Introduction Dual antimicrobial therapy with ceftriaxone plus azithrothmycin 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 amtimicrobial 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. b-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 μg/ml). A total of 32.3% (124/384) of isolates were resistant to azithromycin (MIC ≥1μg/ml), among them 25% (31/124) isolates displayed high-level azithromycin resistance (MIC ≥256 μg/ml). All isolates were susceptible to spectinomycin, cefixime and ceftriaxone. However, 16 isolates (4.3%) had elevated MICs (≥0.125 μg/ml) for cefixime and 38 isolates (10.1%) had an MIC of 0.125 μg/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

O01.4 RECENT RISE IN REDUCED SUSCEPTIBILITY TO CEFTRIAXONE IN *NEISSERIA GONORRHOEAE* IS NOT CAUSED BY STRAINS WITH A *PENA* 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 assesed 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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O01.5 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 (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

findings also demonstrate the benefits of using molecular testing to complement phenotypic NG AMR surveillance.
Disclosure of interest statement Nothing to Declare.

O01.6 EXPLORING THE BENEFITS OF MOLECULAR TESTING FOR GONORRHOEA ANTIBIOTIC RESISTANCE SURVEILLANCE IN REMOTE SETTINGS

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Background The latest nucleic acid amplification tests (NAAT) for gonorrhoea are convenient and accurate, and are often used in place of culture-based tests for diagnosis. However the increasing use of NAATs in remote settings in Australia has compromised surveillance for gonorrhoea antimicrobial resistance (AMR). A molecular resistance test that can make use of samples collected for NAAT diagnosis may provide a means to enhance surveillance in remote settings where the availability of samples suitable for culture-based AMR testing is declining. We used a mathematical model to assess the potential benefit of a molecular test in terms of the timeliness of detection of gonorrhoea AMR.
Methods An individual-based mathematical model was developed to describe the transmission of gonorrhoea in a remote Indigenous population in Australia. We estimated the impact of the molecular test on the time delay between first importation and the first confirmation that the prevalence of gonorrhoea AMR has breached the WHO-recommended 5% threshold (when a change in antibiotic should occur).
Results The model suggests that when culture is the only means of testing for AMR, the breach will only be detected when the actual prevalence of AMR in the population has already reached 8 – 18%. With the addition of a molecular AMR test and assuming AMR can be determined for all samples, the breach will be detected when the actual prevalence of AMR in the population has reached 6%, which only slightly exceeds the recommended notification threshold of 5%.
Conclusion Molecular tests have the potential to provide more timely warning of the emergence of gonorrhoea AMR in remote settings where surveillance is compromised by the increased use of NAATs for diagnosis. This in turn will facilitate earlier treatment switching and more targeted treatment, which has the potential to reduce the population impact of gonorrhoea AMR.
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O02 - Point-of-care STI diagnosis

O02.1 POINT-OF-CARE TESTING AND IMMEDIATE TREATMENT OF CURABLE SEXUALLY TRANSMITTED AND GENITAL INFECTIONS AMONG ANTENATAL WOMEN IN PAPUA NEW GUINEA

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Background *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (NG), *Trichomonas vaginalis* (TV) and bacterial vaginosis (BV), are associated with adverse maternal and neonatal health outcomes, particularly preterm birth and low birth weight. These infections are highly prevalent in many low-income settings but remain undiagnosed and therefore untreated in pregnancy because of a lack of suitable diagnostic technology. In 2014, we conducted the first feasibility study of newly-available, easy to use and highly-accurate point-of-care (POC) STI assays in a routine clinical setting in Papua New Guinea (PNG) in preparation for a large-scale field trial to evaluate the potential of this strategy to improve pregnancy outcomes.
Methods Women aged 18–35 years attending their first antenatal visit were invited to participate. Following informed consent procedures, women completed a short interview, obstetric examination, and provided self-collected vaginal specimens for clinic-based STI testing, conducted by trained clinic staff: CT/NG and TV were tested using the Cepheid GeneXpert platform, and BV tested using the BVBlue Test. Participants were provided with same-day POC test results, and antibiotic treatment as indicated. Women were also provided routine onsite antenatal HIV and syphilis screening.
Results A total of 125 women were enrolled. The prevalence of CT was 20.0%; NG, 11.2%; TV, 37.6%; BV 18.4%; and more than half (67/125) had one or more of these infections. Over 70% of those with a POC-confirmed STI would not have been detected on clinical grounds alone. The prevalence of HIV was 1.6% and active syphilis, 4.0% in this population. All women with an STI and their sexual partners were successfully treated.
Conclusion Antenatal POC STI testing and treatment proved feasible in an antenatal setting in PNG. If this strategy is proven to be effective in our future field trial (2015–18), it has the potential to improve pregnancy outcomes in all high-burden, low-income countries worldwide.
Disclosure of interest statement Nothing to Disclose