

**Results** Fifty-two participants with a median age of 18 (range 12–23) years participated in the study with 53.8% being female. Utilising a pill count to assess adherence, 45 (86.5%) participants had a greater than 95% adherence to their PI regimen. However using the MEMS cap only, 4 (7.7%) participants had a greater than 95% adherence. Twenty-three of the 52 participants had a viral load greater than 50 (median = 21,228 cells/ml; range = 52–1,884,215) with a median adherence level of 100% (range = 93–100%) as determined by a pill count and a median adherence level of 41% (range = 3–100%) as determined by the MEMS cap.

**Conclusion** Pill counts and self-reported adherence overestimated adherence in adolescent patients on PIs as part of an anti-retroviral regimen. Pill dumping phenomenon was observed in participants with high viral loads and greater than 95% adherence when assessed by pill count.

**Disclosure of interest statement** The authors have no conflict of interests to declare.

#### 004.5 THE INFLUENCE OF SEXUAL DEBUT ON SELECTED VAGINAL, RECTAL AND ORAL MICROBIOTA AND VAGINAL INFLAMMATORY MARKERS IN BELGIAN ADOLESCENT GIRLS: A COHORT STUDY

<sup>1</sup>V Jespers\*, <sup>2</sup>L Hardy, <sup>1</sup>A Buvé, <sup>1</sup>J Loos, <sup>3</sup>A Tsoumaris, <sup>3</sup>J Buyze, <sup>2</sup>T Crucitti. <sup>1</sup>Unit of Epidemiology and Control of HIV/STD, Department of Public Health, Institute of Tropical Medicine, Antwerp, Belgium; <sup>2</sup>HIV/STI Reference Laboratory, Department of Clinical Sciences, Institute of Tropical Medicine, Antwerp, Belgium; <sup>3</sup>Clinical Trials Unit, Department of Clinical Sciences, Institute of Tropical Medicine, Antwerp, Belgium

10.1136/sextrans-2015-052270.101

**Introduction** Little research has been done on the composition of the vaginal microbiota and vaginal inflammatory markers in adolescent girls and how these are affected by initiation of sexual activity.

**Methods** We conducted a cohort study for which we recruited adolescent girls at 4 sary schools in Antwerp. Three times over a period of 8 months, participants completed an electronic questionnaire and self-collected vaginal, rectal and oral swabs. Five vaginal *Lactobacillus* species, *G. vaginalis*, and *A. vaginae* employing qPCR; eight inflammatory markers by Luminex; and BV by Nugent score 7–10 were measured in the vaginal specimens. In the oral and rectal specimens, measurements were limited to *Lactobacillus* genus, *G. vaginalis*, and *A. vaginae*. The association of sexual activity (none, penetrative sexual intercourse and non-penetrative activity) with the vaginal, oral and rectal microbiota, BV and vaginal inflammatory markers was assessed by bivariate analysis.

**Results** Of the 93 adolescents (14–20 years), 53 (57%) were virgins, 35 (37.6%) had had penetrative sexual intercourse and 5 (5.4%) had engaged in non-penetrative activity. Cross-sectional, sexual activity was associated with an increased presence of vaginal *G. vaginalis* ( $p = 0.016$ ), rectal *G. vaginalis* ( $p = 0.027$ ), and rectal *A. vaginae* ( $p = 0.010$ ); with higher IL-1 $\alpha$  ( $p < 0.001$ ), IL-8 ( $p = 0.002$ ) and MIP-1 $\beta$  ( $p = 0.030$ ); and with BV ( $p = 0.009$ ). During follow-up, 9 (9.7%) participants had penetrative sexual intercourse for the first time. At individual level this was associated with a higher IL-1 $\alpha$  (+0.37 log;  $p = 0.010$ ) compared to girls who remained virgin over the three visits. Similarly, in girls who reported sexual intercourse IL-1 $\alpha$  and IL-8

was higher (+0.39 log;  $p < 0.0001$ ; +0.43 log;  $p = 0.003$ ) compared to the virgins.

**Conclusion** Sexual debut is associated with the presence of BV related species and the inflammatory status of the vaginal milieu. Consequently, around this period in life adolescent girls have increased vulnerability to HIV and other sexually transmitted infections.

**Disclosure of interest statement** This work was supported by the European Commission on the grand Combined Highly Active Anti-Retroviral Microbicides (CHAARM) N° 242135. No pharmaceutical grants were received in the development of this study.

