

anal high grade intraepithelial neoplasia (HSIL) was higher in HIV-positive than in the HIV-negative participants (46.9% vs 32.3%, $p < 0.001$). Among those with HSIL at baseline, the clearance rate was similar between HIV-positive and -negative participants (38.4 vs 38.0 per 100PY, $p = 0.636$).

Conclusions Gay men in SPANC reported multiple sexual partners across the adult age-range, and incident HPV16 continued to be detected in men up to their seventh decade of life. This suggests that HPV vaccination of adult gay men may prevent infection and have a role in cancer prevention. Anal HSIL is highly prevalent, particularly among HIV-positive men, but there are high rates of clearance without treatment. These data suggest that a screening test which can distinguish persistent from transient HSIL is required. The role of HPV biomarkers in identifying those HSIL lesions most likely to persist should be investigated.

Oral Presentations

001 - Spread of antimicrobial-resistant gonorrhoea

001.1 EVOLUTION AND SPREAD OF ANTIBIOTIC-RESISTANT GONORRHOEA

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Introduction *Neisseria gonorrhoeae* has developed resistance to all classes of antimicrobials that have been used to treat it and strains that are resistant to multiple classes of antimicrobials have evolved. Only one antimicrobial (ceftriaxone) can now be used for empirical treatment in many countries. Hence, it is important to understand the dynamics and drivers of resistance evolution.

Methods First, we estimated rates of resistance evolution from antimicrobial resistance surveillance data from the USA and from England and Wales for heterosexual men (HetM) and men who have sex with men (MSM). Second, we developed dynamic transmission models to reconstruct the observed dynamics of *N. gonorrhoeae* transmission and resistance evolution in both HetM and MSM.

Results We found that resistance to ciprofloxacin and cefixime initially spreads exponentially at rates between 0.2 and 2.4 per year. These rates suggest that the proportion of resistant strains doubles every 3 to 35 months. We found lower rates of spread in HetM (0.2 to 0.8) compared with MSM (0.9 to 2.4). The models show that the treatment rate is the driving force for the spread of resistance.

Conclusion There is a trade-off in optimising the treatment rate to provide individual patient care to all those who are infected and to keep the spread of resistance as low as possible. These findings have implications for developing antimicrobial treatment strategies and point-of-care tests to detect resistance.

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001.2 AZITHROMYCIN-RESISTANT *NEISSERIA GONORRHOEA* IN MEN WHO HAVE SEX WITH MEN (MSM) IN SEATTLE, WASHINGTON: 2014–2015

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Background The emergence of azithromycin-resistant *Neisseria gonorrhoeae* threatens recommended first-line treatment regimens.

Methods We investigated cases of azithromycin-resistant gonorrhoea detected at Public Health – Seattle and King County STD Clinic between January 2014 and February 2015. In 2012–2013, zero of 237 MSM urethral isolates were azithromycin-resistant. The US Centres for Disease Control and Prevention (CDC) and Clinical and Laboratory Standards Institute (CLSI) do not define an azithromycin-resistance breakpoint. CDC uses ≥ 2 mcg/mL as an “Alert Value” minimal inhibitory concentration (MIC) (here called resistant). We used agar dilution to determine MICs.

