## O034 WHOLE GENOME SEQUENCING TO PREDICT *NEISSERIA GONORRHOEAE* ANTIBIOTIC SUSCEPTIBILITY: TOWARD TAILORED ANTIMICROBIAL THERAPY

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**Background/introduction** Absence of genotypic resistance-associated markers in *Neisseria gonorrhoeae* (NG) may predict antibiotic phenotypic susceptibility (APS). NG Whole genome sequencing (NG-WGS) on nucleic acid amplification test (NAAT) positive samples may allow for the avoidance and preservation of first line treatments such as ceftriaxone. However, NG-WGS predictive accuracy for APS should first be established.
**Aim(s)/objectives** To evaluate NG-WGS "wild-type" predictive value for tetracycline, ciprofloxacin and azithromycin APS.
**Methods** NG-WGS was performed on prospectively collected NG isolates from a London clinic in 2013, using Illumina MiSeq. Presence of 31 known single nucleotide polymorphisms (SNPs) and other resistance markers for tetracycline, ciprofloxacin, and azithromycin, were compared against a wild-type reference NG strain (FA1090).
**Results** Of 57 samples, APS to tetracycline, ciprofloxacin, and azithromycin was 14%, 72% and 87% respectively. Genotypic susceptibility (*GeSu*) was defined as absence of SNPs and other resistance-associated markers. For tetracyclines, ciprofloxacin and azithromycin, *GeSu-Tet*, *GeSu-Cip* and *GeSu-Azi*, accurately predicted APS in 7/8 (87.5%; 95% CI 52.9%–97.8%), 40/41 (97.6%; 95% CI 87.4%–99.6%) and 25/25 (100%; 95% CI 86.7%–100%) respectively. One phenotypically resistant *GeSu-Tet* isolate had "Intermediate" resistance. Of seven isolates, both genotypically and phenotypically susceptible to tetracyclines, all were also susceptible to ciprofloxacin, 24/25 isolates susceptible to azithromycin were also susceptible to ciprofloxacin.
**Discussion/conclusion** NG-WGS accurately predicted ciprofloxacin and azithromycin but not tetracycline APS. If validated on NG NAAT positive samples, this may allow for new precision ceftriaxone-sparing or ceftriaxone-adjunctive treatment combinations, for a substantial proportion of patients.

## O035 IS CEFIXIME BACK? TRENDS IN GONOCOCCAL RESISTANCE TO CURRENT AND PREVIOUS FRONT LINE THERAPIES IN ENGLAND AND WALES SINCE THE 2011 GUIDELINE CHANGE

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**Background/introduction** Antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* threatens effective treatment and infection control. Treatment guidelines for gonorrhoea are revised when the prevalence of resistance to first-line therapy exceeds 5%; in the UK this last occurred in 2011, prompting a treatment guideline change from cefixime to dual therapy with ceftriaxone and azithromycin.
**Aim(s)/objectives** Describe emerging trends in gonococcal resistance to current and previous first-line therapies using data from the Gonococcal Resistance to Antimicrobials Surveillance Programme (GRASP).
**Methods** GRASP collects *N. gonorrhoeae* isolates from July–September annually from 27 genitourinary medicine clinics in England and Wales. The minimum inhibitory concentration (MIC) of each isolate to seven antimicrobials is determined, then linked to demographic, clinical and behavioural data. Data from 2011–2014 were considered in this analysis. For each antimicrobial, the test for trend in resistance was determined and MIC distributions were compared using the Kolmogorov–Smirnov test.
**Results** In 2014, there was no ceftriaxone resistance (MIC $\geq$ 0.125 mg/L), but the modal MIC drifted to 0.004 mg/L from 0.002 mg/L in 2011 ($p < 0.001$). Azithromycin resistance (MIC $\geq$ 1.0 mg/L) increased from 0.5% in 2011 to 1.0% in 2014 ($p = 0.09$). The prevalence of cefixime resistance (MIC $\geq$ 0.125 mg/L) declined below 5% for the first time since 2011, but the modal MIC drifted from 0.008 mg/L in 2011 to 0.015mg/L in 2014 ($p < 0.001$).
**Discussion/conclusion** Despite the decline in resistance in cefixime, the drifting MIC distribution suggests isolates are less susceptible than previous years. Ongoing monitoring of AMR with strong compliance with national treatment guidelines is essential to retain gonorrhoea as a treatable infection.

## O036 AN OUTBREAK OF HIGH LEVEL AZITHROMYCIN RESISTANT GONORRHOEA IN A UK CITY - ACTIONS TAKEN BY THE CLINICAL TEAM AND LESSONS LEARNT

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**Background** Between November 2014 and March 2015, eight high level azithromycin resistant *Neisseria gonorrhoeae* (NG) isolates (MIC > 256 mg/l) were identified by Sexually Transmitted Bacteria Reference Unit Microbiology Services (STBRU) from our clinic. An Outbreak Control Team was established to actively manage the outbreak. We report the actions and outcomes of the clinical team.
**Immediate actions** Clinicians reminded to take cultures from all exposed sites when NG suspected and before any treatment; first face-to-face contact is most effective in obtaining partner details; TOC at 2 weeks essential. Enhanced PN commenced. Where initial PN incomplete, or withheld, at least two further attempts of face-to-face interview or phone call. TOC non-attendees contacted by phone call and letter, giving further opportunity to pursue PN. Advice sought from STBRU about treating pharyngeal infections to avoid pressure on ceftriaxone by its use as monotherapy. Investigation of how the first eight cases were missed despite clinic systems in place for checking positive NG cultures.
**Outcomes** By December 2015: 16 infected people identified with whole genome sequencing suggesting clonal outbreak. All were heterosexual, most aged 16–20 years. No ethnic or geographic clustering. 12/16 attended for TOC which were negative. 28 contacts disclosed, 16 traceable all attended - 3 NG negative, 13 NG positive, (12/13 azithromycin resistant, 1 NAAT positive but culture negative). PN identified 1 cluster of 4 and 3 clusters of 2
**Lessons learned** NG cultures and sensitivities remain essential to detect antimicrobial resistance. Despite enhanced PN there are many untraceable contacts in young heterosexuals. Clinics need robust administrative systems for timely detection of antimicrobial resistance