#### 004.6 HIGH PREVALENCE OF BACTERIAL VAGINOSIS AMONG ADOLESCENT GIRLS ATTENDING SECONDARY SCHOOL IN TANZANIA

<sup>1</sup>SC Francis\*, <sup>1,2</sup>C Hansen, <sup>2</sup>J Irani, <sup>1,2</sup>A Andreasen, <sup>3</sup>V Jespers, <sup>4</sup>S Nnko, <sup>3</sup>T Crucitti, <sup>4</sup>C Chungalucha, <sup>1,2</sup>D Watson-Jones, <sup>3</sup>A Buve. <sup>1</sup>London School of Hygiene and Tropical Medicine; <sup>2</sup>Mwanza Intervention Trials Unit/National Institute of Medical Research; <sup>3</sup>Institute of Tropical Medicine; <sup>4</sup>National Institute of Medical Research

10.1136/sextrans-2015-052270.102

**Introduction** Prevalence and incidence of HIV infection and other sexually transmitted infections (STI) are particularly high among adolescent girls in sub-Saharan Africa. One area in need of further research is the role played by the vaginal microbiota in the susceptibility to HIV and other STI in adolescent girls. The aim of this study was to characterise the vaginal microbiota of adolescent girls in Tanzania around the time of their sexual debut.

**Methods** Girls attending secondary schools in Mwanza City, ages 17 and 18 years old, were invited to join a cross-sectional study. After informed consent/assent, girls were interviewed and nurse-assisted, self-collected swabs were obtained for STI and BV testing. BV was considered as a binary outcome: Nugent scores 7–10 were considered BV positive. Factors associated with prevalent BV were analysed using multivariable logistic regression.

**Results** Of the 403 girls who enrolled in the study, 176 (44%) reported having had sexual intercourse and 8 (2%) reported receiving cunnilingus. Ninety-five (25%) girls had BV, 9 (2%) were infected with *Chlamydia trachomatis*, 8 (2%) had *Neisseria gonorrhoea*, 18 (5%) had *Trichomonas vaginalis*, 85 (21%) had Human papilloma virus and 6 (2%) *Mycoplasma genitalium*. Six (2%) girls were infected with HSV-2. Among girls who were sexually naïve, 19% had BV compared to 32% in sexually active girls. BV was independently associated with sexual debut (aOR = 2.11; 95% CI: 1.32,3.39); oral sex (aOR = 7.94; 95% CI: 1.53,40.3); >1 sex partner (aOR = 2.55; 95% CI: 1.21,5.39); and HPV (aOR = 1.73; 95% CI: 1.02,2.94).

**Conclusion** In this study among girls attending secondary school in Mwanza, Tanzania, sexual debut was associated with BV; however, 19% of girls who were sexually naïve had BV. This suggests that sexual intercourse may not be a prerequisite for BV. Oral sex was also associated with BV although the reported prevalence of this sexual behaviour was low.

**Disclosure of interest statement** The authors do not have a conflict of interest. No pharmaceutical grants were received in the development of this study.

## 005 - Detecting antimicrobial resistance and treatment failure

### 005.1 REAL-TIME PCR AND MELT CURVE ANALYSIS TARGETING GYRA GENE FOR PREDICTION OF CIPROFLOXACIN RESISTANCE IN CLINICAL *NEISSERIA GONORRHOEAE* ISOLATES

<sup>1</sup>P Hemarajata\*, <sup>1</sup>S Yang, <sup>2</sup>OO Soge, <sup>1</sup>RM Humphries, <sup>3</sup>JD Klausner. <sup>1</sup>Department of Pathology and Laboratory Medicine, David Geffen School of Medicine, UCLA, USA; <sup>2</sup>Neisseria Reference Laboratory, GISP Regional Laboratory, University of Washington Harborview Medical Center, USA; <sup>3</sup>Division of Infectious Diseases, Center for World Health and Department of Epidemiology, David Geffen School of Medicine and Fielding School of Public Health, UCLA, USA

10.1136/sextrans-2015-052270.103

**Introduction** Increasing antimicrobial resistance in *Neisseria gonorrhoeae* has been a major problem worldwide, limiting effective empirical therapeutic options in patients infected with multi-drug resistant strains. Guidelines from U.S. CDC no longer recommend treatment with fluoroquinolones (FQs) due to emergence of resistance nationally. However, current prevalence of resistance in the US is still low at 12% and treatment with FQs may be a viable option for susceptible isolates. A rapid molecular test predicting FQ susceptibility in *N. gonorrhoeae* isolates would help physicians in determining an effective treatment plan for each patient.

**Methods** Twenty-three ciprofloxacin (CIP)-susceptible and 77 CIP-resistant clinical *N. gonorrhoeae* isolates were obtained from Neisseria Reference Laboratory at University of Washington and grown on chocolate agar plates. To determine the association between mutations in *gyrA* gene and CIP resistance in those isolates, we extracted DNA from culture and performed real-time PCR on a Lightcycler 480 based on the HybProbe system targeting *gyrA* gene followed by melt curve genotyping.

**Results** Melt curve genotyping analysis demonstrated wild-type melt patterns in all (100%) 23 CIP-susceptible isolates, while all 77 (100%) CIP-resistant isolates demonstrated mutant melt patterns.

**Conclusion** There was a 100% concordance between PCR melt genotypes and CIP susceptibility among all clinical isolates tested. The assay is currently being validated for testing on DNA extracted directly from clinical specimens ultimately to be offered for use in clinical practice.

