O19.2 MYCOPLASMA GENITALIUM IS AS FREQUENT A CAUSE OF URETHRITIS AS CHLAMYDIA TRACHOMATIS, AND HAS HIGH RATES OF GENOTYPIC RESISTANCE TO MACROLIDE ANTIBIOTICS

doi:10.1136/sextrans-2013-051184.0192

M J Pond, A Nori, A A Witney, R Lopeman, P D Butcher, **S T Sadiq.** *St George's, University of London, London, UK*

Background When choosing empirical anti-microbial therapy for non-gonococcal urethritis (NGU) and cervicitis, efficacy against Chlamydia trachomatis over Mycoplasma genitalium is prioritised. However, M.genitalium is associated with reproductive sequelae in women and first-line recommended therapy with macrolide antibiotics differs to that for Chlamydia infection. We determined: M. genitalium and C.trachomatis frequency among symptomatic men with and without urethritis; prevalence of macrolide and fluoroquinolone associated genotypic resistance in M.genitalium; and the phylogenetic spread of genotypic M.genitalium antimicrobial resistance using a validated dual-locus typing system.

Methods Urethritis was diagnosed by combining urethral smear and clinical criteria. Nucleic acid amplification was used for detecting M.genitalium and C.trachomatis. Single nucleotide polymorphisms (SNPs) in the 23S ribosomal RNA gene (23S rRNA), in gyrA, gyrB, and parC were detected by DNA sequencing. MG191 SNP typing and MG309 variable number tandem analysis were utilised to assess M.genitalium strain diversity.

Results 217 men were recruited. C.trachomatis and M.genitalium prevalence was 14.7% (95% CI: 7.8–21.6) and 16.7% (95% CI: 9.5–24.0) respectively in NGU cases and both significantly higher than in those with no urethritis. 9/22 (41%; 95% CI: 20%–62%) of M.genitalium strains had markers of macrolide associated genotypic resistance. Of 15 M.genitalium strains analysed only one possessed a parC mutation, associated with fluoroquinolone resistance. Dual-locus typing assigned all M.genitalium strains to two major clusters, both of which contained diverse strains carrying resistant mutations. All strains were phylogenetically dispersed among international reference controls, typed using MG191.

Conclusion Frequency of M.genitalium was as high as C.trachomatis in NGU patients. More than 40% of M.genitalium strains had SNPs associated with macrolide resistance but fluoroquinolone associated genotypic resistance was rare. All strains were phylogenetically dispersed indicating that these infections were probably not part of a local clonal expansion. Treatment guidelines for NGU require re-appraisal in light of these findings.

O19.3 ESTIMATE OF THE PREVALENCE OF TRANSMITTED DRUG RESISTANCE (TDR) AND ACQUIRED DRUG RESISTANCE (ADR) IN A HIV RESISTANCE STUDY OF THE GERMAN CLINSURV-HIV COHORT

doi:10.1136/sextrans-2013-051184.0193

[1]**B Bartmeyer**, [1]D Schmidt, [1]C Kollan, [2]G Fätkenheuer, [3]H Stellbrink, [4]J Bogner, [5]B O Jensen, [6]M Stoll, [1]C Kücherer, [1]O Hamouda. *[1]Robert Koch Institute, Berlin, Germany; [2]Clinic for Internal Medicine, University of Cologne, Germany; [3]ICH Study Centre Hamburg, Hamburg, Germany; [4]Dept. of Infectious Diseases, Medical Clinic, Ludwig Maximilians University Munich, Germany; [5]Clinic of Gastroenterology and Hepatology, Heinrich Heine University Düsseldorf, Germany; [6]Clinic for Immunology and Rheumatology, Medical University Hanover, Germany*

Aim To estimate the prevalence of HIV-TDR and ADR in one resistance study of the German ClinSurv-HIV cohort.

