discriminating influence were *Lactobacillus*, *Anaerococcus*, and *Staphylococcus*. In crude analysis, cytokines TNF-α/IP-10/IL-10 were elevated among MSWomen ($p<0.05$, each); IL-8 did not differ by group; IL-1β was higher among MSM ($p=0.03$). Cytokine concentration increased in response to *Corynebacterium* (IL-8/TNF-α/IP-10/IL-1β), *Gardnerella* (IL-8/IP-10/IL-1β), *Veillonella* (IL-8/IP-10/IL-1β), and *Peptoniphilus* (IL-8/IL-1β). Microbiome composition did not account for the difference in TNF-α, IP-10, or IL-10 between groups; the difference in IL-1β became non-significant after accounting for taxa. Among MSWomen, IL-1β ($p=0.01$) and IL-8 ($p=0.05$) were elevated if the female partner had BV.

Conclusion To our knowledge, this is the first comparison between MSM and MSWomen of penile microbiome and urinary cytokines. Future studies should examine whether microbiome and mucosal inflammation differences between MSM and MSWomen cause differential risk of HIV/STI acquisition or differential impact on efficacy of HIV/STI interventions.

Disclosure No significant relationships.

P858 2018/2019 SURVEILLANCE UPDATE ON *NEISSERIA GONORRHOEAE* ISOLATES

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Background The global prevalence of antimicrobial resistance (AMR) in Neisseria gonorrhea (GC) is increasing and of specific concern is the emerging resistance to third generation cephalosporins worldwide. In Africa, exceedingly limited AMR data is available. The study determined the AMR in GC isolates a public referral clinics offering HIV and STI testing and treatment to people living in Nairobi and the region

Methods The survey on men presenting with urethral discharge at the special treatment Clinic (STC-Casino Clinic) collected samples from symptomatic men, inoculated on modified Thayer martin media (MTM) and identified by standard bacteriological methods. The MICs of five antibiotics Azithromycin, Gentamycin, ciprofloxacin, cefixime and ceftriaxone are determined by the Etest method (AB Biodisk, Solna, Sweden) and results defined as susceptible, intermediate and resistant. WHO reference strains were used as controls.

Results A total of 153 samples have been collected with 96 samples having tested culture positive, giving a 62.7% prevalence on samples collected from 25th June 2018 to 5th Februry, 2019. The mean MIC of 0.016 was recorded for Azithromycin, cefixime, while a mean MIC of 1.41 and 2.0 was recorded for Ciprofloxacin and Gentamycin respectively. The MIC range for Ciprofloxacin and Gentamycin was from 0.004 to 6 and from 0.125 to 8 respectively.

Conclusion This is a continuous study on the Gonoccocal surveillance program to describe antimicrobial resistance profiles of antibiotics used in the region. It confirms that N. gonorrhea isolates from Nairobi in 2018 possessed high level resistance to Ciprofloxacin an antimicrobials previously recommended for the treatment of gonorrhea. Cefixime, ceftriaxone and azithromycin are still useful drugs for treatment of gonococcal infections in Kenya. The outcome of this study together with other additional studies will enable revisions of the gonorrhea treatment guidelines in Kenya and support in antimicrobial resistance in the region.

Disclosure No significant relationships.

P859 GENOTYPING *gyr*A AND *pen*A FROM REMNANT *NEISSERIA GONORRHOEAE* POSITIVE CEPHEID XPERT® CLINICAL SPECIMENS

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Background *Neisseria gonorrhoeae* (NG) has developed resistance to most antibiotics, making it increasingly difficult to treat. Molecular methods have been used to predict antimicrobial susceptibility based on the *gyr*A codon serine 91 and the mosaic XXXIV allele on the penicillin-binding protein 2 (*pen*A) gene using Roche Cobas and APTIMA clinical specimens. We aimed to determine if the same methods could be successfully used on remnant NG-positive Cepheid Xpert® specimens.

Methods We tested NG-positive pharyngeal, rectal, and vaginal/urine specimens from adolescents aged 14–24 years. We extracted 100uL DNA from each sample using the Roche® MagNA Pure. The Roche LightCycler® 480 was used to genotype *gyr*A and *pen*A in a multiplex PCR using high resolution melt curve analysis. The fluorescent labels of the detection probes for the *pen*A mosaic XXXIV target (Cyanine-5 dye) differed from that of *gyr*A (LightCycler® 640 probe) so that both genes could be detected simultaneously at various wavelengths. We used isolates with previously confirmed presence of the NG mutant *gyr*A, NG wild type *gyr*A, and mosaic *pen*A XXXIV allele for internal controls.

Results Of the clinical specimens, 62% (38/61) were successfully genotyped. Urine specimens were most likely to be genotyped (5/6, 83%) followed by rectal (19/26, 73%), pharyngeal (12/24, 50%), and vaginal specimens (2/5, 40%). Of the 38 genotyped specimen, 8 had the *pen*A XXXIV allele (2/26 rectal, 6/24 pharyngeal) and 16 had a mutated *gyr*A (10/26 rectal, 3/24 pharyngeal, 2/6 urethral, 1/5 vaginal). Of the 8 *pen*A XXXIV positive specimens, 6 were *gyr*A indeterminate, 1 was *gyr*A wild type, and 1 was *gyr*A mutant. Of the 30 specimens without the *pen*A XXXIV mosaic allele, 15 were *gyr*A wild type and 15 were *gyr*A mutant.

Conclusion Genotyping specific NG genes from Cepheid Xpert® clinical specimens was feasible. Our study was limited by its small sample size and lack of concurrent antimicrobial testing.

Disclosure No significant relationships.

P861 NOVEL MUTATION CONFERRING HIGH-LEVEL AZITHROMYCIN RESISTANCE IN *NEISSERIA GONORRHOEAE*

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Background Azithromycin resistance in *Neisseria gonorrhoeae* has been attributed to several resistance-associated mutations