds in 2016 in heterosexual women in WIAs; no exceedance was seen in NINEAs. In 2016, heterosexual women with IS were more likely to be UK-born in WIAs than in NINEAs (78% vs. 39%; $p<0.001$). A greater proportion of MSM were bisexual in WIAs than in NINEAs (11% vs. 8%; $p<0.001$).

Conclusion Increased syphilis transmission in some sexual networks of MSM and a higher proportion of bisexual men in WIAs may have created more opportunities for IS acquisition in women. Efforts to raise awareness of the potential risk of acquiring syphilis during pregnancy are needed.

P3.154 CLONAL SPREAD OF AZITHROMYCIN RESISTANT NEISSERIA GONORRHOAE IN CANADA (2014–2015)

¹I Artin, ¹P Sawatzky, ²B Lefebvre, ³V Allen, ⁴P Naidu, ⁵L Hoang, ⁶G Horsman, ¹MR Mulvey. ¹Public Health Agency of Canada, Winnipeg, Canada; ²Laboratoire De Santé Publique Du Québec, Ste-Anne-De-Bellevue, Canada; ³Public Health Ontario, Toronto, Canada; ⁴Alberta Health Services, Edmonton, Canada; ⁵British Columbia Centres For Disease Control, Vancouver, Canada; ⁶Saskatchewan Disease Control Laboratory, Regina, Canada

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Introduction *Neisseria gonorrhoeae* have acquired resistance to many antimicrobials including third generation cephalosporins and azithromycin, which are the current co-therapy recommended by the Canadian STI guidelines for gonorrhoea treatment. Minimum inhibitory concentrations (MIC) to azithromycin and molecular sequence types were determined for *N. gonorrhoeae* circulating in Canada.

Methods Between 2014 and 2015, *N. gonorrhoeae* strains isolated by Canadian provincial public health laboratories were submitted to the National Microbiology Laboratory (NML) ($n=4,720$) for azithromycin MIC determination (resistance MIC ≥ 2.0 mg/L) by agar dilution. *N. gonorrhoeae* multi-antigen sequence typing (NG-MAST) was used for molecular typing.

Results Azithromycin resistance was identified in 3.3% (127/3,809) and 4.7% (198/4,190) of *N. gonorrhoeae* in 2014 and 2015, respectively, a significant increase since 2013 ($p<0.001$). MICs ranged from 2 to 16 mg/L. The most common sequence types identified in 2014 were ST10451 ($n=40$), ST10567 ($n=38$) and ST11765 ($n=10$). ST11765 is closely related to ST10451, differing by 1 bp in the por allele. In 2015, the prevalent sequence types were ST12302 ($n=110$), ST10451 ($n=34$) and ST9047 ($n=23$). ST10451, identified in Quebec, Ontario and Alberta, was newly identified in 2014 and also identified in 2015. ST10451 is related to ST1407 (differing by 1 bp in the por allele) which is an internationally-

recognised epidemic strain, harbouring resistance to cephalosporins. ST12302 was newly recognised in 2015 and identified in two provinces, Quebec and Ontario.

Conclusion *N. gonorrhoeae* isolates in Canada show a significant increase in azithromycin resistance in 2014–2015. Azithromycin resistance in Canadian *N. gonorrhoeae* isolates are approaching the 5% level at which the WHO states an antimicrobial should be reviewed as an appropriate treatment. Continued surveillance of antimicrobial susceptibilities and sequence types of *N. gonorrhoeae* is necessary to identify clusters, inform treatment guidelines and mitigate the impact of resistant gonorrhoea.

P3.155 ASSESSMENT OF *ATOPOBIUM VAGINAE* AND *GARDNERELLA VAGINALIS* CONCENTRATIONS IN A COHORT OF PREGNANT SOUTH AFRICAN WOMEN

¹Mathys J Redelinghuys, ¹Marthie M Ehlers, ¹Janine E Bezuidenhout, ¹Piet J Becker, ²Marleen Kock. ¹University of Pretoria, Pretoria, South African Republic; ²University of Pretoria/National Health Laboratory Service, Pretoria, South African Republic

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Introduction: *Atopobium vaginae* and *Gardnerella vaginalis* are bacterial species that are present in the vagina in increased concentrations during bacterial vaginosis (BV). Numerous studies have proposed a molecular diagnosis of BV by targeting several BV-related bacteria in a polymerase chain reaction (PCR); however, these studies evaluated separately the threshold concentrations of these bacteria. The purpose of this cross-sectional study was to assess *A. vaginae* and *G. vaginalis* concentrations in pregnant women of different age groups, gestational age groups, vaginal flora categories and HIV status and also to determine which combination of DNA threshold concentrations, rather than individually, best discriminated between bacterial vaginosis (BV) and non-BV categories.

