

Background Increasing reports of *Neisseria gonorrhoeae in vitro* decreased susceptibility and resistance, and treatment failures with third generation cephalosporins are of major concern as these drugs are the last remaining options for effective antimicrobial therapy in many settings.

Methods The European Gonococcal Antimicrobial Surveillance Programme (Euro-GASP), a sentinel surveillance programme funded by the European Centre for Disease Prevention and Control since 2009, monitors antimicrobial susceptibility patterns across the European Union (EU/EEA). Participating laboratories performed susceptibility testing by Etest or agar dilution breakpoint method, or sent isolates to reference laboratories in Denmark, Sweden or the United Kingdom for testing. Euro-GASP validated proficiency and result accuracy through an external quality assessment scheme.

Results In 2011, 1902 isolates from 21 countries were collected and tested. The percentage of tested isolates with decreased susceptibility to cefixime (8.0%) remained stable compared to 2010 (8.7%), but was still significantly higher than in 2009 (5.1%, $p < 0.01$). Isolates with decreased susceptibility to cefixime were reported from 17 countries in 2011, the same as in 2010; however three countries reported such isolates for the first time in 2011. For the first time, ten isolates with decreased susceptibility to ceftriaxone were reported from two countries. Rates of ciprofloxacin (49%) and azithromycin (5.3%) resistance remained high. Minimum inhibitory concentration of gentamicin remained low (MIC₅₀: 4 mg/L; MIC₉₀: 8 mg/L).

Conclusions Although the rapid increase and spread of decreased susceptibility to cefixime in 2010 has not continued, the detection of isolates with decreased susceptibility to ceftriaxone is concerning. ECDC has published a response plan which aims to strengthen surveillance of gonococcal antimicrobial susceptibility in the EU/EEA; ensure that capacity for culture and susceptibility testing is maintained; establish a system for collection and verification of data on clinical treatment failure; and to recommend public health actions at national and European level.

003.3 MAXIMISING THE EFFICIENCY OF GONORRHOEA TREATMENT BY TARGETING THE USE OF PREVIOUS FIRST LINE THERAPIES TO SUSCEPTIBLE PATIENTS

doi:10.1136/sextrans-2013-051184.0097

K Town, ¹C Obi, ²S Chisholm, ¹G Hughes, ²C A Ison. ¹HIV/STI Department, Health Protection Agency, London, UK; ²Sexually Transmitted Bacteria Reference Unit, Health Protection Agency, London, UK

Background Gonorrhoea treatment guidelines change when less than 95% of the infected population is successfully treated with the recommended antimicrobial. Isolates with decreased susceptibility to ceftriaxone, the current recommended therapy, have been identified and if treatment failure becomes problematic there are no new antimicrobials approved. However, *Neisseria gonorrhoeae* remains susceptible to penicillin, ciprofloxacin and cefixime in at least two thirds of patients (82%, 68%, and 98% respectively) so it may be possible to target previously recommended antimicrobials to specific population sub-groups.

Methods Descriptive data from the Gonococcal Resistance to Antimicrobials Surveillance Programme (GRASP) were analysed for trends in penicillin, ciprofloxacin and cefixime susceptibility across patient sub-groups. Patient characteristics associated with antimicrobial susceptibility were identified using univariate and multivariable analyses. All analyses were performed separately for heterosexuals and men who have sex with men (MSM).

Results Heterosexual patients whose infection was susceptible to penicillin, ciprofloxacin or cefixime were of black ethnicity, penicillin: 94%, adjusted odds ratio (OR) 3.52 (95% confidence interval (CI) 2.62–4.72), ciprofloxacin: 92%, OR 5.35 (CI 4.08–7.0), cefixime: 99%,

OR 3.62 (CI 1.91–6.84), or with concurrent chlamydia infection (penicillin: 94%, 2.34, 1.75–3.13, ciprofloxacin: 92%, 3.37, 2.59–4.38, cefixime: 99%, 2.32, 1.23–4.39). Additionally isolates susceptible to penicillin were found in patients aged 13–24 years (92%, 3.54, 2.63–4.77) or without symptoms (92%, 1.75, 1.28–2.4). All isolates from heterosexuals were fully susceptible to cefixime. In all sub-groups of the MSM population the proportion of isolates susceptible to penicillin, ciprofloxacin or cefixime was below 90%.

