P685 EVALUATION OF EXTRAGENITAL SWABS FOR SIMULTANEOUS *NEISSERIA GONORRHOEAE* CULTURE AND NUCLEIC ACID AMPLIFICATION TESTING

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Background Nucleic acid amplification testing (NAAT) has replaced culture as the predominant test for *Neisseria gonorrhoeae* (GC). However, antimicrobial susceptibility testing requires culture. We assessed whether a single swab specimen could be used for both NAAT and culture testing for GC.
Methods From May to December 2018, we collected paired specimens from patients presenting to the municipal STD clinic in Seattle, WA who met clinical criteria for gonorrhea culture. One specimen was collected using the BBL CultureSwab plus Amies Gel with Charcoal and one was collected using the Aptima collection kit. Approximately half of BBL specimens were collected by clinicians and half were self-collected by patients. BBL specimens were sent to the laboratory at ambient temperature where they were cultured for GC and then processed and tested using Aptima Combo 2. The second swab was placed in an Aptima transport tube and processed according to the manufacturer's instructions (clinical NAAT). We calculated the agreement between Aptima GC test results among clinical and BBL specimens and the sensitivity of BBL NAAT using the clinical NAAT result as the gold standard.
Results We collected 109 paired rectal specimens (53 clinician-collected and 56 patient-collected) and 104 paired pharyngeal specimens (49 clinician-collected and 55 patient-collected). Twenty-nine (27%) rectal specimens and 19 (18%) pharyngeal specimens were culture positive. Among rectal specimens, 44 (40%) clinical NAATs and 33 (30%) BBL NAATs were positive (90% agreement, BBL 75% sensitive). Among pharyngeal specimens, 59 (57%) clinical NAATs and 39 (38%) BBL NAATs were positive (81% agreement, BBL 66% sensitive). None of the BBL specimens tested positive in the absence of a paired positive clinical NAAT. The sensitivity of NAAT of BBL specimens did not vary substantially between clinician and patient collected specimens.
Conclusion Aptima testing of BBL CultureSwab specimens collected in Amies Gel with Charcoal is insensitive for GC.
Disclosure No significant relationships.

P686 THE ENHANCED SURVEILLANCE OF ANTIMICROBIAL-RESISTANT GONORRHEA (ESAG) IN CANADA

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Background Gonorrhea (GC) is the most commonly reported drug resistant sexually transmitted infection (STI) in Canada with 23,708 cases reported in 2016, double the 11,874 cases reported in 2007, corresponding to an 81% increase in rates. Only about 19% of these were cultured, meaning that direct AMR data was only available for one-fifth of GC cases. The Public Health Agency of Canada (PHAC) launched the Enhanced Surveillance of Antimicrobial-Resistance Gonorrhea (ESAG) program in 2013 in three jurisdictions (Alberta, Manitoba, and Nova Scotia) in order to improve the understanding of current trends of AMR-GC. This enhanced laboratory-epidemiological linked surveillance program collects data not available via its existing routine and laboratory surveillance.
Methods All cultures and data from participating jurisdictions are included in the surveillance program. The National Microbiology Laboratory performs antimicrobial susceptibility testing for a panel of antimicrobials and sequence typing. Enhanced epidemiological data collected includes treatment information and risk factors.
Results From 2014–2017, ESAG captured 2767 cultures from 2566 cases. The majority of the cases were male (81%) and less than 40 years old (83%). There was a 25% decrease from 2014 to 2017 in the number of cases from men who have sex with men. The proportion of isolates demonstrating resistance to at least one antibiotic agent steadily increased from 2014 (54%) to 2016 (66%), dropping to 58% in 2017. Large declines in decreased susceptibility to both cefixime (91%) and ceftriaxone (88%) and increasing rates of resistance to azithromycin were observed.
Conclusion ESAG data for 2014–2017 demonstrated decreased susceptibility to the preferred therapy antimicrobials, suggesting that resistance to these key antimicrobials could complicate GC treatment considerably in the future. The expansion of ESAG remains a priority with negotiations currently underway with the remaining jurisdictions with the goal national representation.
Disclosure No significant relationships.

P687 SEXUAL NETWORK AND GENOTYPIC ANALYSIS OF AN OUTBREAK OF GONORRHEA IN WINNIPEG, CANADA

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Background Alongside traditional epidemiologic tools, network analyses and molecular epidemiology offer deeper insights into the structure of STBBI epidemics. In the context of a 2014 gonorrhea (NG) outbreak, this study sought to compare molecular networks to case-contact networks constructed from public health investigations.
Methods Data were from enhanced public health investigations of NG in Winnipeg, Canada. NG-MAST was used to determine the molecular subtypes of NG. Subtypes were described by socio-demographic/clinical characteristics. Multivariable logistic regression models were used to assess the association of socio-demographic/clinical characteristics, and having the most frequently reported subtype. Networks constructed from case-contact investigations were visualized; components were characterized with univariate network statistics, including degree centralization. Conditional uniform graph (CUG) tests assessed observed degree centralization.
Results In total, 126 NG cases were genotyped, with 41 subtypes found. Five subtypes accounted for 51% of all subtypes,