P855 MULTI-PEPTIDE ELISAS OVERCOME CROSS-REACTIVITY AND INADEQUATE SENSITIVITY OF *CHLAMYDIA TRACHOMATIS* AND *C. PNEUMONIAE* SEROLOGY

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Background *Chlamydia* spp. serology is compromised by cross-reactivity of classical antigens. For specific detection of anti-*trachomatis* (Ctr) and anti-*C. pneumoniae* (Cpn) antibodies, we developed and validated novel peptide ELISAs.

Methods Strongly reactive peptide antigens of 24 Ctr- and 48 Cpn-specific B-cell epitopes of multiple immunodominant chlamydial proteins were used in this study. For specific detection of anti-Ctr and anti-Cpn antibodies, 185 human sera were tested in colorimetric ELISAs with mixtures of 12–24 Ctr or Cpn peptide antigens using polyclonal anti-human IgG-HRP conjugates. For comparative evaluation, these sera were tested with 4 Ctr and 4 Cpn commercial IgG ELISAs.

Results In commercial ELISAs, Ctr and Cpn individual serum reactivity was 54% biased towards positivity for both species (co-positivity), but unbiased in Ctr and Cpn peptide antibody assays. This finding suggested a severe specificity problem (cross-reactivity) of commercial ELISAs, but not peptide assays. Using hyperimmune mouse sera against each of 11 *Chlamydia* spp., we confirmed that commercial Ctr and Cpn ELISA antigens are cross-reactive among all *Chlamydia* spp., but Cpn and Ctr peptide antigens react specifically only with antisera against the cognate chlamydial species. By comparison at 90% specificity to a Ctr-peptide composite reference standard (CRS) for human anti-Ctr antibody status, the Ctr mixed peptide assays showed 86–83% sensitivity, significantly higher than the 59–34% sensitivity of 4 commercial anti-Ctr ELISAs. Relative to a Cpn-peptide CRS, the Cpn mixed peptide assay showed 86–80% sensitivity at 90% specificity, significantly higher than the 48–25% sensitivity of 4 commercial anti-Cpn ELISAs.

Conclusion For detection of anti-Ctr and -Cpn antibodies, commercial ELISAs are not suitable due to cross-reactivity. In contrast, mixed peptide assays are accurate with simultaneous high specificity and sensitivity, and reliably determine anti-Ctr and anti-Cpn antibody prevalence. With convenient use for non-specialized laboratories, these peptide ELISAs will improve Ctr and Cpn serodiagnosis.

Disclosure No significant relationships.

P856 PRIVACY AND TECHNOLOGY FOR YOUNG BLACK MEN WHO HAVE SEX WITH MEN IN THE SOUTHERN US RELATED TO SEXUAL CARE AND RESEARCH

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Background Technology, such as text messaging and mobile apps, has been integrated into health care. Technology preferences of underrepresented young black men who have sex with men (YB MSM) remain unknown but likely influence the use of health care services. The objective was to query the preferences of YB MSM related to technology regarding sexual health care and research. We hypothesized that YB MSM

would prefer the use of social media and mobile applications (apps).

Methods We recruited YB MSM in Birmingham, Alabama to participate in a discrete choice analysis of sexual health preferences. Participants were given a link to an electronic survey, which queried their sociodemographic status and preferences for STI testing and research. We specifically queried the use of technology to notify of STI results and recruit for research in addition to privacy concerns.

Results 33 YB MSM met criteria: median age was 28, most were homosexual (n=27, 82%) and the remaining bisexual, 17 (52%) had HIV, 24 (73%) reported a prior STI, 16 (48%) live below the state federal poverty level, and 11 (33%) were uninsured. When asked, the best and worst way to be contacted with STI testing results, 21/33 (64%) preferred phone notification. Further, (52%) and (39%) said texting and email were the worst option, respectively. When asked the best way to recruit YB MSM for sexual health research, 16/33 (48%) reported social media. The most frequently recommended social media sites were Facebook (33%) and Instagram (27%). When asked their greatest concern about STI testing, 8/33 (24%) reported privacy concerns. None expressed concerns about limited access to technology.

Conclusion YB MSM in the Southern U.S. prefer social media and mobile apps for research recruitment but not for communication about personal health. When it comes to STI testing, privacy remains a significant concern for YB MSM.

Disclosure No significant relationships.

P857 PENILE MICROBIOME AND URINARY CYTOKINES OF KENYAN MEN WHO HAVE SEX WITH MEN AND MEN WHO HAVE SEX WITH WOMEN

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Background MSM are disproportionately affected by HIV and STIs compared to men who have sex with women (MSWomen). This may be due in part to different burden of mucosal inflammation. We compared penile microbial composition between MSM and MSWomen and association with mucosal inflammation.

Methods In this cross-sectional study, we enrolled 43 MSM and 43 MSWomen, who were HIV negative and matched on age and circumcision status. The penile microbiome was assessed via meatal swab, with 16S rRNA gene amplicon sequencing. Urinary cytokine concentrations (TNF- α /IL-1 β /IL-8/IL-10/IP-10) were measured using Luminex. Random Forest (RF) identified genus-level taxa differing between MSM and MSWomen. Taxa from RF were regressed on cytokine outcomes, with multiple testing correction and information criterion model selection.

Results Men were median age 24 and 77% circumcised. There were substantial differences in educational attainment, employment, alcohol and drug use, condom use, and number of sexual partners, with MSM having greater behavioral risks. Microbiome composition differed markedly between MSM and MSWomen: RF discriminated between MSM and MSWomen with 84% accuracy. Taxa with greatest

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-1 β was higher among MSM ($p = 0.03$). Cytokine concentration increased in response to *Corynebacterium* (IL-8/TNF- α /IP-10/IL-1 β), *Gardnerella* (IL-8/IP-10/IL-1 β), *Veillonella* (IL-8/IP-10/IL-1 β), and *Peptoniphilus* (IL-8/IL-1 β). Microbiome composition did not account for the difference in TNF- α , IP-10, or IL-10 between groups; the difference in IL-1 β became non-significant after accounting for taxa. Among MSWomen, IL-1 β ($p = 0.01$) 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 February, 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 Gonococcal 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 *gyrA* AND *penA* FROM REMNANT NEISSERIA GONORRHOEAE POSITIVE CEPHEID XPRT® 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 *gyrA* codon serine 91 and the mosaic XXXIV allele on the penicillin-binding protein 2 (*penA*) 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 *gyrA* and *penA* in a multiplex PCR using high resolution melt curve analysis. The fluorescent labels of the detection probes for the *penA* mosaic XXXIV target (Cyanine-5 dye) differed from that of *gyrA* (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 *gyrA*, NG wild type *gyrA*, and mosaic *penA* 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 *penA* XXXIV allele (2/26 rectal, 6/24 pharyngeal) and 16 had a mutated *gyrA* (10/26 rectal, 3/24 pharyngeal, 2/6 urethral, 1/5 vaginal). Of the 8 *penA* XXXIV positive specimens, 6 were *gyrA* indeterminate, 1 was *gyrA* wild type, and 1 was *gyrA* mutant. Of the 30 specimens without the *penA* XXXIV mosaic allele, 15 were *gyrA* wild type and 15 were *gyrA* 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