Epidemiology of Clostridioides difficile Infection in Canada: A six-year Review of Provincial Surveillance Data

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Two vaccines against Clostridioides difficile infections (CDI) are currently in phase III trials. To enable decision-making on their potential use in public health programs, national disease epidemiology is necessary. This study aims to determine the epidemiology of hospital-acquired CDI (HA-CDI) and community-associated CDI (CA-CDI) in Canada, using provincial surveillance data from ten Canadian provinces and provide a comprehensive discussion of current provincial surveillance programs. **Methods:** We used publicly-available CDI provincial surveillance data from 2011 to 2016 with the most common surveillance definition for each province. Pooled HA-CDI incidence rates and CA-CDI proportions (%) were calculated for each province. Both HA-CDI and CA-CDI incidence rates (IRs) were examined for trends. **Results:** Data from Manitoba were excluded given the substantial differences in the surveillance definition. HA-CDI rates from other provinces ranged from 2.1 – 6.5/10,000 inpatient-days, with a decreasing trend over time, while available data on CA-CDI show that both rates and proportions have been increasing over time. The absence of a common case definition for CDI surveillance is problematic and impacts both the number of cases and denominators reported. Discrepant denominators were identified as a major problem. **Conclusion:** There is a need for a nationally adopted common case definition for CDI, CDI classification, and common methods for total inpatient-days determination. We also need a quality assessment system to ensure that standardized and quality data are reported. This study highlights the limitations of current provincial CDI surveillance, in particular, when attempting to calculate a pan-Canadian burden of illness.
Detection of *Pneumocystis jirovecii* with qPCR to Differentiate Between Colonization and Pneumonia

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**Background and Objectives:** Pneumocystis pneumonia (PCP) is an opportunistic infection caused by the fungus *Pneumocystis jirovecii* (*Pj*). Diagnosis of PCP remains difficult and relies on microscopic methods with low sensitivity (direct immunofluorescent assay-DFA). Our study objective was to evaluate the use of qPCR to differentiate *Pj* infection from colonization and to investigate clinical and laboratory characteristics of patients with PCP.

**Methods:** We screened 415 consecutive bronchoalveolar lavage (BAL) specimens collected between January 2013 and September 2017 for *Pj* using a qPCR targeting the mitochondrial large subunit (mtLSU) gene. *Pj*-positive specimens were further assayed with a qPCR targeting a cyclin-dependent kinase (CDC-2) gene. Two Infectious Diseases physicians, blinded to qPCR values, performed standardized retrospective chart review to classify patients as PCP or *Pj* colonized. Cycle threshold values (Ct) estimating fungal burden were compared to clinical diagnosis as the reference standard. **Results:** *Pj* was detected by mtLSU-qPCR in 59 patients, in whom PCP was diagnosed in 13 patients by a combination of clinical and laboratory criteria excluding qPCR. DFA diagnosed PCP in 8 and qPCR was positive in all 13 patients. Ground-glass and interstitial changes on chest radiography were more frequent in PCP (*p* < .01). Higher fungal burden was found in PCP compared to colonized patients using mtLSU target (median Ct 26 and Ct 35 respectively; *p* < .01) and using CDC-2 target (median Ct 36 and Ct 39 respectively; *p* < .01). The thresholds corresponding to a specificity of 100% were 21 for mtLSU and 32 for CDC-2 target. **Conclusions:** qPCR showed value diagnosing PCP in 5 additional patients compared to DFA. Clinical context is important in interpretation of indeterminate qPCR results. Further work to identify Ct values for diagnosis of PCP is needed.
Novel metabolomics approach for the diagnosis of respiratory viruses directly from nasopharyngeal specimens

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Objectives: Respiratory virus infections, including influenza A and B, are important causes of morbidity and mortality among pediatric and adult patients. These viruses infect respiratory epithelial cells, where they may induce metabolite alterations. As a proof-of-concept, we investigate the novel use of liquid chromatography (LC) combined with mass spectrometry (MS) for the study of host cell metabolite alterations to diagnose and differentiate respiratory viruses. Methods: We studied nasopharyngeal swab samples positive for respiratory viruses by multiplex reverse transcriptase-polymerase chain reaction assay (RT-PCR) (GenMark Diagnostics, Carlsbad, CA). Banked, frozen samples (-80°C) stored in viral transport media were retrieved and thawed. Aliquots of 100µL were centrifuged at 13.3 x g for 15 minutes and analyzed by Agilent 6545 Quadrupole Time-of-Flight (Q-TOF) LC/MS (Agilent Technologies, Santa Clara, CA). Agilent Mass Profiler 3D principal component analysis was performed, and compound identification was completed using the METLIN metabolite database. Results: A total of 130 samples were tested by Q-TOF LC/MS, including 120 positive samples [10 samples of each including adenovirus, coronavirus, influenza A H1N1 and H3N2, influenza B, human metapneumovirus, parainfluenza viruses 1, 2, 3, and 4, respiratory syncytial virus (RSV), and rhinovirus] as well as 10 negative clinical specimens. Q-TOF LC/MS allowed identification of key metabolites that distinguished all virus positive samples compared to the negative group, as well as differentiating these respiratory viruses from one another including between influenza A H1N1 and H3N2 subtypes. Conclusions: Preliminary data from our Q-TOF LC/MS analysis show that respiratory viruses exhibit different host cell metabolomic profiles that allow viral differentiation to the species level, and for influenza A virus, the subtype level. This metabolomic approach has substantial potential for diagnostic applications in infectious diseases directly from patient samples and may be eventually adapted for point-of-care testing.
Applying a Next-generation Sequencing Pipeline in a Clinical Microbiology Laboratory for Surveillance and Outbreak investigations: Defining the Genomic Epidemiology of Klebsiella aerogenes and Identifying Determinants of Carbapenem Resistance and Virulence

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Background: Next-generation sequencing (NGS) is a powerful resource to clinical microbiology laboratories for surveillance and outbreak investigations. Two temporally spaced clusters of carbapenem-resistant K. aerogenes (CR-KA) isolates (n=15, 2017; n=3, 2018) from patients admitted to a cardiac intensive care unit (CICU) were prospectively investigated to identify genetic relatedness, population structure, and determinants of carbapenem resistance and virulence. Methods: 31 patient strains (18 CICU-associated, 13 other wards) were sequenced (Illumina Miseq) and analyzed by a modular, in-house bioinformatics pipeline designed to flexibly address multiple clinical applications. A modified CFSAN-SNP module performed Hq-variant calling and markers corresponding to MLST, antibiotic resistance and virulence factors were identified using curated databases. Comparative genomics of local and global strains (publicly available K. aerogenes genome assemblies, n=111) was assessed using Harvest and Kleborate suites. Results: Phylogenomic analyses indicated that every CICU-associated CR-KA isolate was part of a clonal cluster (<9 SNPs apart), indicating protracted intra-ward transmission. No clonal relationships were observed between the CICU isolates and those from other hospital wards. Genes encoding carbapenemases were not detected and carbapenem resistance was attributed to mutations impacting AmpD activity and membrane permeability. The CICU strains harbored an integrative conjugative element (ICEKp10) that is associated with hypervirulent Klebsiella pneumoniae lineages. Comparative genomics showed the outbreak-associated strains to group closely with global ST4 strains, which may represent a dominant K. aerogenes lineage associated with human infections. Conclusion: Along with high-resolution tracking of transmission events and assessment of the effectiveness of infection control measures, NGS facilitates investigation of cryptic drug-resistance and virulence. For poorly characterized pathogens, scaling analyses to include sequenced genomes from public databases offers tremendous opportunity to identify emerging trends and dominant clones associated with specific attributes, syndromes and geographical locations.
Investigation of the Presence and Impact of Environmentally-Adapted *Escherichia coli* in Private Well Water in Southeastern Ontario

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**Background:** The fecal contamination of drinking water causing acute gastrointestinal illness remains a threat to public health in Canada, including Ontario. To determine potability, water is assessed for the presence of fecal indicator bacteria (FIB) to indicate contamination with harmful fecal pathogens. *Escherichia coli* remains the most frequently employed FIB, given it is a natural inhabitant of the gastrointestinal tract (GIT) of warm-blooded animals. The use of *E. coli* as a FIB has been questioned in recent years with the identification of populations of environmentally adapted *E. coli* capable of surviving outside of the GIT and thus do not represent a recent fecal contamination event. **Methods:** A total of 325 *E. coli* isolates from southeastern Ontario private wells were characterized by comparing their phylogenetic origin using Clermont phylotyping, and identifying unique genetic fingerprints through qPCR. Six accessory genes previously shown to distinguish environmentally-adapted from fecal *E. coli* in surface water were investigated, including *iutA*, *ccdB*, *clpXET1*, *hra1*, *phd* and *tratT*. For comparison, 234 isolates from animal feces were also characterized. **Results:** Of the 76 private wells analyzed, 66% had evidence of environmentally adapted-*E. coli*. Further, 37% of these same wells had only environmentally adapted strains in the subset of *E. coli* isolates selected. Environmentally adapted *E. coli* were determined to have originated from several distinct phylogroups, including B1, B2, A, D and cryptic clades III-V. **Conclusions:** Environmentally-adapted *E. coli* are common in private well water in southeastern Ontario and come from several phylogroups. This has potential implications for *E. coli* as a FIB and for water quality testing methodologies and interpretations. The potential health risk associated with drinking water containing environmentally-adapted populations of *E. coli* is not understood. Current work includes assessing these environmentally adapted strains in the context of virulence, disease and as potential reservoirs of antimicrobial resistance genes.
ORAL PRESENTATIONS
Thursday, April 4, 2019
11:15 – 12:30 Session B
Room: Governor General II