Conclusion The efficiency of gonorrhoea treatment could be maximised by targeting the use of previous first line therapies to specific heterosexual population sub-groups if the treatment threshold is reduced to 90%. Treatment of any MSM with penicillin, ciprofloxacin or cefixime would not be appropriate, as the proportion susceptible to these antimicrobials is much less than for the heterosexual population.

003.4 GENOMIC EPIDEMIOLOGY OF NEISSERIA GONORRHOEA WITH REDUCED SUSCEPTIBILITY TO CEFIXIME IN THE UNITED STATES

doi:10.1136/sextrans-2013-051184.0098

^{1,2}Y H Grad, ³R Kirkcaldy, ³D Trees, ⁴J Dordel, ¹E Goldstein, ³H Weinstock, ⁴J Parkhill, ¹W P Hanage, ⁴S Bentley, ^{1,5}M Lipsitch. ¹Center for Communicable Disease Dynamics, Department of Epidemiology, Harvard School of Public Health, Boston, MA, United States; ²Division of Infectious Diseases, Brigham and Women's Hospital, Harvard Medical School, Boston, MA, United States; ³Division of STD Prevention, Centers for Disease Control and Prevention, Atlanta, GA, United States; ⁴Wellcome Trust Sanger Institute, Hinxton, UK; ⁵Department of Immunology and Infectious Diseases, Harvard School of Public Health, Boston, MA, United States

Background Genome sequencing of pathogens has yielded insights into transmission networks and the spread of antibiotic resistance. Here, we report a large-scale genomic epidemiology study of *Neisseria gonorrhoeae* to investigate the emergence and spread of isolates with reduced susceptibility to cephalosporins.

Methods We sequenced the genomes of 242 gonococcal isolates collected by CDC's Gonococcal Isolate Surveillance Program (GISP). These isolates comprise all 141 isolates from GISP in 2009–10 with reduced susceptibility to cefixime (cef^{RS}; cefixime MICs ≥ 0.25 μ g/ml) and 141 susceptible isolates matched by location, collection date, and sexual orientation of the infected individual. We assessed diversity and association of genes known to contribute to antibiotic resistance, correlated location and phylogenetic clustering to determine sexual networks, and characterised the extent of recombination.

Results Phylogenetic analysis of single nucleotide polymorphisms (SNPs) within the core genome (34959 SNPs) demonstrates that most cef^{RS} isolates in the US fall into two distinct lineages. We identify several independent acquisitions of a mosaic *penA* allele, including evidence of a partial mosaic in an isolate with cef^{RS} and of reversion to an allele conferring cephalosporin susceptibility. Correlating the phylogeny with sexual orientation and geographic location provides evidence for clones circulating in sexual networks, some of which appear geographically restricted and others widespread. Analysis of predicted recombinant regions shows evidence of exchange with other *Neisseria* spp., consistent with prior observations of interspecies mosaicism.

Conclusions Cef^{RS} isolates in the US predominantly derive from two lineages that share the same mosaic *penA* sequence, and reflect sexual networks at local and regional scales. Additionally, we quantify the extent of recombination and the correlation of selected alleles with resistance phenotypes. Genomic methods offer detailed insights into the spread of resistant infections, with potential for enhanced surveillance and improved diagnostics.

