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,

with ST-3672 (n=22) predominant. At the bivariate level, infection with ST-3672 was associated with younger age (62% of those infected were 15–19 years old, p=0.002), and chlamydia co-infection (67% vs 37%, p=0.012). In multivariable analysis, age group remained significant, while an interaction between inner-core residency and chlamydia co-infection was detected. Case-contact networks were highly-fragmented, consisting mainly of dyads and triads. Of 85 components, the largest component included 6 nodes, while 61% were dyads. CUG testing indicated in-degree centralization was lower than expected (p<0.05). Genotyping combined with case-contact data increased the potential size and geographic reach of each component. Of potential components found after incorporating subtypes, 32% (10/33) were dyadic, with the largest component consisting of 45 nodes.
Conclusion Molecular data revealed connections that were not apparent from case-contact investigations alone, leading to more cases potentially linked together, and over a wider geographic area. A handful of subtypes were responsible for the majority of infections. Early identification of dominant subtypes may potentially curtail transmission of NG.
Disclosure No significant relationships.

P688 RECENT INCREASES IN RATES OF GONORRHEA IN TORONTO, ONTARIO, 2012–2018

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Background In Toronto, gonorrhea is the second most commonly reported sexually transmitted infection, after chlamydia. From 2000 to 2012, rates of gonorrhea in Toronto were stable, ranging from 56/100,000 to 72/100,000. However, rates started to rise in 2013. In 2018, rates increased by 37% from 2017, the largest observed annual increase since 2000, reaching a high of 158/100,000. This study aimed to describe gonorrhea trends in Toronto between 2012 and 2018.
Methods Data for gonorrhea cases reported between 2012 and 2018 were extracted from the integrated Public Health Information System on January 29 2019. Analyses were conducted in SAS 9.4.
Results In 2018, 4,549 gonorrhea cases were reported in Toronto, 135% higher than 1,939 cases (71/100,000) reported in 2012. The increase was driven by a rise in reports among males, increasing by 192% while females increased by 24%; males comprised 81% of cases in 2018. Males most commonly reported engaging in sex with men (MSM), and the proportion with this risk factor increased from 55% in 2012 to 69% in 2018. Conversely, the proportion of males reporting sex with women declined from 25% in 2012 to 17% in 2018. Females in 2018 most commonly reported not using a condom (77%) in the last sexual encounter, slightly higher than 2012 (71%). In 2018, 38% of cases (44% of males, 9% of females) had rectum and/or pharyngeal gonorrhea, higher than 20% of cases in 2017.
Conclusion The rising rates in gonorrhea, particularly among MSM, may be due to changes in screening guidelines in 2013 that included extragenital screening of gonorrhea. In April 2018, both rectal and pharyngeal specimens were approved for Nucleic Acid Amplification Testing in Ontario, potentially playing a role in the additional increase in 2018. This study demonstrates that it is important that physicians continue to screen for extragenital gonorrhea among MSM.
Disclosure No significant relationships.

P689 TURNING GONORRHEA AGAINST HIV: LATENT HIV 'SHOCK-AND-KILL' USING A GONOCOCCAL-DERIVED METABOLITE

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Background Clinical studies have long indicated that a pathological synergy exists between *Neisseria gonorrhoeae*and HIV, with gonococcal infection increasing HIV transmission between HIV serodiscordant sexual partners. In trying to understand this association, we discovered that *N. gonorrhoeae* liberate a small molecule that stimulates HIV replication from latently infected CD4+ T cells. This led to our discovery that heptose phosphate (HP)-containing metabolites, 7-carbon phospho-sugars not produced by animals, serve as a molecular cue that bacteria are present in the tissues and elicit an NF-κB-dependent transcriptional response. Based upon these observations, this study aims to test the hypothesis that HP can function both to (i) drive the virus from latency and (ii) stimulate the antiviral response to work in synergy with available highly active antiretroviral therapies to cure HIV infection.
Methods We have used a combination of cell line and primary human leukocyte-based models to test the effect of natural and synthetic analogues of HP to stimulate HIV from latency, both alone and in combination with potential latency reversing agents, and to understand their effect of HPs on different leukocytic populations that have potential to either promote or inhibit HIV infection.
Results We show that HP has a superior combination of HIV latency reversal without toxicity often evident with conventional LRAs, and HP activity synergizes with other LRAs such that these can be administered at lower concentrations. Finally, we observed that HP stimulates primary human leukocytic responses with anti-viral potential.
Conclusion Our findings suggest that HP-based agonists are a novel LRA capable of both driving HIV from latency and stimulating immune responses so as to help control the infection. By virtue of its synergy with other LRAs and clinically available anti-retroviral agents, this represents an enticing new avenue in ongoing efforts to develop a cure for established HIV infection.
Disclosure No significant relationships.

P690 ESTABLISHMENT OF THE GONORRHEA MOUSE MODEL FOR PRE-CLINICAL TESTING OF ANTIBIOTICS THAT FOLLOW THE PK DRIVER FAUC/MIC

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Background New antibiotics for gonorrhea are needed due to the emergence of resistance to extended-spectrum cephalosporins in *Neisseria gonorrhoeae* (*Ng*). We recently established the 17β-estradiol mouse model of gonococcal lower genital tract