B01

WITHDRAWN
Evaluation of Five Commercial Nucleic Acid Tests for Bacterial Gastroenteritis in Alberta, Canada

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Objective(s): Compare the performance of commercial nucleic acid tests (NATs) for enteric bacteria in Alberta, Canada. Methods: BD Max Enteric Bacterial Panels, Fast-Track Diagnostics Bacterial Gastroenteritis, Prodesse Progastro SSCS, RidaGene Bacterial Stool Panel I and EHEC/EPEC, and Seegene Allplex Gastrointestinal Panels were used to test both patient feces and contrived specimens representing circulating serotypes and species in Alberta (see table for organisms in contrived specimens). Patient fecal samples that were culture-negative (n=46) and positive for Campylobacter (n=40), Salmonella (n=40), Shigella (n=15), shiga toxin(stx)-producing E. coli (STEC) (n=20), or Y. enterocolitica (n=10) were tested. Clinical specimens with a false negative NAT result were retested with the DNA extract; if the repeat result was negative, the original specimen was re-extracted and tested. Contrived specimens with false-negative results on a NAT were repeated with the specimen and/or isolate suspension. Results: Based on consensus (minimum two positive NATs), the percent agreement of the NATs for each organism result were as follows: Shigella 100%, Salmonella 97.6-100%, Campylobacter 95-100% (n=5 C. coli, n=35 C. jejuni), STEC 90-100%, Y. enterocolitica 70-90%, negative for these five targets 78.5-100%. The following isolates in the contrived specimen panel were missed by the denoted assays: C. upsaliensis (all NATs), Y. non-enterocolitica spp. (all NATs), stx2f (all except RidaGene), stx1d (Prodesse). Conclusion: Commercial NATs reliably detect Salmonella, Shigella, C. jejuni, C. coli and the most prevalent STEC subtypes with the exception of Yersinia spp.

Organism | Isolates in contrived specimen panel
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Salmonella (n=25) | Predominant serotypes from human (n=20) and food sources (n=5).
Shigella (n=19) | S. flexneri, dysenteriae, and boydii serotypes isolated >twice in Alberta 2009-2016 (n=18). S. sonnei (n=1).
STEC (n=10) | 1a/2a;1c/2b;1d/2a;2b/2e;2d;2e;2f;2g
Campylobacter (n=4) | C. coli, upsaliensis, jejuni subsp jejuni and doylei.
Yersinia (n=9) | Y. rohdei, federiksenii, intermedia, and pseudotuberculosis (n=4). Different Y. enterocolitica serotypes (n=5).
Comparison of Prevalence of Pathogenic Protozoa in Stool Samples Using Molecular testing Compared to Traditional Microscopy

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Background: Giardia intestinalis, Cryptosporidium spp. and Entamoeba histolytica are the most common diarrhea-causing parasitic protozoa. Diagnosis of these parasites is usually performed by microscopy; however, at our institution, a molecular platform was implemented as a primary diagnostic test for detection of parasitic protozoa. Objective: To compare the positivity by PCR testing in the detection of pathogenic protozoa to the positivity using Microscopy. Method: Data for Microscopy results for the period 2016-2018 were compared to the results of PCR using Seegene Allplex PCR technology. Microscopy was performed on stool samples received in SAF. Concentrated specimen and direct smears were performed for the detection of protozoan cysts, helminth eggs and larvae in small numbers. A Kinyoun/Hematoxylin stain was used for the detection and identification of protozoan cysts and trophozoites including Cryptosporidium and Cyclospora. PCR testing was performed using Allplex Seegene technology. Stool samples for molecular testing were collected in Copan swabs with Cary Blair. Results: A total of 190,817 specimens were tested using microscopy over 3 years from 2016-2018. Blastocystis hominis had the highest prevalence at 5.22% positivity, followed by Dientamoeba fragilis at 2.84%, Giardia intestinalis at 0.90%, Entamoeba histolytica/dispar at 0.62%, Cyclospora spp at 0.19% and Cryptosporidium at 0.11%. PCR testing as primary diagnostic testing started in late 2017. Total number of specimens tested by PCR was 89,928. The prevalence of pathogenic protozoa were as follows: Blastocystis hominis 10.92%, Dientamoeba fragilis 5.55%, Giardia intestinalis 1.45%, Entamoeba histolytica 0.03%, Cryptosporidium 0.67% and Cyclospora spp 0.17%. Conclusion: Detection of pathogenic protozoa in stool samples is higher using molecular testing for primary testing compared to the microscopy for most protozoa except for Cyclospora spp. The most noticeable increase was detected for Cryptosporidium spp. Entamoeba detection was lower since molecular testing detects only Entamoeba histolytica while microscopy does not differentiate between histolytica/dispar.
Molecular Detection Of Non-O157 Shiga Toxin-Producing Escherichia coli (STEC) Directly From Stool Using Real-time Multiplex PCR Assays

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Objectives: Non-O157 Shiga-toxin producing E. coli (STEC) can cause outbreaks that have great economic and health impact. Since implementation of all STEC screening in Alberta in 2018, it is also essential to have a molecular serotyping method with faster turn-around time for cluster identification and surveillance purposes. This study sought to 1) evaluate 2 molecular assays for prediction of the top 6 non-O157 [O26, O45, O103, O111, O121, and O145] serotypes and 2) to perform molecular serotyping directly from stools. Methods: Two multiplex serotyping PCR assays were used to determine the sensitivity and specificity. Sensitivity was assessed by extracting DNA from 10 fold cell dilutions of the top 6 serotypes. PCR assays were performed as singleplex and multiplex for comparison. Specificity was determined using a panel of bacteria (N=27), non-top 6 STEC isolates (N=45) and top 6 STEC (N=157). The final phase was to test blinded stool specimens (N=60) or broth samples (N=44) submitted from frontline laboratories for STEC investigation. Our serotyping results were further confirmed by the Public Health Agency-National Microbiology Laboratory using conventional serotyping method. Results: Both singleplex and multiplex assays were comparable and we observed 100% sensitivity and specificity. Direct molecular serotyping from stool specimens correlated with conventional serotyping from cultured isolate serotype. Furthermore, top 6 non-O157 STEC mixed infections were identified and confirmed by culture and serology. Conclusion: We have shown that detection of non-O157 STEC can be done directly from stool specimens using multiplex PCR assays with the ability to observe mixed infections, which would otherwise remain undetected by conventional serotyping of a single colony. This method can be easily implemented into a frontline diagnostic laboratory as we move to culture independent assays in the near future.
Inferring Amoxicillin-clavulanate Susceptibility from Penicillin Susceptibility for Clinical Isolates of *Streptococcus pneumoniae* – Rethinking the Cut-off Value

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**Objectives:** Current CLSI guidelines indicate that a penicillin minimum inhibitory concentration of ≤0.06 mg/L can be used to infer susceptibility to oral amoxicillin and amoxicillin-clavulanate in *S. pneumoniae*. However, given the high bioavailability (80%) and higher susceptibility breakpoint of amoxicillin, this relatively low penicillin MIC cut-off has the potential of over-calling amoxicillin resistance thus limiting the use of these oral agents for the treatment of respiratory infections. We sought to compare penicillin and amoxicillin-clavulanate MICs to establish an optimal penicillin MIC cut-off value to predict amoxicillin-clavulanate susceptibility.

**Methods:** Isolates were collected from the annual, ongoing CANWARD study between 2007 and 2017. Antimicrobial susceptibility testing and interpretation of susceptibility were performed using broth microdilution panels prepared following CLSI recommendations. Sensitivity, specificity and accuracy of penicillin MIC cut-offs ranging from 0.06 mg/L to 8mg/L for accurately predicting amoxicillin-clavulanate resistance were determined.

**Results:** 2577 *S. pneumoniae* isolates were included. 2466 (95.7%) isolates were penicillin-susceptible (MIC ≤0.06 mg/L) and 111 (4.3%) were penicillin-non-susceptible. 54 (2.1%) of the 2577 isolates were non-susceptible to amoxicillin-clavulanate. The sensitivity, specificity and accuracy of various penicillin cut-offs for predicting amoxicillin-clavulanate resistance were as follows:

<table>
<thead>
<tr>
<th>Penicillin MIC cut-off (mg/L)</th>
<th>Sensitivity (for resistance)</th>
<th>Specificity (for resistance)</th>
<th>Accuracy</th>
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</thead>
<tbody>
<tr>
<td>≤0.06</td>
<td>100%</td>
<td>84.4%</td>
<td>84.7%</td>
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<tr>
<td>≤0.12</td>
<td>100%</td>
<td>90.5%</td>
<td>90.7%</td>
</tr>
<tr>
<td>≤0.25</td>
<td>100%</td>
<td>93.4%</td>
<td>93.5%</td>
</tr>
<tr>
<td>≤0.5</td>
<td>100%</td>
<td>95.4%</td>
<td>95.5%</td>
</tr>
<tr>
<td>≤1</td>
<td>96.3%</td>
<td>97.7%</td>
<td>97.7%</td>
</tr>
<tr>
<td>≤2</td>
<td>46.3%</td>
<td>99.4%</td>
<td>98.3%</td>
</tr>
<tr>
<td>≤4</td>
<td>5.6%</td>
<td>100%</td>
<td>98.0%</td>
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<tr>
<td>≤8</td>
<td>1.9%</td>
<td>100%</td>
<td>97.9%</td>
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**Conclusion:** The current penicillin cut-off of ≤0.06 mg/L will misclassify 15.6% of amoxicillin-clavulanate-susceptible isolates as resistant. A penicillin MIC cut-off of ≤0.5 mg/L will accurately predict amoxicillin-clavulanate resistance in 100% of resistant isolates and accurately predict amoxicillin-clavulanate susceptibility in 95.4% of susceptible isolates. Despite better accuracy of higher cut-off values, ≤0.5 mg/L represents a better cut-off given the importance of accurately classifying resistant isolates.
Outcomes of Administering Cefazolin vs. Other Antibiotics in Penicillin Allergic Patients with Anaphylactic Reactions for Surgical Prophylaxis at a Major Canadian Teaching Hospital