Method The ClinSurv study is a national open multi-centre long term observational cohort with 15 participating clinical centres (n = 16,750 patients; 31.12.2011). In a resistance study all ClinSurv patients in five centres were identified. Sequences were processed through the Stanford University Genotypic Resistance Interpretation Algorithm (www. hivdb.stanford.edu; HIVdb version 6.1.1F; 2012 webService version beta-1.0.1) to identify mutations and to determine drug susceptibility. Sequences were analysed by using different lists of mutations (Bennett D. 2009; Johnson V. 2011). Trends in the prevalence of drug resistance mutations were calculated by logistic regression.

Results A total of 9,528 patients from five study centres were included into analysis. 4,989 viral sequences were collected from 34% (3,267/9,528) of these patients. 47% (2,365/4,989) of sequences were produced from patients being treatment naïve and 50% (2,495/4,989) from patients under treatment. TDR was identified in 10% (203/1,950) of viral strains. The prevalence of TDR over time was stable at 10.4% (95% CI 9.1–11.8; OR: 0.98; 95% CI 0.92–1.04; $p_{for\ trend}$ = 0.6; 2001–2011). NRTI-resistance was determined in 7% (128/1,950), followed by 3% NNRTI- and PI-resistance, respectively (NNRTI: 61/1,950; PI: 56/1,950). Prevalence of ADR in treated patients was high (61%; 1,500/2,453 of sequences) but declined significantly over time (OR: 0.8; 95% CI 0.77–0.83; $p_{for\ trend}$ < 0.001; 2001–2011). Within drug classes NNRTI-resistance was predominant (56%; 834/1503), followed by NRTI-resistance in 52% (1,139/2,194) of sequences of patients with ADR exposed to these drug classes. PI-resistance was identified in 30% (543/1778). Integrase-resistance was determined in 8% (13/161) of integrase-sequences.

Discussion Prevalence of TDR is highly stable in this unselected study population, whereas ADR declined significantly over the time, indicating that this decline was presumably influenced by ART related effects, broader resistance testing and resistance test guided therapy.

O19.4 ACCEPTABILITY OF HPV VACCINATION AMONG PARENTS OF ADOLESCENT SCHOOL GOING GIRLS IN MYSORE CITY, INDIA

doi:10.1136/sextrans-2013-051184.0194

[1,2]**K Krupp**, [1]V Srinivas, [3]L Marlow, [2]T Li, [2]A Albetini, [1]S Gowda, [2]A Arun, [1]P Jaykrishna, [2,1]P Madhivanan. *[1]Public Health Research Institute of India, Mysore, India; [2]Robert Stempel College of Public Health & Social Work, Florida International University, Miami, FL, United States; [3]Health Behavior Research Centre, Department of Epidemiology and Public Health, UCL, London, UK*

Background One in every four reported cases of cervical cancer occurs in India. While mortality from the disease has all but disappeared in industrial countries, 74,000 Indian women still die each year from this preventable cancer. It has been estimated that widespread uptake of HPV vaccine by adolescent girls could reduce this high incidence and mortality by approximately two-thirds. This study explores correlates of HPV vaccine acceptability among parents of adolescent school-going girls in urban Mysore, India.

Methods Between August and December of 2011, participants were selected by stratified, multi-stage random sampling in schools located in Urban Mysore. Questionnaires were sent home with a random sample of 800 adolescent girls 11–15 years of age attending 10 schools in Mysore city to be completed by a parent. Logistic regression was used to assess factors associated with parental acceptability of HPV vaccine.

Results 797 completed surveys (99.6%) were received back from parents. About 72% of respondents would accept the HPV vaccine for their daughters. Vaccine acceptance was higher among participants who had experienced cancer in their family (OR: 1.69, 95% CI: 1.07, 2.65), or perceived that their family doctor (5.04; CI 3.27, 7.76) or spouse (5.01; CI: 3.20, 7.87) would approve. Parents having concerns about vaccinations in general (0.38; CI: 0.25, 0.57), vaccine side-effects (0.65; CI: 0.45, 0.94), vaccine safety (0.64; CI: 0.42, 0.97) or the possibility that their daughter might become sexually active (0.71; CI: 0.28, 0.76) had lower odds of accepting HPV vaccination.