Results Of 179 urethral, 83 pharyngeal and 87 rectal isolates from MSM, 11 (6.1%), 6 (7.2%) and 5 (5.7%) had azithromycin MIC ≥ 2 mcg/mL, respectively. We identified no cases of azithromycin-resistance among 56 heterosexuals. Overall, 19 (6.9%) of 276 MSM with culture-positive gonorrhoea had an azithromycin-resistant isolate. The median azithromycin MIC was 4.0 mcg/mL (range 2 to >256 mcg/mL). Eight patients’ isolates also demonstrated tetracycline resistance (MIC ≥ 2 mcg/mL); one was ciprofloxacin-resistant (MIC 16.0 mcg/mL). None exhibited reduced susceptibility to cefixime or ceftriaxone. Clinicians treated thirteen (68%) cases with ceftriaxone and azithromycin, one (5.3%) with ceftriaxone and doxycycline, two (10.6%) with study drug, and three (15.8%) with 2g of azithromycin. Two of three men treated with azithromycin-monotherapy had a test of cure (TOC) and both had persistent infection; their isolates demonstrated azithromycin MICs of 32 mcg/mL and 4.0 mcg/mL. One rectal treatment-failure was cured with 360 mg of gentamicin intramuscularly; the other (urethra/pharynx positive), was treated with ceftriaxone and doxycycline. He did not undergo repeat TOC. The individual with high-level azithromycin-resistance (MIC >256 mcg/mL) was an international traveller and not locatable for TOC.

Conclusions Clinically important azithromycin-resistant *Neisseria gonorrhoeae* now are found in $>5\%$ of MSM with gonorrhoea in Seattle. These findings support new CDC recommendations to avoid treating gonorrhoea with azithromycin alone.

Disclosure of interest statement This work was funded by the US National Institutes of Health and CDC. No pharmaceutical grants were received in the development of this study.

001.3 HIGH-LEVEL AZITHROMYCIN RESISTANCE IN *NEISSERIA GONORRHOEA* CLINICAL ISOLATES IN NANJING, CHINA, 2013–2014

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Introduction Dual antimicrobial therapy with ceftriaxone plus azithromycin has recently been recommended for uncomplicated gonorrhoea in the United States, the United Kingdom and Canada because of increases in MICs of *N. gonorrhoeae* for extended-spectrum cephalosporins. However, emergence of high-level azithromycin resistance in *N. gonorrhoeae* have been reported in many countries. No high-level azithromycin-resistant isolates of *N. gonorrhoeae* have been reported in China. Azithromycin has been added into antibiotic susceptibility panel since 2013. In this study, we present the results of antimicrobial susceptibility testing of 384 gonococcal strains isolated between 2013 and 2014 and evidence of high-level azithromycin resistance in Nanjing, China.

Methods 384 *N. gonorrhoeae* isolates were isolated sequentially from male adults with symptoms/signs of urethritis attending a single STD clinic in Nanjing, China between 2013 and 2014. Minimum inhibitory concentrations (MICs) of *N. gonorrhoeae* to penicillin, tetracycline, ciprofloxacin, spectinomycin, azithromycin, cefixime and ceftriaxone were determined by the agar dilution technique. β -lactamase production was determined by paper acidometric testing.

Results Resistance to penicillin and tetracycline was 72.1% (277/384) and 85.9% (330/384), respectively; 46.9% (180/384) of strains were PPNG and 34.6% (133/384) were TRNG. All isolates (100%) were resistant to ciprofloxacin (MIC ≥ 1 μ g/ml). A total of 32.3% (124/384) of isolates were resistant to azithromycin (MIC ≥ 1 μ g/ml), among them 25% (31/124) isolates displayed high-level azithromycin resistance (MIC ≥ 256 μ g/ml). All isolates were susceptible to spectinomycin, cefixime and ceftriaxone. However, 16 isolates (4.3%) had elevated MICs (≥ 0.125 μ g/ml) for cefixime and 38 isolates (10.1%) had an MIC of 0.125 μ g/ml for ceftriaxone.

Conclusion The present study shows a high prevalence of *N. gonorrhoeae* isolates displaying resistance to penicillin, tetracycline, azithromycin and ciprofloxacin and reduced susceptibility to extended-spectrum cephalosporins. High-level azithromycin resistance in *N. gonorrhoeae* has emerged in Nanjing, China.

