(NG). Antimicrobial resistant (AMR) NG is a global public health concern, which may emerge *de novo* or be imported to the UK when individuals infected abroad have subsequent sexual partners at home. We investigated whether patients who reported sex outside the UK ('sex abroad') were more or less likely to be diagnosed with AMR NG.

Methods Logistic regression was used to model the association between reported recent sex abroad and decreased susceptibility (DS) to ceftriaxone (MIC (mg/L)>0.015) and cefixime (0.125) and azithromycin AMR (>1) stratifying by sexual orientation (men who have sex with men (MSM) and heterosexual men and women) from isolates in England and Wales collected within the Gonococcal Resistance to Antimicrobials Surveillance Programme, 2004–2015.

Results Over 10% of MSM and heterosexuals reported sex abroad. Among heterosexuals, infection with a strain of NG with DS to ceftriaxone was associated with sex abroad after adjusting for potential confounders: ceftriaxone (DS prevalence, adjusted odds ratio (95% confidence interval)): 14%, 1.8 (1.3–2.3). Infection with NG DS/AMR to cefixime or azithromycin was not associated with reported sex abroad after adjusting for potential confounders: cefixime 4%, 1.6 (0.9–2.7); azithromycin 2%, 1.5 (0.7–3.3). For MSM, no association was found between infections with DS/AMR NG and sex abroad.

Conclusion In the UK, heterosexuals with NG infection who report sex abroad are at a higher risk of DS to ceftriaxone, suggesting that sex abroad might be the source of some AMR NG within heterosexual networks and highlighting the importance of condom use for travellers. In contrast, DS/AMR NG was not associated with sex abroad among MSM, which might reflect established AMR within MSM networks in the UK. Genetic comparison of these isolates using whole genome sequencing might further elucidate how AMR NG is imported and disseminated in the UK.

O05.6 THE IMPACT OF A RAPID GENOTYPIC *NEISSERIA GONORRHOEAE* ASSAY ON TARGETED CIPROFLOXACIN THERAPY

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10.1136/sextrans-2017-053264.29

Introduction Multidrug-resistant *N. gonorrhoeae* infections are a threat to public health. In November 2015, UCLA Health began routine gyrase A (*gyr*A) genotyping all *N. gonorrhoeae* positive specimens, and reporting genotype and treatment recommendations for wild-type infections. Physicians were educated about wild-type *gyr*A genotypes predicting ciprofloxacin susceptibility. In May 2016 we began sending electronic reminders to providers of genotype results and treatment recommendations.

Methods We reviewed records for all laboratory confirmed *N. gonorrhoeae* cases from January 1st 2015 - November 30th2016. Infections in different anatomic sites were considered unique infections, while unique infections in a single patient on the same date were considered a case. Empiric therapy was defined as treatment within one day of specimen collection.

Results Among 381 patients (32% HIV infected) there were 411 cases and 459 anatomic site-specific *N. gonorrhoeae* infections. Of cases, 290 (71%) were treated non-empirically. The average time to treatment among non-empirically treated cases (n=256) was 5.2 days (SD 4 days). After November 2015, there were 319 infections: 131 (41%) were wild-type *gyr*A genotypes, 92 (29%) mutant, 92 indeterminate and 4 were not attempted. Of the 92 indeterminate results 68 (74%) were from the pharynx, compared to 24 (26%) from other sites (p-value<0.001). Among non-empirically treated cases, ceftriaxone was used in 119 (96%) of 124 before versus 132 (72%) of 184 after assay introduction (p-value<0.001). Among 59 non-empirically treated wild-type *gyr*A infections, 17 (29%) were treated with ciprofloxacin; 2 (9%) of 23 before electronic reminders began compared to 15 (50%) of 30 after (p-value=0.001), six cases had missing data. There was no ciprofloxacin use prior to assay implementation.

Conclusion A large health system successfully implemented routine *N. gonorrhoeae gyr*A genotyping with a reduction in ceftriaxone use. Targeted ciprofloxacin therapy increased with the use of electronic provider reminders.

Oral Presentation Session 6

Host-Pathogen Interactions and Vaginal/Urethral Microbiota

O06.1 INVESTIGATING THE INTERACTION OF THE STEALTH PATHOGEN AND CAUSATIVE AGENT OF SYPHILIS, *TREPONEMA PALLIDUM*, WITH HUMAN PLATELETS

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10.1136/sextrans-2017-053264.30

Introduction *Treponema pallidum* ssp. *pallidum*, the causative agent of syphilis, is a highly invasive pathogen that interacts with a diverse repertoire of host cells during infection. The pathogen invades immunologically privileged sites and crosses the placental, blood-brain, endothelial and blood-retina barriers to establish widespread infection. *Treponema pallidum* disseminates via the circulatory and lymphatic systems, avoiding the prevalent inflammatory reactions raised against other blood-borne pathogens. In this study we investigate if *T. pallidum* uses an interaction with human platelets, key mediators of homeostasis and immune surveillance, to facilitate host persistence. We demonstrate that *T. pallidum* adheres to human platelets enabling survival for an extended period, and we discuss how this interaction may aid *T. pallidum* pathogenesis.

Methods Platelet rich plasma prepared from donor blood was incubated under host-mimicking microaerophilic conditions with viable *T. pallidum*, followed by examination for *T. pallidum*-platelet interactions via darkfield microscopy and flow cytometry analyses. Viability was confirmed using microscopic and fluorescent staining methodologies.