P660 EXTRA-GENITAL CIPROFLOXACIN-RESISTANT *NEISSERIA GONORRHOEAE* INFECTIONS AMONG SEXUAL-HEALTH CLINIC USERS IN LIMA, PERU

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Background The increasing prevalence of drug-resistant *Neisseria gonorrhoeae* (NG) infections has caused great concern. NG susceptibility to ciprofloxacin can be reliably predicted using a real-time polymerase chain reaction (PCR) assay for the determination of mutation at codon 91 of the gyrase A (*gyr*A) gene. Ciprofloxacin remains the empiric antimicrobial recommended to treat NG infections in Peru, however local data are limited regarding the prevalence of ciprofloxacin resistance.
Methods Clinical swab specimens from pharyngeal and rectal anatomic locations were collected quarterly between 2013 and 2016 from a cohort of men who have sex with men (MSM) and transgender women in Lima, Peru. NG detection was done using Aptima Combo 2 assay (Hologic Inc, USA). NG-Positive samples were selected for DNA extraction using High Pure PCR Template Preparation Kit (Roche Inc, USA). DNA was amplified using a probe-based Real-time PCR assay to determine point mutations at codon 91 of the *gyr*A gene.
Results Overall, 156 individuals had at least one sample that tested positive for NG by the Aptima assay, 61 (39%) of whom reported a previous sexually transmitted infection diagnosis and 50 (32%) were HIV-infected. Of the 80 participants with *gyr*A genotype results available, 67 (84%) had at least one sample with a *gyr*A mutant NG strain; also, 5 individuals alternated between wild type and mutant NG strain infections during follow up in the same anatomical site.
Conclusion We report the prevalence of individuals with extra-genital NG infections with a *gyr*A mutation conferring ciprofloxacin resistance. While most countries of the region recommend ceftriaxone for NG treatment, Peruvian guidelines need to be updated urgently given the high frequency of ciprofloxacin resistance. The use of molecular genetic markers may facilitate surveillance for antimicrobial resistance.
Disclosure No significant relationships.

P662 CELL ENVELOPE DAMAGE OF *N. GONORRHOEAE* AFTER 15-MIN BETA-LACTAM EXPOSURE ENABLES RAPID ANTIMICROBIAL SUSCEPTIBILITY TESTING

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Background Designing diagnostic tools to perform phenotypic antimicrobial susceptibility testing (AST) at the point-of-care (POC) is a vital step in tackling the global threat of antimicrobial resistance. Gonorrhea infections with resistance to the first-line dual therapy have already emerged, highlighting the impending threat of untreatable gonorrhea. A rapid, phenotypic AST could enable evidence-based (instead of empirical) therapy and improve surveillance. The focus of this work is to develop innovative strategies to measure the phenotypic antimicrobial susceptibility of *Neisseria gonorrhoeae* clinical isolates after just 15–30 min of exposure with an antibiotic. We focused on the duration of the exposure step because it remains the bottleneck for phenotypic AST with fastidious and slow-growing microorganisms.
Methods We selected nucleic acid readout because our long-term goals include building fully integrated POC devices that determine the phenotypic response to antibiotic of a specific pathogen rapidly. We have been developing rapid phenotypic ASTs based on quantification of nucleic-acid concentrations in antibiotic-exposed samples. We describe a new phenotypic AST that does not depend on the speed of DNA replication and applies to beta-lactams penicillin, ceftriaxone, and cefixime acting on clinical isolates of *N. gonorrhoeae* very rapidly.
Results Our assay had 100% categorical agreement with the gold-standard agar dilution AST when *N. gonorrhoeae* isolates were incubated for 15-min with penicillin, and 100% categorical agreement when incubated for 30 min with ceftriaxone and cefixime, and steps can be performed within 35 min measured from contrived urine samples exposed to penicillin.
Conclusion By designing techniques which allow us to rapidly determine the antibiotic phenotype, evidence-based prescription of antibiotics will become possible.
Disclosure No significant relationships.

P663 SHARP INCREASE OF CIPROFLOXACIN RESISTANCE OF *NEISSERIA GONORRHOEAE* IN YAOUNDÉ, CAMEROON

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Background We hypothesize that in Yaoundé, Cameroon, the circulating *Neisseria gonorrhoeae* strains would have acquired resistance mechanisms to ciprofloxacin since the availability of the antibiotic under the form of a generic drug formulation in 2012.
Methods We conducted a retrospective study (2012–2017) using data collected at the Centre Pasteur du Cameroun. Antimicrobial susceptibility results of *N. gonorrhoeae* isolates were retrieved from the laboratory information system and the laboratory worksheets. We included results of the disk method for tetracycline, azithromycin, spectinomycin and the minimal inhibitory concentrations (MICs) obtained with the E-test method for penicillin, ceftriaxone and ciprofloxacin. Data on the beta-lactamase activity was included, if available. European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints were applied.
Results Over the years *N. gonorrhoeae* isolates showed resistance towards all tested antibiotics: the MICs of ciprofloxacin shifted to higher concentrations (with MIC90% of 6 mg/l in 2013 to 32 mg/l in 2017) and 84% of the tested strains were resistant in 2017; resistance to penicillin was highest in 2016 (91%) and overall mainly plasmid mediated; the highest MIC values of 1 and 1.5 mg/l for ceftriaxone were detected in 2017 in 2 isolates; a total of 7 and 8 isolates resistant to