**Disclosure of interest statement** This study was funded in part by NIH R21AI109005.

### 005.2 DIAGNOSTIC AND CLINICAL IMPLICATIONS OF GENOTYPIC FLUOROQUINOLONE SUSCEPTIBILITY DETECTION FOR *NEISSERIA GONORRHOEAE*

<sup>1</sup>MJ Pond\*, <sup>1</sup>C Hall, <sup>2</sup>M Cole, <sup>1</sup>KG Laing, <sup>1</sup>V Miari, <sup>1</sup>H Jagatia, <sup>3</sup>E Harding-Esch, <sup>1,2</sup>I Monahan, <sup>1,4</sup>T Planche, <sup>1</sup>J Hinds, <sup>2</sup>C Ison, <sup>2</sup>S Chisholm, <sup>1</sup>PD Butcher, <sup>1,5</sup>ST Sadiq. <sup>1</sup>Institute for Infection and Immunity, St George's University of London, London, UK; <sup>2</sup>Sexually Transmitted Bacteria Reference Laboratory, Public Health England, London, UK; <sup>3</sup>HIV/STI Department, Public Health England, London, UK; <sup>4</sup>Department of Medical Microbiology, St George's University Hospitals NHS Foundation Trust, London, UK; <sup>5</sup>Department of Genitourinary & HIV Medicine, St George's University Hospitals NHS Foundation Trust, London, UK

10.1136/sextrans-2015-052270.104

**Introduction** Antibiotic resistance poses major challenges to empirical treatment of *Neisseria gonorrhoeae* (NG), potentially addressable if antimicrobial susceptibility point of care (POC) tests were available. The performance of a POC compatible real-time PCR assay (GCSNP), enabling detection of fluoroquinolone susceptible NG directly on clinical samples from multiple anatomical sites and on diverse circulating strains, was evaluated.

**Methods** Residual routine nucleic acid amplification test samples, derived from patients who were also culture positive for NG at the same clinical attendance were GCSNP tested. Assay performance was further verified using a phenotypically characterised fluoroquinolone resistant and susceptible strain panel which was sequence-typed using NG-MAST (NG Multi Antigen Sequence Typing).

**Results** 290 residual samples derived from 222 clinical episodes (56 female; 166 male) were tested by GCSNP, yielding result in 90% (n = 262/290), with assay failure more likely in non-genital compared to genital samples (16.4% vs. 5.2%, p = 0.002). 29.7% (n = 66/222) of NG cases were attributable to fluoroquinolone resistant strains in at least one anatomical site. GCSNP predictive values for fluoroquinolone susceptibility were 100% (95% CI: 95.9–100%) and 100% (82.8–100%), respectively for urogenital (n = 173) and rectal samples (n = 37). In four episodes of multi-anatomical-site infection (3 male, 1 female) different antimicrobial susceptibility profiles were observed across sample sites but all were correctly genotyped using GCSNP. GCSNP panel testing correctly identified all of 92 phenotypically susceptible (n = 52) and resistant (n = 40) strains. A total of 66 diverse NG-MAST sequence types were observed in the panel.

**Conclusion** GCSNP testing enables accurate genotypic detection of fluoroquinolone susceptible NG from clinical samples, from multiple anatomical sites and across diverse circulating gonococcal strains, enabling use of tailored anti-gonococcal therapy following NAAT positivity. If multi-site infection is suspected, genotypic testing on all anatomical sites is necessary in order to account for the presence of infections with mixed susceptibility.

**Disclosure of interest statement** This study was funded under the UKCRC Translational Infection Research (TIR) Initiative supported by the Medical Research Council (Grant Number G0901608) with contributions to the Grant from the Biotechnology and Biological Sciences Research Council, the National Institute for Health Research on behalf of the Department of Health, the Chief Scientist Office of the Scottish Government Health Directorates and the Wellcome Trust.

### 005.3 MULTIPLEX REAL-TIME PCR WITH HIGH RESOLUTION MELTING ANALYSIS FOR DETECTING RESISTANCE MECHANISMS IN *NEISSERIA GONORRHOEAE*

<sup>1</sup>V Dona\*, <sup>2</sup>N Low, <sup>1</sup>YN Guilarte, <sup>1</sup>A Lupo, <sup>3</sup>H Furrer, <sup>4</sup>M Unemo, <sup>1</sup>A Endimiani. <sup>1</sup>Institute for Infectious Diseases, University of Bern, Bern, Switzerland; <sup>2</sup>Institute of Social and Preventive Medicine, University of Bern, Bern, Switzerland; <sup>4</sup>Örebro University Hospital, Örebro, Sweden; <sup>3</sup>Department of Infectious Diseases, Bern University Hospital and University of Bern, Bern, Switzerland

10.1136/sextrans-2015-052270.105

**Background** Molecular tests to detect antimicrobial resistance in *Neisseria gonorrhoeae* (NG) are urgently needed. Genetic methods are the mainstay of NG detection in many settings, but resistance testing still requires conventional phenotypic tests. The objective of this study was to develop an assay to detect the