003.5 RECENT INCREASES IN GONORRHOEA IN EUROPE

doi:10.1136/sextrans-2013-051184.0099

G Spiteri, K Haar, O Sfetcu, M van de Laar. European Centre for Disease Prevention and Control, Stockholm, Sweden

Background Recent reports have described increasing trends of gonorrhoea among men who have sex with men (MSM) in the United Kingdom and women in Sweden. European Union (EU/EEA) surveillance data has also shown increasing rates of gonorrhoea since 2008. We analysed surveillance data to identify the contributions of key populations to this increase.

Methods Surveillance of gonorrhoea in the EU/EEA is co-ordinated by the European Centre for Disease Prevention and Control (ECDC). Data reported to ECDC in 2008 and 2011 were compared, focusing on countries with an increasing number of gonorrhoea cases, to analyse changes among key populations.

Results In 2011, 39 179 cases of gonorrhoea were reported from 28 EU/EEA countries. Of these countries, 21 reported a median increase in the number of reported cases of 31% (interquartile range: 22–79%). Among countries reporting increasing cases, 15–24 year olds accounted for 43% of reports in 2011; males accounted for 72%; MSM for 40%. Among MSM, the largest proportion of cases was reported among 25–34 year olds (42%).

Between 2008 and 2011, the number of reported cases increased by 37%. Increases were observed among all age-groups, particularly among 25–34 year olds (61%) and those aged 45+ (78%). Reported cases increased by 51% among males compared to 30% among females. Transmission among MSM increased by 124% since 2008 and, among MSM, the largest increase in reported cases was among those aged 45+ (192%) and 25–34 year olds (173%).

Conclusions Although reported cases of gonorrhoea increased among all age-groups and both genders between 2008 and 2011, the highest increase occurred among MSM above 25 years of age. Increasing trends may be due to increased awareness and testing, and improved reporting; increased transmission, however, is also likely. Prevention messages targeting these groups need to be reinforced.

003.6 USING MOLECULAR TYPING TO INVESTIGATE *N. GONORRHOEAE* STRAIN TURNOVER: A COMPARATIVE STUDY OF GISP ISOLATES COLLECTED FROM BALTIMORE AND SAN FRANCISCO

doi:10.1136/sextrans-2013-051184.0100

¹K Espinosa, ¹J Gerrity, ²M Pandori, ³V Marsiglia, ⁴J Hardick, ⁴M Barnes, ¹D Hess, ⁴C Gaydos. ¹Santa Clara University, Santa Clara, CA, United States; ²San Francisco Department of Public Health Labs, San Francisco, CA, United States; ³Baltimore City Health Department, Baltimore, MD, United States; ⁴Johns Hopkins University, Baltimore, MD, United States

Background One internationally accepted method for the molecular epidemiologic typing of *Neisseria gonorrhoeae* is *Neisseria gonorrhoeae* Multi Antigen Sequence Typing (NG-MAST). NG-MAST utilises DNA sequencing of two variable regions of the *N. gonorrhoeae* genome to classify gonococcal isolates into strain types.

Method We assessed the genetic diversity of *N. gonorrhoeae* isolates in Baltimore (N = 277) spanning the years 2009–2011 compared to San Francisco (N = 539) from 2005–2011, using NG-MAST. All isolates in this project were obtained from the CDC Gonococcal Isolate Surveillance Project (GISP). San Francisco strains were mostly from MSM, while the Baltimore isolates were mostly from a heterosexual population.

Results NG-MAST results from isolates across that time period revealed a surprising degree of sequence type turnover within the Baltimore area. When compared to the data from San Francisco, the *N. gonorrhoeae* genetic diversity trends revealed minimal overlap in sequence families between the two metropolitan areas; SF8238, SF210, and SF 2992 were present in both populations. However, a pair-wise comparison of other strain families revealed two relatively distinct populations; the most prevalent strain families in San Francisco were SF437, SF23, SF3935, and SF1407, while those in Baltimore were SF8234, SF8240, SF865, and SF8262.

