

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 $\mu\text{g/ml}$). A total of 32.3% (124/384) of isolates were resistant to azithromycin (MIC ≥ 1 $\mu\text{g/ml}$), among them 25% (31/124) isolates displayed high-level azithromycin resistance (MIC ≥ 256 $\mu\text{g/ml}$). All isolates were susceptible to spectinomycin, cefixime and ceftriaxone. However, 16 isolates (4.3%) had elevated MICs (≥ 0.125 $\mu\text{g/ml}$) for cefixime and 38 isolates (10.1%) had an MIC of 0.125 $\mu\text{g/ml}$ 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 GONORRHOEAE* 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

¹ Whiley DM, Limnios EA, Ray S, et al. Diversity of *penA* alterations and subtypes in *Neisseria gonorrhoeae* strains from Sydney, Australia, that are less susceptible to ceftriaxone. *Antimicrob Agents Chemother.* 2007;**51**:3111–6

001.5 AN AUSTRALIA-WIDE MOLECULAR STUDY OF *NEISSERIA GONORRHOEAE* 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 (MIC 0.06 – 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