Disclosure of interest statement Nothing to declare

001.4 RECENT RISE IN REDUCED SUSCEPTIBILITY TO CEFTRIAZONE IN *NEISSERIA GONORRHOAE* IS NOT CAUSED BY STRAINS WITH A *PEN A* MOSAIC GENE

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Background Resistance of *Neisseria gonorrhoeae* against third generation cephalosporins is a threat to public health. A known determinant is the presence of a mosaic *penA* gene in *N. gonorrhoeae*, partially derived from commensal *Neisseria* spp. We report resistance figures of *N. gonorrhoeae* against ceftriaxone from 2010 to 2013 and looked at *penA* characteristics of specific strains.

Methods MICs for ceftriaxone were assessed from 2010–13 (4191 strains). A specific PCR identifying strains with a mosaic *penA* gene and partial sequence analysis (aa 180 – 550) of the *penA* gene were used for further characterisation of specific strains.

Results Strains resistant to ceftriaxone were not found during the study period. The frequency of strains with an increased MIC (>0.032) to ceftriaxone was 5.2% in 2010, this rate

dropped to 2.0 and 3.1% in 2011 and 2012 respectively, but increased to 7.8% in 2013. In 2010, 46/48 (96%) strains with an increased MIC against ceftriaxone contained a mosaic *penA* gene; in 2013, only 15/68 (22%) of such strains contained this gene. Sequence analysis of 16 of the strains isolated in 2013 with reduced susceptibility to ceftriaxone and lacking a mosaic *penA* gene showed that they all had an identical *penA* gene which was similar to type XVIII, including a 502 A-T mutation, but lacking the 543 G-S mutation.¹

Conclusion The recent increase of the frequency of strains with reduced susceptibility to ceftriaxone in 2013 is due to strains with a *penA* sequence not yet found in the Netherlands in 2010 among strains with reduced susceptibility to ceftriaxone.

Disclosure of interest statement Nothing to declare

REFERENCE

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001.5 AN AUSTRALIA-WIDE MOLECULAR STUDY OF *NEISSERIA GONORRHOAE* IDENTIFIES FREQUENT OCCURRENCE OF A KEY CEPHALOSPORIN RESISTANCE MECHANISM

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Background *Neisseria gonorrhoeae* (NG) antimicrobial resistance (AMR) has been declared an urgent threat by the United States Centres for Disease Control and Prevention. Ceftriaxone is the mainstay of treatment, however many specific NG strains throughout the world exhibit decreased susceptibility (DS) and, occasionally, high-level resistance. In particular, this emerging resistance has been associated with an NG strain of multi-locus sequence type (MLST) 1901 and harbouring a ‘mosaic’ Penicillin Binding Protein sequence (mPBP2–1901). Here, we sought to measure the prevalence of this strain in Australia.

Methods In the context of the Gonorrhoea Resistance Assessment by Nucleic Acid Detection (GRAND) study, we developed molecular NG-AMR detection methods to test 2225 NG isolates collected in the first half of 2012 from around Australia. These isolates comprised approximately 90% of all NG isolates collected for culture-based AMR testing, and about 30% of all NG diagnoses nationally. The isolates were characterised using the Sequenom iPLEX platform to provide both an MLST type and AMR mutation data. We compared the findings to minimum inhibitory concentration (MIC) results from culture-based AMR surveillance.

Results We identified 186 distinct NG genotypes among the 2225 isolates; the 8 most common comprised 51% of all isolates. The mPBP2–1901 strain was the second most prevalent genotype, accounting for 8.4% (188/2228) of isolates. The prevalence of mPBP2–1901 was highest in Victoria and New South Wales (12% and 10.2%, respectively) compared to the other states (all $<4.3\%$). Of the 188 mPBP2–1901 strains, 64% were classified as sensitive to ceftriaxone by culture (MIC ≤ 0.03 mg/L) and 36% as DS (MIC0.06 – 0.125 mg/L).

Conclusion These findings highlight that a small number of genotypes account for the majority of NG infections in Australia, with the mPBP2–1901 strain accounting for 8% of isolates. The