Methods Pregnant women attending an antenatal clinic of a tertiary academic hospital in Pretoria, Gauteng, South Africa were enrolled in a cross-sectional study from July 2012 to December 2012. Self-collected vaginal swabs were obtained to detect BV with the Nugent scoring system and quantify *A. vaginae* and *G. vaginalis* DNA with a duplex quantitative real-time polymerase chain reaction (PCR) assay.

Results In 220 pregnant women, median concentrations of *A. vaginae* and *G. vaginalis* were not significantly different among various age groups (*A. vaginae* $p=0.98$ and *G. vaginalis* $p=0.18$) or different trimesters (*A. vaginae* $p=0.31$ and *G. vaginalis* $p=0.19$) but differed significantly among the vaginal flora categories (*A. vaginae* $p<0.001$ and *G. vaginalis* $p<0.001$) and HIV status (*A. vaginae* $p<0.001$ and *G. vaginalis* $p=0.004$). An *A. vaginae* DNA concentration of $\geq 10^7$ copies/mL together with a positive *G. vaginalis* result ($\geq 10^6$ copies/mL) (i.e. AV₇GV₀) best discriminated between BV (39/220) and non-BV categories (181/220) with a sensitivity of 85% (95% CI 0.70 to 0.94) and a specificity of 82% (95% CI 0.76 to 0.88).

Conclusion Threshold concentrations for BV detection should be established for specific populations to ensure the development of tailored, sensitive molecular assays.

P3.156 CORRELATION OF THE EXPRESSION OF THE P16INK4A PROTEIN AND HPV DNA IN INDIVIDUALS WITH PENILE CANCER IN THE STATE OF GOIAS, BRAZIL

¹Megmar AS Carneiro, ²LA De Araújo, ³HSCP De Paula, ⁴VA Saddi, ⁵SA Teles, ⁶SH Rabelo-Santos, ³AAP De Paula. ¹Institute of Tropical Pathology and Public Health/Federal University of Goiás, Goiânia, Brazil; ²Institute of Tropical Pathology and Public Health/Federal University of Goiás, Goiânia, Brazil; ³Hospital Araújo Jorge, Goiânia, Goiás, Brazil; ⁴Pontifical Catholic University of Goiás, Goiânia, Goiás, Brazil; ⁵Federal University of Goiás, Goiânia – GO, Brazil; ⁶Federal University of Goiás, Goiânia – GO, Brazil

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Introduction Penile carcinoma (PC) is a rare disease, however it is still considered a serious public health problem. The expression of p16INK4a, a protein associated with tumour suppression, can be used as a marker for the presence of high risk HPV DNA. The upregulation of this protein is understood to be an attempt to stop uncontrolled cellular proliferation in response to HPV infection.

Objectives The goal of this study was to estimate the prevalence of HPV DNA and evaluate the expression and correlation of p16INK4a with HPV DNA in patients with PC in Goiás, Brazil. **Methods:** this retrospective cohort study involved 190 patients with PC treated in the UroOncology service of Hospital Araújo Jorge (HAJ), a unit of the Association Against Cancer in Goiás (ACCG), from January 2003 to November 2015. The paraffin blocks containing the cancerous tissue fragments were subjected to extraction of viral DNA, subsequently subjected to polymerase chain reaction testing with short PCR fragment (SPF PCR) primers to detect HPV DNA. The marking of the p16INK4a protein was performed with immunohistochemistry, using a commercial kit (Mach 4 Universal HRPPolymer Detection System – Biocare Medical, CA, USA). The slides were evaluated independently by two pathologists.

Results Of the 190 samples tested, 89 (46.8%) (CI 95%: 39.8%–53.9%) showed positive HPV DNA and 98 (51.7.0%) (CI 95%: 33.2 to 53.2) showed expression of p16INK4a. The correlation between the presence of HPV DNA and p16INK4a was 63.6% (CI 95%: 46.3 to 78.6). Although there is no expression of p16INK4a in 100% of cases positive for HPV DNA, there was statistical significance between the presence of viral DNA and expression of p16INK4a ($p<0.003$).

Conclusion Some studies suggest that the standard knowledge of the expression of the p16INK4a protein may be a useful marker for HPV activity in patients with penile cancer. The results of this study showed that there are significant differences between the expression of this protein in positive and negative HPV DNA samples.

P3.157 DOES THE EUROPEAN GONOCOCCAL ANTIMICROBIAL SURVEILLANCE PROGRAMME (EURO-GASP) ACCURATELY REFLECT THE TRUE ANTIMICROBIAL RESISTANCE SITUATION IN EUROPE?

¹Michelle Cole, ²Gianfranco Spiteri, ²Chantal Quinten, ¹Neil Woodford, ³Magnus Unemo, ⁴Euro-Gasp Network. ¹National Infection Service, London, UK; ²European Centre of Disease Prevention And Control, Stockholm – Sweden; ³Örebro University Hospital, Örebro – Sweden; ⁴European Centre of Disease Prevention, Stockholm – Sweden

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