cetrixone and spectinomycin, respectively, were detected over the time period; 7% of the isolates was resistant to azithromycin in both 2013 and 2015; a high percentage (mean: 59%) of resistance to tetracycline was observed over the whole period. Overall, 42% of the isolates were resistant to three or more antimicrobials.

Conclusion A sharp increase in ciprofloxacin resistance of N. gonorrhoeae was detected, requiring the revision of the current Cameroonian treatment guidelines recommending ciprofloxacin. In addition, multidrug resistant N. gonorrhoeae strains are present in Yaoundé, Cameroon. A national surveillance program to monitor the antimicrobial susceptibility at national level should be installed and supported.

Disclosure No significant relationships.

P665 RAPID SEQUENCE TYPING FOR ANTIMICROBIAL RESISTANCE SURVEILLANCE IN NEISSERIA GONORRHOEAE USING WHOLE GENOME SEQUENCING

1Laura Phillips, 2Adam Wilney, 3Fernando Izquierdo-Carrasco, 4Qing Zhou, 5Simon Mayers, 6Kenneth Laing, 7Tariq Sadiq*, 1St George’s, University of London, Applied Diagnostic Research and Evaluation Unit (ADREU), London, UK; 2St George’s University of London, Institute for Infection and Immunity, UK; 3Oxford Nanopore Technologies Ltd, UK; 4St George’s University of London, UK; 5St George’s University of London, Applied Diagnostic Research and Evaluation Unit (ADREU), Institute for Infection and Immunity, London, UK

Background The Neisseria gonorrhoeae (NG) genome changes by ~4 single nucleotide polymorphisms (SNP) per genome per year, information which is considered when predicting sexual networks using next generation sequencing to type circulating gonococcal strains. Oxford Nanopore Technologies’ MinION provides opportunities for rapid “run-until” sequencing until a target coverage is achieved. We assessed MinION capacity to rapidly predict NG whole-genome strain type, from patients attending a London sexual health clinic, as an aid to rapid turn-around antimicrobial resistance (AMR) surveillance.

Methods One-directional MinION sequencing using bar-coded DNA library preparations from 44 well characterised NG isolates, prospectively collected from clinic, were run on MinION flow cells (version R9.2; three per flow cell) and Illumina MiSeq platform as a comparator. To determine shortest run-time to accurately predict strain type, MinION sequences at various time points and genome coverages were placed on a phylogenetic tree consisting of the same isolates sequenced on the MiSeq platform, clustered with a large European NG reference collection (Euro-GASP).

Results Total library preparation time was approximately one hour per flow cell. Whole genome coverage for MinION sequences varied per isolate as sequencing proceeded at different rates. In 44 isolates, 90 minutes of MinION sequencing produced a median coverage of 21-fold, and was sufficient for 30/44(68%) isolates to achieve <4 SNP differences compared to the corresponding MiSeq sequence. Estimated median SNP distance between the platforms at 90 minutes (of MinION) was 1.9 SNPs (IQR: 0.4–5.9).

Conclusion MinION sequencing enabled the placement of the majority of NG sequences onto the correct location on a reference tree after 90 minutes of sequencing, suggesting that such a method, particularly with newer iterations of the technology and library preparation protocols, might support early identification of sexual networks that support transmission, as well NG AMR surveillance.

Disclosure No significant relationships.