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Background: Approximately 10% of patients report a history of penicillin allergy. Recent literature suggests cross-reactivity between cephalosporins and penicillins are due to side-chain similarities. Since cefazolin has a unique side-chain from other beta lactams, it can be safely administered in penicillin allergic patients for surgical prophylaxis. Since October 2018, our hospital updated all surgical prophylaxis pre-printed orders to use cefazolin in penicillin allergic patients, except in those with histories of cefazolin-specific allergy or delayed skin reactions (e.g. Stevens-Johnson syndrome). Objectives: This study aims to retrospectively determine outcomes and safety of cefazolin as compared to other antibiotics for surgical prophylaxis in penicillin allergic patients with anaphylactic histories prior to implementation of cefazolin pre-printed orders. Methods: All patients with reported anaphylactic reactions to penicillins prescribed surgical prophylaxis from October 2017 to October 2018 were included. Patients were stratified based on antibiotic received (i.e. cefazolin, clindamycin, vancomycin, other antibiotic) and a retrospective chart review was performed to assess for outcomes and safety. Results: One-thousand-seventy-three prescriptions for prophylactic antibiotics were identified. Of these, 240 cases met inclusion with histories of anaphylaxis to pencillins: 75 (31%) cefazolin, 75 (31%) clindamycin, 39 (16%) vancomycin, and 51 (21%) other antibiotics. General and spinal surgeries used the most cefazolin in penicillin allergic patients, while orthopedics the most clindamycin and thoracics the most vancomycin. Amongst those receiving cefazolin, no critical incidents of allergic reactions were reported and no delays in surgery occurred, as compared to clindamycin and vancomycin. Conclusions: Cefazolin appears to be a safe option for surgical prophylaxis in patients with history of penicillin anaphylaxis. No differences in incidences of allergic reactions, complications or surgical delays were reported, as compared to alternate antibiotics. Further larger studies are needed to confirm our findings and determine rates of adverse events associated with the various antibiotic regimens.
Prescribing and Care by Pharmacists for Uncomplicated Urinary Tract Infections in the Community: Antimicrobial Utilization and Stewardship Results of the RxOUTMAP Study

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Background: Urinary tract infections (UTI) are common infections that often result in suboptimal antibacterial use. In some provinces, pharmacists have the authorization to prescribe medications for the treatment of uncomplicated UTI. Pharmacists are accessible primary care professionals who have an important role to play in antimicrobial stewardship. Our objective was to evaluate the appropriateness of antibacterial prescribing by pharmacists for patients with uncomplicated UTI. Methods: We conducted a prospective registry trial in 39 community pharmacies across New Brunswick. Adult patients were enrolled if they presented to the pharmacy with either symptoms of UTI with no current antibacterial treatment (Pharmacist-Initial Arm) or if they presented with a prescription for an antibacterial to treat UTI from a physician (Physician-Initial Arm). Pharmacists assessed patients and if they had complicating factors or red flags for systemic illness or pyelonephritis, they were excluded from the study. Pharmacists either prescribed antibacterial therapy, modified antibacterial therapy, provided education only, or referred to physician, as appropriate. Antibacterial therapy prescribed was compared between the study arms. Results: There were 750 patients enrolled (87% Pharmacist-Initial Arm). The most commonly prescribed agents in the Pharmacist-Initial Arm were nitrofurantoin (88%), sulfamethoxazole-trimethoprim (TMP-SMX) (8%), and fosfomycin (2%) vs nitrofurantoin (55%), TMP-SMX (26%), and fluoroquinolones (11%) in the Physician-Initial Arm. Nitrofurantoin was prescribed for 5 days in 97% of Pharmacist-Initial orders as compared to Physician-Initial orders where 65% were for greater than 5 days. TMP-SMX was prescribed for 3 days in 88% of Pharmacist-Initial compared to Physician-Initial where 63% were for greater than 3 days. Therapy was guideline concordant in 95% of Pharmacist-Initial compared to 35% of Physician-Initial (p < 0.001). For guideline-discordant therapy from physicians, pharmacists prescribed to optimize therapy for 46% of patients. Conclusion: Treatment was more guideline-concordant when initiated by pharmacists, with longer treatment durations and more fluoroquinolones prescribed by physicians.
C03

The Urine Culturing Cascade: Variation in Nursing Home Urine Culturing Practices and Association with Antibiotic Use and C. difficile infection

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Objectives: Rates of antibiotic use vary widely across nursing homes; a large portion of antibiotic prescribing may be due to variation in diagnosis and inappropriate treatment of asymptomatic bacteriuria. We aimed to obtain a complete portrait of urine culturing practices in Ontario and their association with antibiotic use. Methods: We conducted a retrospective, multilevel evaluation based on quarterly nursing home assessments between April 2014 and January 2017 in 591 nursing homes covering over 90% of nursing home residents in Ontario. Home urine culturing was measured as the proportion of residents with a urine specimen submitted for culture in 14 days before the assessment. Adjustment covariates included: resident age, sex, history of acute care stay, Charlson comorbidity index, functional status, and history of urinary catheterization. Outcomes included receipt of any systemic antibiotic and any urinary antibiotic (defined as ciprofloxacin, norfloxacin, nitrofurantoin, fosfomycin, or trimethoprim and/or sulfonamides) in 30 days and C. difficile infection in 90 days following the assessment. Results: 875,297 quarterly assessments, corresponding to 131,218 unique residents in 591 nursing homes were included. Urine cultures had been submitted in the prior 14 days for 7.9% of assessments. Home urine culturing varied substantially (10th percentile=3.4%, 90th percentile=14.3%). Within 30 days after the assessment, 17.1% of residents received an antibiotic, and 5.4% received a urinary antibiotic. Urine culturing prevalence predicted total antibiotic use (adjusted risk ratio for homes at 90th vs 10th percentile of urine culturing [aRR]=2.23, 95% confidence interval [CI]: 2.00, 2.39), urinary antibiotic use (aRR=3.22, 95%CI: 2.82, 3.86), and C. difficile infection rates (aRR=2.00, 95%CI: 1.33, 3.11). Conclusions: Homes that submit more urine specimens for culture have significantly higher antibiotic use and more C. difficile infection. These findings suggest the broad applicability of antibiotic stewardship interventions aiming to improve the diagnosis and treatment of urinary tract infection.
A "NIMBLE" Approach to Antimicrobial Stewardship: Nudging In MicroBiology Laboratory Evaluation Scoping Review

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¹PublicHealth Ontario, Toronto, ON, Canada, ²Unity Health Toronto, Toronto, ON, Canada, ³University Health Network, Toronto, ON, Canada, ⁴University of Toronto, Toronto, ON, Canada

Background: Antimicrobial stewardship programs (ASP) are most successful when multifaceted. Opportunities to influence prescriber behaviour by modifying the microbiology report may be promising strategies. Nudging guides decision-making through the strategic placement of architecture of choice, while maintaining prescriber autonomy. The purpose of this scoping review was to determine if nudging strategies in microbiology can improve antimicrobial use. Materials/methods: A search in the databases: Ovid MEDLINE: Epub Ahead of Print, In-Process & Other Non-Indexed Citations, Ovid MEDLINE® Daily and Ovid MEDLINE, 1946-August 2018, Embase Classic+Embase 1947- August 2018, PsycINFO 1806-August 2018, and All EBM Reviews 2005-August 2018 was conducted. Simulated and vignette studies were excluded. Two independent reviewers were used throughout screening and data extraction. Results: Of a total of 1334 citations screened, 13 relevant studies were identified. Study types included pre/post intervention (n=9), retrospective cohort (n=3), and randomized controlled trial (n=1). The majority of studies were performed in acute care settings (n=11) and the remainder were in primary care (n=2). Anatomical sites included urine (n=5), multiple sites (n=5), respiratory (n=2), and blood (n=1). The majority of studies used a default choice nudging strategy (i.e., selective reporting). All studies reported at least one outcome of antimicrobial use (utilization n=9, appropriateness n=5, de-escalation n=2, cost n=1). Eleven studies reported a significant change in antimicrobial use with either introducing a nudging strategy or removing the strategy. Four studies evaluated the association of nudging on antimicrobial resistance, with two studies noting improvement in susceptibility rates. Conclusions: There are a limited number of heterogeneous studies evaluating the impact of microbiology laboratory nudging. Opportunities for further study include identifying the optimal design of a microbiology report, performing prospective studies, evaluating the impact of nudging strategies (desired agents at eye level and framing), and determining the impact of nudging on patient clinical outcomes.
Antimicrobial Use among Adult Inpatients at Canadian Nosocomial Infection Surveillance Program (CNISP) Hospital Sites across Canada, 2009 to 2016

