Methods Putative GC collected from patients between 2012 and 2015 were confirmed as GC using standard biochemical and serological methods. Susceptibility to eight different antibiotics was determined by Etest. β-lactamase (ßL) activity was determined by nitrocefin hydrolysis. NG-MAST types were determined by standard methods and WGS analysis.
Results Sixty eight out of 90 isolates examined were confirmed as GC. Antimicrobial susceptibility testing showed a high level of resistance to ciprofloxacin (70%) and lower percentages of resistant strains to other common antibiotics. Although 63% percent of isolates were β-lactamase positive by the nitrocefin test, only 70% of these isolates were Pen^R. The other 30% had reduced susceptibility to Pen (Pen^{RS}). Whole Genome Sequencing (WGS) revealed mutations in the bla_{TEM-1B} gene for these Pen^{RS} isolates. These isolates were collected from different clinics, but showed genetic relatedness based on nucleotide polymorphism (SNP)-based analysis. Several novel NG-MAST types were detected among the isolates.
Conclusion These findings highlight the high prevalence of multidrug resistant GC in Peru. The identification of NG-MAST types not identified in surveillance reports from Europe or the United States is important. Further, WGS allowed us to discern false positive β-lactamase isolates by detecting mutations in the bla_{TEM} genes observed in Pen^{RS} isolates and showed the clonally relatedness of these isolates.
Disclosure No significant relationships.

P646 AGENT-BASED MODELLING STUDY OF ANTIMICROBIAL RESISTANT *NEISSERIA GONORRHOEAE* TRANSMISSION

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Background Antimicrobial resistant (AMR) gonorrhoea is a global public health threat. Diagnoses of gonorrhoea have increased in England over the last decade. Guidelines in UK now recommend single dose ceftriaxone, so preserving the efficacy of ceftriaxone is essential. In England, over half of tested isolates remain sensitive to previously recommended drugs, e.g. ciprofloxacin. We evaluate options for improving antibiotic stewardship, through better use of existing surveillance data or new diagnostic tests.
Methods We previously developed an agent-based stochastic network model of gonorrhoea transmission, including ciprofloxacin-sensitive and resistant strains for MSM. This has been modified, to add a heterosexual population and a full model including bridging between MSM and heterosexuals. A novel feature is the time-varying network which breaks and reforms connections within a fixed cumulative network to capture behavioural heterogeneity in duration and number of partnerships. We explored different strategies to facilitate individualised treatment selection, including discriminatory POCT, and selecting treatment based on either index case or partner susceptibility.
Results Our MSM model suggests, based on 50% resistance to ciprofloxacin at baseline, that using POCT to detect ciprofloxacin-sensitive infections could reduce ceftriaxone doses by 70%. If index case susceptibility information were to be used to determine partner treatment, ceftriaxone use could be reduced by 27%. In the heterosexual model, the prevalence is much lower and could only be maintained through assuming higher transmission probability or duration of infection or via bridging to the higher prevalence MSM group.
Conclusion Novel POCT which identify susceptible infections are likely to come to market soon, but are costly. Mathematical models can evaluate the trade-offs between increasing test costs and reduced time to treatment or between delaying treatment to confirm susceptibility and reduce use of ceftriaxone in partners. The flexible model structure will be used in future to implement evolution of resistance and the impact of vaccination.
Disclosure No significant relationships.

P647 EFFECTIVE MONOTHERAPY DUE TO HIGH RATE OF AZITHROMYCIN RESISTANCE IN *NEISSERIA GONORRHOEAE* INFECTION IN MEN IN SOUTH AFRICA

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Background *Neisseria gonorrhoeae* drug resistance has emerged worldwide. There is limited data about the situation in South Africa where syndromic management is used for sexually transmitted infections (STIs). We investigated the antimicrobial resistance profile of *Neisseria gonorrhoeae* infections in high-risk men.
Methods We conducted a cross-sectional study at three primary healthcare facilities in Johannesburg, South Africa. We recruited: (a) men with persistent or recurrent discharge following recent treatment, and b) men-who-have sex with men (MSM) presenting with urethral discharge. Urethral swab and urine were obtained for culture of *Neisseria gonorrhoeae* on New York city medium followed by drug susceptibility testing using E-test with minimum inhibitory concentration (MIC) as per EUCAST guidelines. Molecular diagnostics for STIs were performed using the TIB MOLBIOL Lightmix Kit 480 HT CT/NG assay and real-time PCR assays for *Trichomonas vaginalis* and *Mycoplasma genitalium*.
Results We recruited 48 men of which 30 (63%) had persistent or recurrent discharge and 18 (37%) were MSM. Urine PCR was positive for *Neisseria gonorrhoeae* in 36 men (75%); *Chlamydia trachomatis* was detected in 9 (19%), *Mycoplasma genitalium* in 13 (27%) and *Trichomonas vaginalis* in 6 (13%). Gonococcal cultures were positive for 25/36 men (69%) with *Neisseria gonorrhoeae* detected molecularly. Isolates showed resistance to ciprofloxacin in 60%, penicillin 32% and tetracycline 60%. Reduced susceptibility to azithromycin was identified in 11/25 (44%) isolates: 5 were resistant (MIC range 1–8 µg/ml) and another 6 showed intermediate resistance. All MIC values for the cephalosporins and spectinomycin were within the susceptible range.
Conclusion The observed high rate of azithromycin resistance in *Neisseria gonorrhoeae* infection in our high-risk population is of great concern as it effectively results in monotherapy. These findings add to the debate on the best regimen choice for syndromic management, and emphasize that the introduction of diagnostics is a priority in our setting.
Disclosure No significant relationships.