P666 INCREASED RESISTANCE TO EXTENDED-SPECTRUM CEPHALOSPORINS IN *NEISSERIA GONORRHOEAE* ISOLATES IN NANJING, CHINA (2013–2018)

[1]Xiaohong Su*, [1]Wenjing Le, [1]Xiangdi Lou, [1]Xuechun Li, [1]Xiangdong Gong, [2]Peter Rice. [1]*Institute of Dermatology, Chinese Academy of Medical Sciences, STD Clinic, Nanjing, China*; [2]*University of Massachusetts Medical School, Worcester, USA*

10.1136/sextrans-2019-sti.733

Background The aim of this study is to monitor the trend in antimicrobial resistance in *Neisseria gonorrhoeae* in Nanjing, China. Gonococcal strains isolated during 2015–2018 were examined for susceptibility to seven antibiotics and compared with results from 2013–14 (Antimicrob Agents Chemother, 2018)

Methods 1173 gonococcal strains were isolated from men with urethritis; n=789 (2015–18), compared with n=384 (2013–14). MICs for seven antibiotics were determined by agar dilution method. Criteria for decreased susceptibility to ceftriaxone (MIC≥0.125 mg/L) and cefixime (MIC≥0.25 mg/L) were defined by WHO. Using CLSI and EUCAST (for azithromycin only) criteria, the following MIC breakpoints were used to ascertain resistance: ≥128 mg/L, spectinomycin; ≥2 mg/L, penicillin and tetracycline and ≥1 mg/L, ciprofloxacin and azithromycin. Resistance determinants were investigated using WGS of two isolates which were resistant to both ceftriaxone and cefixime.

Results The percentage of isolates with decreased susceptibility to ceftriaxone rose from 9.9% in 2013–14 to 23% in 2016 and decreased to 16.7% in 2018 (P=0.01). The percentage of isolates with decreased susceptibility to cefixime rose from 0.3% (2013–14) to 15.7% in 2016 and decreased to 13.7% in 2018 (P<0.0001). 38 isolates displayed MIC≥0.5 mg/L for cefixime, among them 26.3%(10) belonged to ST5308 and one isolate to ST1407 NG-MAST types. Two isolates that exhibited MIC=1 mg/L for ceftriaxone and MIC=2 mg/L for cefixime were detected in 2017 and 2018, respectively. Each possessed mosaic penA-60.001 gene (the same as FC428 isolated in Japan). Azithromycin resistance decreased from 32.3% (2013–14) to 15.2% (2018) and high-level azithromycin resistance (MIC ≥256 mg/L) decreased from 10.4% (2013–14) to 3.4% (2018) (P<0.001). All 1173 isolates were susceptible to spectinomycin, but resistant to ciprofloxacin. 81.3% isolates were resistant to penicillin and 84.8% to tetracycline.

Conclusion The proportion of *N. gonorrhoeae* isolates with decreased susceptibility to extended-spectrum cephalosporins increased significantly from 2013 to 2018. Ceftriaxone-resistant strain has emerged in Nanjing, China.

Disclosure No significant relationships.

P667 GUIDING *NEISSERIA GONORRHOEAE* MANAGEMENT BY MOLECULAR DETECTION OF CIPROFLOXACIN RESISTANCE BY SPEEDX RESISTANCEPLUS GC ASSAY

[1]Seb Cotton*, [2]Michelle Etherson, [2]Jill Shepherd, [2]Naomi Henderson, [2]Kate Templeton. [1]*Royal Infirmary Edinburgh, Edinburgh, UK*; [2]*Royal Infirmary Edinburgh, Edinburgh, UK*

10.1136/sextrans-2019-sti.734

Background There is a growing concern due to the emergence of multi-drug resistance developed in *Neisseria gonorrhoeae*. A rapid molecular test could provide antimicrobial susceptibility knowledge prior to start of treatment and decrease the turnaround time from current culture methods (7 days). The aim was to evaluate the clinical performance of the ResistancePlus GC assay (SpeeDx) compared to the in-house PCR and antimicrobial susceptibility results for ciprofloxacin.

Methods Antimicrobial susceptibility data was captured on all GC culture positives from 2015–2017 in Scotland. A gyrA real-time PCR was used to detect for ciprofloxacin resistance in *N. gonorrhoeae*. In this study 168 samples were selected from a range of sites (Cervical/vaginal, Rectal, Urine or Throat). Results were compared to susceptibility results of cultures isolated from the same patient episode (within 14 days). The culture isolates displayed a range of MICs with 84 susceptible and 84 resistant to ciprofloxacin.

Results Ciprofloxacin resistance was seen in 420/1338 episodes (31.4%) in 2017. The ResistancePlus GC assay was able to detect *N. gonorrhoeae* in all of the samples (100%) and *gyrA* in 164/168 samples (97.6%).The 4 samples with *gyrA* undetected had high Ct's (≥35) in a 2nd line real-time PCR for *porA*. In total 162/164 *gyrA* results matched the phenotype of a culture isolate taken from the same episode (98.7%). Further analysis showed that performing the assay on the discrepant culture isolates matched the phenotype result.

Conclusion The ResistancePlus GC assay performed well on clinical samples and could offer ciprofloxacin susceptibility testing within 4 hours to a laboratory service. This would therefore allow for an alternative antibiotic to be prescribed. Modeling based on current episodes in Scotland could mean that ciprofloxacin would be able to be used in ≥50% of episodes which provides an exciting new approach to GC treatment.

Disclosure No significant relationships.

P668 TRANSFER OF HIGH-LEVEL MACROLIDE RESISTANCE IN *NEISSERIA GONORRHOEAE*

[1]Saïd Abdellati*, [1]Els Verhoeven, [1]Irith De Baetselier, [2]Tania Crucitti, [3]Chris Kenyon. [1]*Institute of Tropical Medicine, Clinical Sciences, Antwerp, Belgium*; [2]*Centre Pasteur du Cameroun, Yaoundé, Cameroon*; [3]*Institute of Tropical Medicine, HIV/STI Unit, Antwerp, Belgium*

10.1136/sextrans-2019-sti.735

Background Previous transformation experiments with *Neisseria gonorrhoeae* (Ng) have established that it is able to acquire high-level antibiotic resistance via transformation. We aimed to assess if a high-level ceftriaxone resistant Ng strain (WHO X) was able to acquire resistance to azithromycin (AZM) via this mechanism.

Methods A mid log phase culture of Ng WHO X (AZM MIC 0.25 µg/mL) was mixed with whole genomic DNA extracted from Ng WHO strain V (AZM ≥ 256 µg/mL). A concentration of 1,5x MIC of AZM was added as a stress factor for the selection of the resistance determinants. Control experiments were conducted by omitting the addition of AZM and/or DNA. Consecutively, the mixture was plated on blood agar plates and incubated at 36°C in a 6% CO_2 atmosphere. Of each blood agar plate 1 or 2 colonies were selected for E testing performed according to CLSI guidelines. Colonies growing alongside the E-test strip at the higher range of the MIC values were selected for further characterization, including whole genome sequencing, and to identify the acquired resistance mechanisms.

Results The MIC for AZM of WHO strain X increased to greater than 256 µg/ml. There was no change in the MICs of Ng in the control experiments. Whole genome sequencing results will be presented demonstrating the pathways to resistance.