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Background: Antimicrobial resistance (AMR) is a serious threat to global public health. Antimicrobial use (AMU) is a major contributor in accelerating the emergence and spread of AMR. Objective: Identify trends and patterns of AMU in acute-care hospitals in Canada. Methods: The Canadian Nosocomial Infection Surveillance Program (CNISP) has conducted sentinel surveillance for adult inpatient AMU since 2009. Data are collected on all prescribed J01 systemic antimicrobials as well as oral vancomycin and oral metronidazole. AMU was analyzed from dispensed medications using Defined Daily Doses (DDD) per 1000 patient-days (pd) as per the World Health Organization. From 2014–2016, AMU was collected by ward type (intensive care unit (ICU) vs. non-ICU). Linear regression was used to test for temporal trends. Results: Between 2009 and 2016, 21–23 hospitals per year participated in surveillance (across 10 provinces). On average, 3.0 million patient-days were included in surveillance annually. Between 2009 and 2016, the total rate of AMU decreased from 645 to 554 DDD/1000pd (P=0.02). The rate of fluoroquinolone use decreased from 126 to 71 DDD/1000pd (P<0.0001) (Figure). The rate of clindamycin use decreased by 50% between 2009–2012 (~14 DDD/1000pd) and 2016 (7 DDD/1000pd; P=0.003). Between 2014 and 2016, the rate of AMU was higher on ICU wards (1276–1370 DDD/1000pd) compared to non-ICU wards (461–513 DDD/1000pd). In 2016, the 5 most commonly used antimicrobials were cefazolin (73 DDD/1000pd), piperacillin/tazobactam (51 DDD/1000pd), ceftriaxone (44 DDD/1000pd), ciprofloxacin (41 DDD/1000pd), and vancomycin (41 DDD/1000pd). The top 5 antimicrobials used on ICU wards were piperacillin/tazobactam (177 DDD/1000pd), vancomycin (173 DDD/1000pd), cefazolin (140 DDD/1000pd), ceftriaxone (116 DDD/1000pd), and meropenem (114 DDD/1000pd). Conclusions: AMU has decreased among CNISP acute-care hospitals most notably among fluoroquinolones. These results support the need for ongoing surveillance of AMU within CNISP to monitor trends and provide Canadian
benchmarks.

Figure: Antimicrobial use for the top 8 antibiotic classes / subclasses for adult inpatients at CNISP hospitals across Canada, 2009 to 2016 [represents 74% of total AMU in 2016].
Identifying Opportunities for Laboratory Stewardship Through Prospective Review of Clostridium difficile Testing Indications at a Tertiary Care Hospital

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Background and Objective: Clostridium difficile infection (CDI) is a leading cause of nosocomial infections in Canada. Molecular testing for C. difficile is highly sensitive but cannot differentiate infection from colonization. Inappropriate test-ordering can lead to increased laboratory costs and unnecessary antibiotic treatment. Our objective was to determine the prevalence of and reasons for inappropriate CDI test-ordering. Methods: From April 26 to May 28, 2018, hospitalized patients with a CDI order at a tertiary care hospital were prospectively reviewed, capturing clinical history, symptoms, vital signs, laboratory data (e.g. WBC and Cr), alternative reasons for diarrhea, ordering provider and C. difficile test results. CDI orders were categorized as appropriate/inappropriate based on clinical presentation and identification of alternate reasons for diarrhea. Results: 89 charts were reviewed. The median length of stay prior to CDI test was 3 days. Physicians ordered 68(76.4%) tests and nurses initiated 21(23.6%). The order location was distributed: Medicine (51), Surgery (12), Critical Care (14), and Emergency (11). Overall, 41(46%) tests were considered appropriate, while 48(54%) tests were assessed as inappropriate (Figure 1). Nurse initiated tests were more likely than physician’s to be inappropriate (85.7% vs 44.1%, p=0.00083). The two primary aetiologies of inappropriate testing were asymptomatic patient and alternative reason for diarrhea. The alternative reasons for diarrhea were laxative only (16), laxative and NG-feed (4), NG-feed only (7), and chemotherapy (3). The excess, direct laboratory costs associated with unnecessary testing was estimated at $2347.68 (48 inappropriate tests at $48.91/test) for the 31-day period.
Conclusions: We identified that 54% of CDI tests ordered were inappropriate; 34% of patients had an alternative reason for diarrhea and 20% of patients tested were asymptomatic. Inappropriate CDI test-ordering was prevalent in our hospital. Diagnostic stewardship interventions to optimize CDI diagnosis should be explored.
Development of a Tool to Assess the Evidence that Hospital Sinks are a Reservoir for Gram-Negative Bacterial Infection

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Objective: Decades of studies suggest that sinks in acute-care facilities are a reservoir for Gram-negative bacterial infection. We sought to develop a tool to assess the strength of evidence for causality. Methods: We adapted the Causal Analysis/Diagnosis Decision Information System (CADDIS) developed by the United States Environmental Protection Agency for use in ecosystems research. We used a modified Delphi process, with input from individuals with expertise in hospital infection epidemiology. Results: Through 4 rounds of feedback and revision, and 2 tests of tool application to score evidence from published articles, we developed the Modified CADDIS Scoring for Assessing Causality in Studies of Hospital Sinks as a Reservoir for Gram-Negative Bacterial Infection or Colonization. For assessment of inter-rater reliability, 8 reviewers scored 4 randomly chosen articles, across 6 domains: Spatial/Temporal Co-occurrence, Temporal Sequence, Stressor-Response Relationship, Causal Pathway, Evidence of Exposure and Biological Specificity, Manipulation of Exposure. Mean percent agreement was 69.6, 81.3, 87.5, 54.5, 85.7, and 80.4 per respective domain in Test 1. In Test 2, 6 reviewers scored 4 articles selected to be difficult to assess, with mean percent agreement 83.4, 65, 83.4, 46.7, 83.4, and 50 per domain. There were 16 (20%) cases of 100% agreement, and the Gwet’s AC statistic (adjusting for chance agreement) ranged from 13.4- 73.5 (median 61.3). Areas of disagreement were felt to result from lack of a priori knowledge of causal pathways from sinks to patients and uncertain influence of co-interventions to prevent organism acquisition. Modifications were made until consensus was achieved that further iterations would not improve the tool. Conclusion: Our modified CADDIS Scoring appears to be a promising tool that we are now applying in a systematic review on sink causality in hospital-acquired infection. Similar processes using a modified CADDIS may assist in assessing causality in other infection prevention and control applications.
**Candida auris Prevalence in Canadian Acute Care Hospitals, 2018**

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**Objectives:** As of July 2018, there were 14 known cases of the emerging drug-resistant yeast *Candida auris* in Canada. We aimed to estimate the prevalence of *C. auris* among Canadian patients deemed to be at-risk in order to inform the development of surveillance and infection prevention and control policies.

**Methods:** High risk patients from 14 Canadian Nosocomial Infection Surveillance Program (CNISP) and 7 non-CNISP Canadian Hospital Epidemiology Committee (CHEC) hospitals from six provinces were screened for *C. auris* between September 4, 2018 and November 6, 2018. For each patient, two pooled axilla/groin swabs were collected and a data collection form completed. One swab was inoculated onto chromogenic agar (CandiSelect® or Brilliance Candida®), and the second swab shipped to the US CDC for culture. *C. auris* was identified by MALDI-TOF and isolates subjected to Illumina whole genome sequencing. **Results:** A total of 475 at-risk patients were screened: 35 (7.4%) hospitalized outside Canada; 53 (11.1%) with travel to the Indian subcontinent; 105 (22.1%) colonized with carbapenemase producing organism (CPO), and 282 (59.4%) present on a ward with high antifungal use. Risk groups overlapped, for example, 49% of CPO-colonized patients reported travel to the Indian subcontinent. Two patients were found to be colonized with *C. auris* (prevalence = 0.42%). Both *C. auris*-colonized patients were recently hospitalized in India and both patients were co-colonized with NDM-1 and OXA-48-like producing organisms. Whole genome sequencing showed that the isolates were highly related to the South Asian clade, consistent with the patients’ recent overseas hospitalization. **Conclusions:** We found the prevalence of *C. auris* in hospitalized patients in Canada to be low and associated with healthcare exposure abroad. The rapid emergence of *C. auris* in the United States and other countries suggests that ongoing surveillance for *C. auris* colonization in patients recently hospitalized outside Canada would be prudent.
Carbapenemase-Producing *Enterobacteriaceae* (CPE) in Household Contacts and Household Environments of CPE-Colonized/Infected Persons

