P1.31 THE COSTS OF TARGETED CIPROFLOXACIN THERAPY VS. EMPIRIC THERAPY FOR *NEISSERIA GONORRHOEAE* INFECTIONS OVER A THIRTEEN-MONTH STUDY PERIOD

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10.1136/sextrans-2017-053264.139

Introduction Novel approaches to combating drug-resistant *N. gonorrhoeae* infections are urgently needed. Targeted therapy with ciprofloxacin for susceptible infections has been made possible by the development of a rapid molecular assay for the determination of mutation in the gyrase A gene of *N. gonorrheoae*, which reliably predicts susceptibility to ciprofloxacin.

Methods Using previously collected data over a thirteen-month study period of all *N. gonorrhoeae* cases diagnosed to UCLA Health System, we determined the costs per-test of running the rapid genotypic gyrase A assay and treatment with 500 mg of ciprofloxacin for wild-type infections and compared these estimations with the costs of the standard of care treatment, which is empiric dual therapy with 250 mg ceftriaxone injection and 1000 mg azithromycin. Cost estimates for non-empiric therapy included assay reagents, labour, refrigerator space, and ciprofloxacin 500 mg. Cost estimates for empiric therapy included costs of ceftriaxone 250 mg, injection, azithromycin 1000 g, needle, syringe, and clinic space.

Results There were 167 non-empirically treated anatomic site-specific *N. gonorrhoeae* infections during the thirteen month study period, 51 (30.5%) of which were wild-type, and 49 (29.3%) were mutant. Using the total number of specimens tested (167) we calculated the cost of running the assay per specimen to be $97.4. With an additional cost of $2.2 per pill of ciprofloxacin, the total cost of non-empiric therapy for wild-type infections was estimated to be $99.6. The cost of empiric treatment with ceftriaxone and azithromycin was estimated to be $141, however there may be additional costs of up to $300 based on the clinic facility fees, which vary greatly by location.

Conclusion We found that the genotypic assay with ciprofloxacin therapy among wild-type infections is less costly than empiric therapy. Furthermore, given the consequences ceftriaxone resistance, including continued transmission and the sequela of untreated infection, the true difference in cost may be even greater.

P1.32 HAND-HELD RAPID WHOLE GENOME NANOPORE SEQUENCING TO PREDICT *NEISSERIA GONORRHOEAE* ANTIBIOTIC SUSCEPTIBILITY: STEPS TOWARDS CLINIC BASED TAILORED ANTIMICROBIAL THERAPY

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10.1136/sextrans-2017-053264.140

Introduction Next generation sequencing can accurately predict antibiotic susceptibility in *Neisseria gonorrhoeae* (NG) allowing preservation of first-line treatments in the face of widespread antimicrobial resistance (AMR). The rapid nature of novel hand-held nanopore sequencing (NPS) gives promise for utility at the point of care. We evaluated time to result post DNA extraction, and accuracy of MinION (Oxford Nanopore Technologies) NPS to predict phenotypic antimicrobial susceptibility (PAMS) of NG to ciprofloxacin and azithromycin.

Methods One-directional (1-D) NPS using bar-coded DNA library preparations from 48 NG isolates, prospectively collected from a London clinic, were run on NPS flow cells (3 per R9.0 flow cell) and illumina MiSeq as a comparator. NPS raw sequences were transferred to the cloud for base-calling, alignment, and variant calling using standard tools.

Results Mean time for 1-D library preparation was roughly 1 hour; NPS and alignment took <40 min per sample with single nucleotide polymorphism (SNP) calling adding little extra time. NPS genome coverage was >30X per isolate. Of 48 samples, PAMS to ciprofloxacin, and azithromycin was 74% and 87% respectively. Accuracy of NPS-based genotypic susceptibility, defined as absence of any known AMR-associated SNP's, to predict PAMS for ciprofloxacin and azithromycin, was 34/34 (100%; 95% CI 89.8%–100%) and 35/40 (87.5%; 95% CI 73.9%–94.5%) respectively. Accuracies improved significantly for azithromycin when only high quality reads were included, and with Illumina sequencing. 30 of the 34 isolates susceptible to azithromycin were also susceptible to ciprofloxacin, and 3 of 6 isolates resistant to azithromycin were also resistant to Ciprofloxacin.

Conclusion NPS accurately predicted ciprofloxacin PAMS but was less accurate for azithromycin. With new iterations of the technology, imminent rapid barcoded library preparation (10 min) and rapid DNA extraction from clinical samples, NPS may allow accurate ceftriaxone-adjunctive treatment combinations, for a substantial proportion of patients.

P1.33 MULTIPLEX ASSAY FOR THE DETECTION OF SYPHILIS AND OTHER PATHOGENS ASSOCIATED WITH GENITAL LESIONS USING PLEXPCR

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10.1136/sextrans-2017-053264.141

Introduction Syphilis is a well-known STI caused by the bacterium *Treponema pallidum*. It can result in genital lesions and substantial morbidity and mortality. Recently, there has been an alarming global resurgence of syphilis with infections rising to unprecedented rates. As such, it is increasingly pertinent to test genital lesions for syphilis.Herpes simplex virus types 1 and 2 (HSV-1 and HSV-2) and Varicella zoster virus (VZV) cause lesions in cutaneous and mucocutaneous sites. While HSV-1 and HSV-2 are commonly known to cause genital lesions, recent publications have also found VZV in genital specimens. This unexpected finding suggests that reactivation of VZV in this atypical presentation is not as uncommon as previously believed. Using our highly specific PlexZyme technology that enables efficient multiplexing in real-time PCR (qPCR), we have developed a genital lesion assay for the detection of syphilis, HSV-1, HSV-2 and VZV to facilitate prompt and correct treatment of these STI pathogens.