Conclusion These data may imply that the traditional understanding of a gonococcal transmission pattern from west to east cannot accurately depict the strain flow of *N. gonorrhoeae* isolates within these populations. Our data revealed a large amount of strain turnover in both metropolitan areas by year. This raises questions about the entry and transmission of *N. gonorrhoeae* within the U.S., and the implications of this turnover in regards to the evolution of this organism.

0.04 - Vaginal infections and PID

004.1 THE INFLUENCE OF HORMONAL CONTRACEPTION AND PREGNANCY ON THE VAGINAL MICROBIOME, SEXUALLY TRANSMITTED INFECTIONS, AND CYTOKINE RESPONSES IN A COHORT OF RWANDAN SEX WORKERS

doi:10.1136/sextrans-2013-051184.0101

^{1,2}M C Verwijs, ¹H Borgdorff, ¹F W N M Wit, ³F H Schuren, ⁴R Lutter, ⁵R Verhelst, ²M J M Bonten, ⁶J H H M van de Wijert. ¹Amsterdam Institute for Global Health and Development (AIGHD), Amsterdam, The Netherlands; ²Utrecht University Medical Center, Department of Medical Microbiology, Utrecht, The Netherlands; ³TNO Microbiology & Systems Biology, Zeist, The Netherlands; ⁴Department of Experimental Immunology, Academic Medical Center, Amsterdam, The Netherlands; ⁵International Center for Reproductive Health (ICRH), Ghent University, Ghent, Belgium; ⁶University of Liverpool, Institute of Infection and Global Health, Liverpool, UK

Background The effects of hormonal contraception and pregnancy on the vaginal microbiome (by molecular methods), acquisition and persistence of sexually transmitted infections (STIs), and genitourinary mucosal immunology are still largely unknown.

Methods HIV-negative, non-pregnant female sex workers (n = 397) in Kigali, Rwanda, were followed for two years. Demographic, behavioural, clinical, STI and pregnancy data were collected at regular intervals. The vaginal microbiome was cross-sectionally determined using a phylogenetic microarray (n = 174). Women with STIs were purposefully oversampled in this subsample. Inflammatory cytokines were measured in cervicovaginal fluid using Luminex and ELISA methodology (n = 343). Hormonal exposure was defined as use of hormonal contraception (oral or injectable) or a positive urine pregnancy test. Women in the exposure groups were compared to non-pregnant women who did not use hormonal contraception. Adjustments were made for demographic data and sexual risk taking.

Results At baseline, 12% of the women used hormonal injectables, and 6% oral contraceptives (OC); 7.7% was pregnant. OC use was associated with higher HPV prevalence (aOR 3.09; 95% CI 1.42–7.72), higher *Chlamydia trachomatis* incidence (aOR 7.13; 95% CI 1.40–36.30), and lower syphilis prevalence (0% vs 7.2% in controls) and incidence (0% vs 1.2%). Hormonal injectables were associated with higher HSV-2 prevalence (aOR 2.08; 95% CI 1.23–3.50). Pregnancy was weakly associated with higher *Trichomonas vaginalis* (aOR 1.67; 95% CI 0.97–2.88) and vaginal yeast (aOR 1.95; 95% CI 0.99–3.82) incidence. Six vaginal microbiome clusters were identified. No associations between hormonal exposure status and vaginal microbiome clusters were found; however, pregnant women had lower *Gardnerella vaginalis* levels. Pregnant women had higher IL-8 levels in cervicovaginal fluids than non-exposed women.

Conclusions Both hormonal contraception and pregnancy were associated with higher STI incidence. Overall, vaginal inflammation and microbiome composition were similar among groups, but pregnant women had lower *Gardnerella* and higher IL-8 levels.

004.2 HORMONAL CONTRACEPTION IS ASSOCIATED WITH A REDUCED RISK OF BACTERIAL VAGINOSIS: A SYSTEMATIC REVIEW AND META-ANALYSIS

doi:10.1136/sextrans-2013-051184.0102