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**Objectives**: CPE have emerged rapidly worldwide. This prospective cohort study aimed to assess the risk of CPE transmission from colonized patients (index cases, ICs) to household contacts (HCs). **Methods**: ICs were identified by population-based surveillance. Groin and rectal swabs, and urine specimens were collected from ICs/HCs at home visits every 3 months; swabs of 10 environmental surfaces (ESs) were also collected. Swabs/specimens were incubated in BHI broth overnight, followed by direct PCR to detect carbapenemase genes and cultures of PCR-positive samples. **Results**: 95 households and 175 HCs participated. 20 (11%) HCs in 20 (21%) households were CPE-colonized. 8/20 (40%) were CPE-colonized at first visit. The probability of initially non-colonized HCs becoming CPE-colonized by month 12 was 11% (Figure). Overall, 15/20 (75%) CPE-colonized HCs probably/possibly acquired CPE from the IC; 5 (25%) probably acquired CPE from another source (4 from travel). HCs were more likely to be older, be the IC’s spouse (OR 17, 95% CI 4.8-63), have an underlying chronic medical illness (OR 4.5, 95% CI 1.7-12), and have travelled abroad (OR 3.8, 95% CI 1.2-12). Households with CPE-positive ESs were more likely to have CPE-colonized HCs (OR 7.89, 95% CI 1.7-36). 299/2887 (10%) ES samples representing 203 unique ESs yielded CPE. CPE yield per ES type was: kitchen sink drain (19%), shower drain (18%), bathroom sink drain (17%), toilet drain (13%), pillow (12%), sofa/chair (10%), bathroom sink tap (9%), toilet handle (6%), telephone (5%), and kitchen sink tap (4%). Of 203 CPE-positive ESs, 70%, 14%, 7%, 2%, and 1% yielded CPE for 1, 2, 3, 4, and 5 visits, respectively. 14/23 (61%) persistently positive samples (positive at ≥3 visits) were from drains. **Conclusions**: After 12 months, transmission occurred to 8.6% of HCs of CPE-colonized patients. CPE contamination of household surfaces, particularly drains, is common.
Randomized Controlled Trial of Chlorhexidine Gluconate, Intranasal Mupirocin, Rifampin, and Doxycycline Versus Chlorhexidine Gluconate and Intranasal Mupirocin Alone for the Eradication of Methicillin-Resistant *Staphylococcus aureus* Colonization: a Preliminary Analysis

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**Background:** To prevent recurrent methicillin-resistant *Staphylococcus aureus* (MRSA) infections, both topical and systemic antibiotic therapies have been studied for decolonization. Clinical equipoise remains with regards to the role of decolonization. Furthermore, the advantages of systemic versus topical decolonization strategies remain unclear. **Objectives:** To compare initial MRSA clearance and subsequent MRSA re-colonization rates over a 12-month period, systemic therapy (topical chlorhexidine gluconate, intranasal mupirocin, oral rifampin, and oral doxycycline) was compared to standard topical therapy at our centre’s Ambulatory MRSA Clinic (topical chlorhexidine gluconate and intranasal mupirocin). **Methods:** MRSA-colonized patients were randomized (3:1 allocation) to receive either systemic or standard therapy. Follow-up for MRSA screening swabs were obtained at 3, 6, and 12 months after completion of therapy, from the anterior nares and rectum, and where relevant additional specimens from skin lesions, Foley catheter urine (excluding lines), medical device exit sites, and any prior MRSA positive sites. Kaplan-Meier survival curves were calculated using the end date of therapy as time (0) and either the date of next positive MRSA sample or censored at either the last date of follow-up for those lost to follow-up or 12 months from the last day of therapy. Survival curves were assessed for significant differences using log-rank tests. **Results:** Of 98 enrolled (73 systemic; 25 standard), 21 patients (16 systemic; 5 standard) were unable to complete the 12-month follow-up. Initial MRSA clearance, defined as 3 sets of negative MRSA cultures immediately following therapy, was achieved in 72.6% (systemic) versus 52.0% (standard). There was a marginally significant difference in the likelihood of remaining MRSA-negative post-therapy (p=0.043, Figure 1). Among those who achieved initial clearance, there was no significant difference in the survival curves over a 12-month period (p=0.970). **Conclusion:** Standard topical decolonization was similar in efficacy compared to systemic decolonization after a 12-month follow-up.

**Figure 1**
Emergence of A Novel ST1478 VRE in Canadian Hospitals Associated with Daptomycin Non-Susceptibility and High Level Gentamicin resistance

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Objective: Infection with vancomycin resistant enterococci (VRE) causes significant morbidity and mortality in hospitalized patients with few antimicrobial treatment options. A novel strain of VRE recently described in Australia was non-typeable by MLST methodology due to loss of the *pstS* gene. We describe the emergence of this strain in Canadian hospitals from 2013-2017 and compare the clinical characteristics of this strain to other VRE strains.

Methods: The Canadian Nosocomial Infection Surveillance Program prospectively collects epidemiologic data on all VRE blood stream infections (BSI) from 65 hospitals in 10 provinces. Isolates are sent to the National Microbiology Lab for typing and antimicrobial susceptibility testing. Whole genome sequencing (WGS) of ST1478 isolates was carried out to determine interrelatedness. Results: There were a total of 45 VRE BSI caused by ST1478 in 15 hospitals across six provinces accounting for an increasing proportion of VRE BSI (2.7% in 2013 to 27.6% in 2017). Patients bacteremic with ST1478 VRE were similar with respect to age, sex, ICU admission and mortality to those with non ST1478 VRE. Patients with ST1478 VRE were more likely to have had a solid organ transplant (30.2%) compared to patients with non ST1478 VRE (11.9%; p=0.002). There was a higher proportion of daptomycin non-susceptibility in the ST1478 strains (11.1%) compared to non ST1478 strains (4.5%; p=0.06). High level gentamicin resistance was also more common in the ST1478 strains (93.3% vs 10.7%; p<0.001). WGS revealed close genetic relatedness, varying from 0-56 SNVs using AUS004 as the reference strain. Conclusions: ST1478 VRE appears to be increasing and may be transmissible in Canadian hospitals. This strain is more prevalent in the solid organ transplant population and is associated with non-susceptibility to daptomycin and high level gentamicin resistance. Further investigation is required to understand the emergence and transmission dynamics of this novel strain.
**Burkholderia cenocepacia ET12 Transmission in Adults with Cystic Fibrosis**

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**Background:** *Burkholderia cenocepacia* is a well-known pathogen in the cystic fibrosis (CF) population. Despite enhanced infection prevention and control (IPAC) precautions, 11 CF patients have been identified as having incident *Burkholderia cenocepacia* ET12 strain (ET12-Bc) infection since 2008 at the Toronto Adult CF centre. **Objectives:** The objective of this study was to describe the investigation of ET12-Bc acquisition in CF patients in this centre. **Methods:** A retrospective chart review of 11 cases of incident ET12-Bc infection was performed at St. Michael’s Hospital, in Toronto, Canada. Patient demographic and clinical characteristics were reviewed and an epidemiologic investigation was conducted. ET12-Bc isolates were analyzed by multilocus sequence typing (MLST) and whole genome sequencing (WGS). **Results:** Ten patients had a hospital admission within the two months preceding their first ET12-Bc positive sputum culture; ET12-Bc was detected 12 months following hospital admission in the eleventh patient. In all but one isolate, the seven MLST loci had a 100% DNA sequence match to these loci in ET12-Bc strain J2315, which represents *Burkholderia* MLST sequence type 28. The remaining isolate had a single nucleic acid polymorphism in one MLST locus. Epidemiologic investigation, together with WGS analysis, suggested that transmission occurred between patients during hospitalization in 8 of 11 patients. To date, 10 of 11 patients with new acquisitions have died (median survival of 379.5 days). **Conclusions:** We identified ET12-Bc nosocomial transmission between CF patients in hospital, despite enhanced IPAC precautions. This led to a change in our hospital policy wherein ET12-Bc positive patients are no longer cared for on the same unit as ET12-Bc negative patients with CF.
**Still rising: A quasi-experimental study of vancomycin resistant Enterococcus (VRE) bacteremia rates in Ontario, 2009-2018**

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**Objective:** In June 2012, some Ontario hospitals discontinued VRE screening and isolation programs; additional hospitals have since followed. In 2015, we observed a significant increase in the incidence of VRE bacteremias in hospitals that had stopped screening. The aim of this study was to update these results through to 2018. **Methods:** All Ontario hospitals are mandated to publicly report VRE bacteremias on a quarterly basis and we used these data for the study period January 2009 to September 2018. An interrupted time series Poisson regression was used to assess the slope change in VRE bacteremia incidence rate (primary outcome) after versus before the discontinuation of screening. Hospitals that continued to screen were the comparison group. Incidence rates were adjusted for hospital type and clustering within hospital site; slope changes were presented as incidence rate ratios (IRR) with 95% confidence intervals (CIs). **Results:** 97 hospital facilities publicly reported at least 1 VRE bacteremia during the study period. Overall, rates of VRE bacteremia increased from 0.74/100,000 in 2009 to 3.54/100,000 in 2018. In ceased-screening hospitals (n=23), there was an increase in slope after screening was discontinued when compared to before (slope change IRR 1.44 [95%CI 1.22–1.71]) [Figure]. In screening hospitals (n=74), the slope was not significantly different after June 2012 compared to before (slope change IRR 1.02 [95%CI 0.70–1.50]). The results were similar when restricted to acute teaching hospitals; ceased-screening hospitals (n=11), slope change IRR 1.77 [95%CI 1.44–2.18]) compared to screening hospitals (n=10, slope change IRR 0.83 [95%CI 0.46–1.52]). **Interpretation:** Since 2009, there has been over a 4-fold rise in the rate of VRE bacteremias in Ontario. The association between discontinuation of VRE screening and isolation and rates of VRE bacteremia is impressive and persistent. Hospitals aiming to minimize VRE bacteremias should consider VRE screening and isolation programs.
Active Charcoal Filters in Hospital Ice Machines as a Source for Contamination of Mycobacterium fortuitum: Update of a Pseudo-Outbreak

