ceftriaxone 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.

P664 *IN VITRO* EVALUATION OF GEPOTIDACIN, AN ORAL ANTIMICROBIAL AGAINST MULTIDRUG-RESISTANT *MYCOPLASMA GENITALIUM*

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Background *Mycoplasma genitalium* has rapidly developed resistance to first-line azithromycin and second-line moxifloxacin. Third-line pristinamycin is difficult to source and only 80% effective. Consequently, there is an urgent need for alternative therapies, and to protect new antimicrobials against development and/or spread of resistance. Resistance-guided therapy and combination with other antimicrobials are important tools. Gepotidacin is a novel, first-in-class triazaacenaphthylene topoisomerase II inhibitor inhibiting DNA replication by a mechanism distinct from fluoroquinolones. Limited studies have shown activity against fluoroquinolone susceptible *M. genitalium* strains

Methods We determined the gepotidacin minimal inhibitory concentration (MIC) and minimal bactericidal concentration (MBC) in 54 *M. genitalium* isolates by the Vero-cell culture method. Macrolide resistance was present in 31 isolates, fluoroquinolone resistance in 18 (33%) isolates; 17 had dual resistance. Synergy testing was performed for gepotidacin and doxycycline by checkerboard titration for four macrolide or dual resistant isolates.

Results Gepotidacin was active against all 54 *M. genitalium* isolates with median and modal MIC of 0.125 mg/L and MIC_{90} at 0.25 mg/L (range ≤0.016–0.5 mg/L). No difference in MIC between macrolide resistant and susceptible isolates (p=0.24) or between fluoroquinolone and dual-resistant and susceptible isolates (p=0.2) was demonstrated. Gepotidacin MBC was available for 45 *M. genitalium* isolates with a median MIC of 0.064 and a median MBC of 0.125 mg/L and all isolates had ≤4 fold difference between MIC and MBC suggesting bactericidal effect. Checkerboard titrations showed synergistic or additive effect with a Fractional Inhibitory Concentration Index (ΣFIC) of 0.5 for two isolates (one macrolide resistant and one dual resistant) and additive effect (ΣFIC at 0.62 and 0.75) for a macrolide and a dual resistant isolate, respectively.

Conclusion Gepotidacin warrants further evaluation in clinical treatment trials for *M. genitalium*. Combination therapy with doxycycline should be clinically studied to assess effect and potential protection against development and/or spread of resistance.

Disclosure No significant relationships.

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

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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 sequencing) 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.

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