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Background: We report a follow up to a nosocomial pseudo-outbreak of respiratory tract colonization with Mycobacterium fortuitum believed to have originated from a contaminated ice machines. We wanted to further delineate the source of contamination and our hypothesis was that the charcoal filters were the ultimate source. Methods: Ice machines from the affected hospital campus and unaffected campus were compared in terms of type of filtration system. We increased the scope of our investigation to include environmental samples collected from different hospital sites as well as additional sites in the ice machines. Environmental sampling was repeated after removal of the charcoal filters. Specimens were cultured with use of a continuously monitored broth system for the isolation of mycobacteria. Samples positive for mycobacteria were sent to the regional Public Health Laboratory for identification or by MALDI-TOF MS once implemented in our laboratory. Environmental isolates were compared by genotyping using ERIC-PCR. Data regarding the water quality including pH, temperature, turbidity and anionic makeup between hospital campuses was collected by PHL representatives. Results: The affected campus ice machines involved a Pentek GS-10ALS filtration system which was not included in the ice machines of the unaffected campus. When sampling the ice machines, M. fortuitum was consistently isolated from the water sampled after charcoal filtration. Of note some ice machines remained positive other species of non-tuberculosis Mycobacterium. Repeat sampling from the ice machines post cleaning and filter removal were negative for M. fortuitum. Further investigations will involve measuring M. fortuitum rates in our patient population after filtration removal. Conclusion: Water treatment using a charcoal filtration lead to a pseudo-outbreak of M. fortuitum. Active charcoal filters may allow for M. fortuitum biofilm formation and contamination of the water supply.
The Economic Burden of Vancomycin Resistant Enterococcus (VRE) Bacteremia: A Population-Based Matched Cohort Study

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Objective: To evaluate the costs attributable to VRE bacteremia from the healthcare payer perspective. Methods: We conducted a population-based matched cohort study of hospitalized patients with confirmed VRE bacteremia in Ontario, Canada, between January 2009 and December 2013. Infected (i.e., exposed) subjects were identified and hard-matched to up to three unexposed subjects based on age, sex, comorbidities, admission date, rurality, neighborhood income, hospital type and pre-hospitalization resource utilization. All subjects were followed until December 31, 2017. The primary study outcomes were costs up to 1-year post index date (C$ 2014). Results: We identified 217 exposed subjects and in preliminary analysis, we matched 127 exposed to 344 unexposed subjects. In the exposed group, mean age was 62.9 years (SD 17.1), 40% were female, and common comorbidities were cancer (33%), heart disease (21%), and renal failure on hemodialysis (10%). In the unexposed group, mean age was 62.8 years (SD 16.5), 39% were female, and common comorbidities included cancer (24%), heart disease (4%) and renal failure on hemodialysis (5%). Length of stay was 63 days for exposed versus 8 days for unexposed subjects. Mortality within 30 days was 19% for exposed subjects, 68% within 1 year, and 83% within the follow-up period, versus 7%, 17% and 35% for unexposed subjects, respectively. Approximately half (53%) of exposed subjects died during index hospitalizations versus 6% of unexposed subjects. Mean cost for index hospitalization was $134,542.69 for exposed versus $10,838.46 for unexposed subjects. Mean unadjusted costs for exposed subjects at 30 days, and 1 year were $63,762.56 and $190,931.86 versus mean unadjusted costs for unexposed subjects of $17,722.31 and $51,153.35. Conclusion: VRE bacteremia is associated with increased healthcare costs, extending well beyond the index hospitalization.
Metronidazole-associated Neurologic Toxicity: A Nested-Case Control Study

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Objectives: There have been numerous case reports of peripheral and central nervous system toxicity among metronidazole users. We sought to confirm an association of metronidazole with neurologic toxicity, to quantify the magnitude of these risks, and to assess whether these phenomena are dose dependent. Methods: We conducted a nested case control study in Ontario from April 1 2003 to March 31 2017. The cohort nest included all older adults age ≥ 66yrs, who received at least one outpatient prescription of metronidazole or clindamycin, without a history of neurologic disorders or recent prolonged hospitalizations prior to index date. The cases were patients that experienced new cerebellar dysfunction, encephalopathy, or peripheral neuropathy, as identified in province-wide emergency department and hospital datasets. Ten control patients were matched to each case based on age, sex and recent hospital exposure. The primary exposure of interest was metronidazole treatment in the 100d preceding the index date. Conditional logistic regression was used to test the association of metronidazole (versus clindamycin) exposure with neurologic toxicity. Results: Among 140,556 older Ontarians with incident outcomes of neurologic dysfunction, there were 1,212 cases with metronidazole or clindamycin exposure, but not both, in the 100 days preceding the outcome event; these patients were matched to 12,098 controls. Metronidazole use was associated with increased neurologic toxicity compared to clindamycin (odds ratio (OR) 1.72, 95%CI 1.53-1.94), which persisted after accounting for patient demographics, comorbidities and other medication exposures (adjusted OR (aOR) 1.43, 95%CI 1.26-1.63). The increased neurologic toxicity was detected among patients with low, medium and high cumulative doses of metronidazole. Conclusions: Metronidazole is associated with a statistically significantly increased risk of peripheral and central nervous system toxicity; clinicians and patients should be aware of these rare but serious adverse events.
Cutaneous Leishmaniasis: a 10 Years Experience in a Canadian Reference Centre for Tropical Diseases

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Background/Objectives: Cutaneous leishmaniasis (CL) is one of the “Neglected Tropical Diseases”. Migration and travel has led to increasingly encountered CL cases in non-endemic country such as Canada. The objectives are to describe the epidemiology, clinical presentations, diagnostic methods and treatments used for CL in our center. Clinical differences between Old World (OW) and New World (NW) CL were evaluated as well as the sensitivities of the diagnostic methods. Methods: A retrospective observational study was performed with all the laboratory confirmed diagnoses of CL between January 2008 and October 2018. Demographic, epidemiologic and clinical characteristics, diagnostic methods, treatments and outcomes were abstracted from computerized patient records. Clinical response was determined based on the degree of re-epithelialization at 1 year after treatment. Results: A total of 52 cases were identified, clinical data was available for 48 cases (NW: 33, OW: 15 – average age: 41 years (range: 1 - 75); male: 28 [58%]). Lower extremities (n=15 [31%]) and face/neck (n=13 [27%]) were the most common locations. At initial presentation, NW CL presented more often as ulcers (n=28 [85%]) compared to OW CL that mostly presented as plaques (n=9 [60%]); p=0,006. Adenopathy was seen in 9 (27%) NW CL but not in OW CL (p=0,0248). PCR had the highest estimated sensitivity with 98% compared to 68% for smear, 64% for histopathology and 65% for culture. Among all cases, 38 patients had documented treatment, 36 of them (95%) received systemic treatment as first-line. Liposomal amphotericin B was the most commonly used in 20/38 (53%). Of all CL cases, clinical response was achieved in 32 patients (67%). Conclusion: This study represents the largest Canadian case series of CL. Non-endemic countries encounter a diversity of CL species. PCR is an essential tool for diagnosis and treatment leads to complete re-epithelialisation in most cases.
Management of *Mycobacterium tuberculosis* Prosthetic Joint Infection: A Case Report and Literature Review

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**Background:** *Mycobacterium tuberculosis* prosthetic joint infection (TBPJI) is a rare complication but can be seen in immunocompromised patients or those at-risk of tuberculosis (TB). Lacking clinical suspicion and experience with TBPJI often lead to delays in diagnosis. We report a case of left hip TBPJI in a Hungarian-Canadian immigrant, treated with concurrent surgical and medical therapy. We also performed a literature review on TBPJI case reports outlining their diagnosis and management. **Methods:** A comprehensive search was conducted on English language literature published from 1980 to July 2018 on TBPJI, using EMBASE, OvidMEDLINE, PubMed, and Google Scholar. Data analysis focused on patient demographics (age/gender, risk factors), time elapsed from arthroplasty to symptom onset, diagnosis, therapy, and outcomes. **Results:** Our literature review identified 53 cases of TBPJI from 38 published articles, most involving hip or knee infections. Symptom onset from arthroplasty ranged from 2 weeks to 38 years. Delays in diagnosis up to 3 years were reported, often after failing empiric antibiotics and/or repeated surgeries with no bacterial growth from intraoperative cultures. Diagnosis was confirmed via fluid/tissue acid-fast bacillus testing, TB culture/PCR, or pathology. Except for 2 cases, all patients received anti-mycobacterial therapy (AMT). AMT drug combinations and duration varied greatly. 11 cases received AMT alone, while most required surgery (13 with DAIR [Debridement-Antibiotics-Implant-Retention], 18 staged revisions, 11 hardware removals). Of the 11 medically managed cases, 2 were declined surgery. Our case was unique as the surgeon suspected an infected native joint intraoperatively and opted for cemented spacer, until diagnosis of TBPJI was made 3 months later, where she successfully responded to 12 months of AMT followed by second-stage revision. **Conclusion:** Though medical management alone is possible our literature review and experience recommend managing TBPJI with both AMT and surgical consultation/intervention as a safer option.
Hit or miss? Comparison of Neisseria gonorrhoeae detection limits of automated molecular methods used across Nova Scotia

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Objectives: Testing for Neisseria gonorrhoeae (GC) is often performed concurrently with Chlamydia trachomatis (CT). Due to the low prevalence of GC in Nova Scotia, confirmatory testing is reflexively performed following an initial positive (or indeterminate) GC result. Given the different commercial assays are used for these purposes in NS, the analytical sensitivity of methods used for GC testing was assessed. Methods: Panels were sent to each NS laboratory performing CT/GC testing consisting of 10-fold serial dilutions of GC, with the final dilution in the recommended buffers for each method. GC screening methods included the Hologic Panther, BD Viper, BD Max, and Roche 4800 systems. GC confirmatory testing was evaluated on the Hologic Panther system, BD Max, or Cepheid Xpert. To assess analytical specificity, non-GC strains of N. meningitidis (serotypes B and C), N. lactamica, N. cineria, N. sicca, and N. subflava were also tested at high concentrations (>10⁷ CFU/ml). Results: In the specificity analyses, the BD Viper was the only assay that showed cross reactivity (with N. lactamica). In the analytical sensitivity analyses, the Hologic Panther and BD Viper systems were the most sensitive screening methods for GC with LoD of 11 ± 1 CFU/ml, followed by the BD Max at 27 ± 4, and the least sensitive method was the Roche 4800 at 295 ± 37 CFU/ml. GC confirmation on the Hologic Panther had equivalent sensitivity to the primary testing method, whereas testing algorithms using BD Max or Xpert for GC confirmation were less sensitive than their screening method at 27 ± 4 and 31 ± 4 CFU/ml, respectively. Conclusions: The most sensitive methods for GC detection and confirmation were the Hologic Panther assays. Given the lower sensitivity of other methods used in Nova Scotia for GC screening and confirmation, testing algorithms may need to be revised.
Understanding why PrEP uptake is low among the most at risk individuals

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Background: In July 2018, there were 25 new HIV seroconversions in 6 months compared to 15 in 2017. These infections occurred in people who use drugs, within a discrete geographic area. PrEP (Pre-exposure prophylaxis) has been publicly funded in NS since July 2018, however there has been no uptake among the most at risk individuals. The barriers to access were unclear. Our objective is to determine self-perceived risk of HIV transmission, awareness of prevention methods, and PrEP knowledge in a high incidence region.

Methods: Using an ethics approved questionnaire, 210 individuals were surveyed. Questionnaires were collected from pedestrians within the geographic area of the outbreak. Participants were asked “Yes” or “No” questions about their (1) awareness of PrEP, (2) self-perceived risk of contracting HIV, (3) knowledge of HIV prevention methods, and (4) willingness to use a daily medication to reduce HIV risk. The aggregate questionnaire responses were reported as percent answering “Yes” or “No” to each question.

Results: 40/210 individuals self-identified as “at-risk” for HIV infection, 100% (40/40) of these individuals were aware of an HIV prevention method, 52% (21/40) were aware of PrEP, and 90% (36/40) would consider PrEP if told they were at high risk of HIV infection. 170/210 individuals self-reported as “not-at-risk” for HIV infection, 94% (160/170) were aware of an HIV preventative method, 29% (49/170) were aware of PrEP, and 81% (138/170) would consider PrEP if told they were at high risk of HIV infection.

Conclusions: Less than 20% of individuals surveyed in this high incidence area consider themselves at risk of HIV infection. Willingness to use a daily medication to reduce the risk of contracting HIV was high among all participants, however awareness of PrEP was low. These findings support efforts to increase harm reduction, as well as specific community awareness and PrEP prescribers.
ORAL PRESENTATIONS
Friday, April 5, 2019
16:30 – 18:00 Session G
Room: Governor General I

G01

Assessing Adolescent Immunization Options for Pertussis in Canada: a Cost-Utility Analysis

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Objective: In Canada, adolescent pertussis vaccination helps prevent transmission. Trade-offs with respect to disease prevention and effectiveness can be associated with immunization timing. The objective of this study is to assess the cost-utility of different adolescent pertussis immunization strategies. Methods: A cost-utility analysis was conducted using a Markov model, with adolescents (beginning at age 10 years) as the cohort of interest. The model assessed three vaccination strategies: 1) immunization of 10 year olds, 2) removal of adolescent vaccination, or 3) immunization of 14 year olds (status quo comparator). The analysis was conducted from a healthcare payer perspective and used a lifetime time horizon. Primary outcomes included life years, quality-adjusted life years (QALYs), health system costs, and incremental cost-effectiveness ratio (ICER). Costs and outcomes were discounted at 1.5% annually. Deterministic and probabilistic sensitivity analysis was conducted to assess parameter uncertainty. Results: The current recommended adolescent immunization strategy (at 14 years old) resulted in an average of 40.4432 expected QALYs at a cost of $34.36 per individual. This strategy was dominated by immunization at 10 years and no immunization. Compared to no immunization, immunizing at 10 years of age had an ICER of $108,703.01 per QALY. Results were robust across a series of deterministic and probabilistic sensitivity analyses; findings were most sensitive to infection probability, vaccine cost, vaccine effectiveness, probability of mortality, and cost of inpatient care. At a cost-effectiveness threshold of $50,000/QALY, removal of the adolescent vaccine represented the most cost-effective strategy in 97% of simulations. However, at a threshold of $100,000/QALY, immunization at 10 years of age is marginally cost-effective relative to no immunization, with a 58% probability of being cost-effective. Conclusion: Findings suggest that alternatives to the current Canadian adolescent pertussis vaccine schedule – especially no immunization – are more cost-effective relative to current immunization of 14 year olds.
The Lower Saint-Lawrence River of Quebec, a hot spot for sheepfold-associated Q fever (Coxiella burnetii infection) in Canada: review of 254 cases

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**Background**: The Lower Saint-Lawrence region (LSLRR) has a 15-fold higher incidence Q fever (Coxiella burnetii infection) compared to Quebec provincial rate, frequently associated with sheepfolds. This study aims to review the Q fever clinical cases in the LSLRR. **Methods**: All Q fever cases were retrieved from the microbiology logs, the medical records of Rimouski hospital (250-bed acute-care community center) and Public Health records between 1991 and 2018. Confirmed acute cases included positive PCR, antibody titers > fourfold rise (CF or IFA). Probable acute cases included titers > 1/40 CF or > 1/128 IFA IgG phase 2. Chronic cases had positive PCR, antibody titers > 1/320 CF or > 1/1024 IFA IgG phase 1. Data were analyzed using EPI-INFO 7.2.2.6. **Results**: Of 295 screened cases, 243 were acute (239 confirmed, 4 probable), 11 chronic. Median age was 46 years (range 3-84), 75% were male. For acute Q fever, prominent symptoms were fever (99%), headache (81%), chills (79%), sweating (72%), myalgia (68%), fatigue (66%). Acute cases included Hepatitis 83%, Pneumonia 4% and Endocarditis 1%. Antimicrobial was provided in 92%, mostly Doxycycline (93%). Seasonal peak was observed from May to July, with 56% of acute cases. Chronic cases included 4 Hepatitis, 3 Endocarditis and 1 Aortitis. Comorbidity was observed in 22% of patients and 37% were hospitalized. Among the 8 counties in LSLRR, most cases (56%) were within the 2 counties with higher ovine production. Exposure to sheepfold was prominent 81%, including 34% shepherds, 20% sheepfold visitors and 37% indirect. **Conclusions**: To our knowledge, this is the largest retrospective study of Q fever in Canada. Fever with hepatitis were the most common manifestation of C. Burnetii in the Quebec LSLRR. Most patients (81%) were exposed to sheepfold. Protective measures should be implemented in the sheep industry to reduce Q fever in our region.
Schistosoma and Strongyloides Screening in Immigrants as Part of HIV Care in Alberta

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Background: People who previously lived in regions endemic to Schistosoma and Strongyloides are at high risk of chronic infections, even when they have immigrated to non-endemic regions. These parasitic infections can have serious and sometimes fatal consequences for people co-infected with HIV. While screening guidelines and data exist pertaining to parasitic prevalence for immigrant populations, these do not exist for HIV positive populations. Objectives: Assess the prevalence of chronic parasitic infections in immigrant/refugee HIV positive individuals and identify epidemiologic and laboratory characteristics to enable more focused screening. Methods: 243 HIV positive individuals, born outside of Canada and receiving care at a centralized HIV clinic in Alberta between 2015 and 2018 were screened for Schistosomiasis and Strongyloidiasis using serology and stool analysis. Epidemiologic and laboratory values were analyzed using univariate logistic regression. Results: Defined by serology, the prevalence of Schistosomiasis was 19.9% and Strongyloidiasis 4.8%. Stool microscopy identified no Schistosoma or Strongyloides parasites. Age between 40 and 50 years (OR 2.50, 95%CI 1.13-5.50), being a refugee (OR 3.55, 1.72-7.33), country of origin within Africa (OR 10.11, 1.25-82.00) or within East Africa (14.93, 1.94–114.89), eosinophilia (OR 3.56, 1.25–10.16) and CD4 count less than 200 cells/mm³ (OR 2.46, 1.017–5.92) were associated with positive Schistosoma serology. Eosinophilia was associated with positive Strongyloides serology (OR 11.57, 2.81-47.65). Eosinophilia had poor sensitivity for identification of chronic parasitic infection. Conclusion: In the HIV positive immigrant population, Schistosomiasis and Strongyloidiasis are found at a similar prevalence as in the refugee population and at significantly high rates to warrant targeted screening with serology. Schistosoma serology should be performed for all HIV positive individuals originating from Africa. Stool microscopy and eosinophil counts are not useful for parasitic screening in this context.
Decreasing Unnecessary Antibiotics for Clostridium difficile Colonization with a Nudge from Microbiology Reporting

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Objective: Patients who test positive for C. difficile by polymerase chain reaction (PCR) testing, with a negative toxin immunoassay (EIA) are commonly colonized and do not require treatment, yet clinicians often treat in the setting of a “positive” result. We evaluated the clinical impact of a nudge, changing from reports that included both assay results along with treatment recommendations, to the current “Clostridium difficile organism present but toxin not detected by EIA. Consider C. difficile colonization or early infection”.

Methods: We conducted a retrospective cohort study of all adult patients admitted to our multisite community hospital with a positive C. difficile PCR result and negative toxin EIA from January 1, 2016 – June 30, 2018, including 15 months pre and post intervention. Patients dying within 24 hours of testing were excluded. Recurrent episodes were included if they were off treatment and >7 days from initial testing. The primary outcome was total days of therapy (DOT) for TID metronidazole, oral vancomycin and fidaxomicin and statistical process control charting determined special cause variation. Secondary outcomes included subsequent toxin positive disease (TPD), colectomy, all cause mortality, and length of stay (LOS). Results: 369 episodes were identified in total, 169 occurring after the intervention. Mean DOTs/episode decreased from 13.7 to 7.7 (p<0.05) post-intervention, with SPC indicating special cause variation. Patients who did not receive any treatment increased from 6.0% to 23.7% post intervention (P<0.05). Pre and post-intervention, no significant change in adverse outcomes including subsequent TPD (9.9% vs. 6.5%), colectomy (0% vs. 0.6%), or mortality (8% vs. 11.8%) occurred (all p values >0.05). LOS was statistically unchanged at 52 days pre-intervention and 43 days post-intervention (P>0.05). Conclusions: A significant decrease in antibiotic utilization and exposure occurred after introduction of a reporting nudge raised the possibility of C. difficile colonization, without increasing subsequent disease.
Recurrent Endocarditis in Persons Who Inject Drugs

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Objective: The incidence of infective endocarditis (IE) and recurrent IE is increasing among persons who inject drugs (PWID); however, literature studying recurrent IE in PWID is limited. Our objectives were to understand and compare the microbial etiology, clinical characteristics and variables associated with mortality between initial and recurrent IE episodes in PWID. Methods: A retrospective cohort study based on chart review was conducted between February 2007–March 2016. We included adult inpatients (>18) at tertiary care centers in London, Ontario who met a diagnosis of definite IE based on the Modified Duke’s Criteria. Results: 390 patients had endocarditis with 212/390 in PWID. 68/212 (32%) PWID had a second episode with 28/212 (12%) having additional recurrences. Second episode IE is more common in PWID (14/179 [6.2%] vs 68/212 [24.3%]; p<0.001) with injection drug use increasing the risk of second episodes more than fourfold (RR 4.46, 95% CI 2.21-8.99; p<0.001). There are few clinical differences between first and second IE episodes in PWID; however, the microbial etiology varies. There are significantly less S. aureus infections (165/212 [78%] vs 43/68 [63%]; p=0.03) and a wider variety of infectious organisms are seen causing second episode IE (Figure 1). In particular, fungal IE is more common in second episodes (1/212, 0.5% vs 5/68, 7.4%, p=0.002). Additionally, fungal infection in recurrent endocarditis was associated with increased mortality in PWID with an adjusted HR of 4.43 (95% CI 1.27-15.5, p=0.02). Conclusions: PWID are at significantly higher risk of recurrent IE. Fungal endocarditis is more common in recurrent endocarditis and is associated with increased mortality, suggesting that providers should consider empiric antifungal therapy in PWID with suspected IE and a history of previous IE.
Microbiology of First Episode Infective Endocarditis in PWID
(n=212, #, %)

- Staphylococcus aureus: 165 (78%)
- Coagulase-negative staphylococci: 13 (6%)
- Viridans group streptococci: 1 (0.5%)
- Non-viridans group streptococci: 1 (0.5%)
- Enterococci: 5 (2.4%)
- Enterobacter: 1 (0.5%)
- Pseudomonas & acetinobacter: 1 (0.5%)
- Fungal: 1 (0.5%)
- Culture Negative / Unknown: 1 (0.5%)
- Other: 1 (0.5%)
- Polymicrobial: 1 (0.5%)
Figure 1: Microbial Etiology of First Episode and Recurrent Endocarditis in PWID

a) first episode etiology b) recurrent episodes etiology
Cost Analysis of Outpatient IV Clinic Daptomycin Use compared to Inpatient Vancomycin Use in the Treatment of Patients with Resistant Gram Positive Infections

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Objectives:} Assess the most cost effective method of delivering treatment to patients with resistant gram positive infections who are not eligible for Home Parenteral Therapy (HPT) and identify patient factors leading to barriers to discharge with HPT. \textbf{Methods:} A six-month retrospective chart review at an inner city, tertiary care hospital in Edmonton, AB, identified patients receiving daptomycin as an inpatient or outpatient for serious MRSA or VRE infections. A cost analysis was done for the patients with serious MRSA infections who either started or completed their course of daptomycin therapy in the outpatient antimicrobial therapy (OPAT) clinic because they were not eligible for HPT with vancomycin due to no fixed address, no refrigeration in home, no medication coverage, or were denied by the HPT Program for other reasons. Hospital stay, OPAT visit, antibiotic drug (based on an 80 kg patient with normal renal and liver function) and administration costs were provided by Alberta Health Services. \textbf{Results:} 21 patients started or completed their daptomycin treatment courses in the OPAT clinic. Seven patients (33.3\%) received daptomycin without an appropriate indication and were excluded from the cost analysis. Four patients (19.0\%) received daptomycin due to allergy to vancomycin or infection with vancomycin resistant organisms. Ten patients (47.6\%) received daptomycin via OPAT as they could not be discharged on vancomycin via HPT. Compared to inpatient vancomycin, using daptomycin in OPAT resulted in a 45\% cost savings and using vancomycin in OPAT would have resulted in a 20\% cost savings for these 10 patients. \textbf{Conclusions:} OPAT clinic daptomycin use is a cost-effective way to facilitate discharge for patients requiring vancomycin that are not eligible for HPT.

Table 1:

<table>
<thead>
<tr>
<th></th>
<th>Cost (Canadian dollars)</th>
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<tbody>
<tr>
<td>Vancomycin (inpatient)</td>
<td>131,965</td>
</tr>
<tr>
<td>Vancomycin (IV clinic)</td>
<td>98,916</td>
</tr>
<tr>
<td>Daptomycin (IV clinic)</td>
<td>72,630</td>
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</table>
THE ONTARIO PROGRAM TO IMPROVE ANTIBIOTIC USE (OPTIMISE): Defining Appropriate Antibiotic Prescribing in Primary Care – a Modified Delphi Panel Approach

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Background: More than 90% of antibiotic use in Canada occurs outside hospital settings; however, there is currently no consensus or benchmark defining appropriate antibiotic use in Canadian primary care settings. The objective of this study was to define expected appropriate outpatient antibiotic prescribing rates for 23 clinical conditions using a modified Delphi method. Method: An initial online questionnaire on percentage of visits for which an antibiotic should be prescribed for each condition was sent to a nine-member multidisciplinary expert panel; including community and academic family physicians, adult and paediatric infectious disease physicians, and antimicrobial stewardship pharmacists. Conditions that did not reach consensus were discussed during face-to-face meetings with anonymous voting. This process was repeated until 100% consensus was reached. Results: Three of 69 clinical scenarios (23 conditions by three age groups) reached consensus online. The remaining 66 were discussed face-to-face. The average number of rounds required to reach consensus was 2.6 (min: 1; max: 5). Appropriateness rates, some of which differed by age groups (i.e., <2, 2-18, >18 years) where appropriate, were: pneumonia (100%); pyelonephritis (100%); non-purulent skin and soft tissue infections (SSTI) (100%); other bacterial infections (100%); reproductive tract infections (100%); urinary tract infections (95-100%); prostatitis (95%); epididymo-orchitis (85-88%); chronic obstructive pulmonary disease (50%); purulent SSTI (35-50%); otitis media (30-40%); pharyngitis (18-40%); acute sinusitis (18-20%); chronic sinusitis (14%); bronchitis (5-8%); gastroenteritis (4-5%); dental infections (4%); eye infections (1%); otitis externa (0-1%); asthma (0%), common cold (0%), influenza and other non-bacterial infections (0%). Conclusions: Using a rigorous method this study defined the levels of appropriate antibiotic prescribing among community primary care providers. These results can be applied to community antimicrobial stewardship programs to define the level of inappropriate use and therefore set targets to optimize outpatient antibiotic use.
Marked Reduction in Urine Cultures Collected from Long-Term Care Residents after Targeted Use of Intensive Education and a Long-Term Care Urinary Tract Infection Medical Directive

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Background: Asymptomatic bacteriuria is exceedingly common in the elderly population, particularly in residents of long-term care (LTC) facilities. Urine cultures are frequently ordered leading to unnecessary and often harmful treatment. Our primary objective was to determine if there was a reduction in urine cultures before and after implementing two different targeted strategies at LTC sites in the province. The first strategy was a medical directive at two public LTC sites, the second strategy being intensive education to private LTC sites. Methods: A Urinary Tract Infection (UTI) Medical Directive was implemented at one of 9 public LTC sites in March/April 2016 and at the second site in September 2017. Intensive education on asymptomatic bacteriuria was given at 5 of 9 private facilities and to all of the private LTC directors starting in November 2016 and finishing in April 2017. All urine cultures collected were evaluated from January 2015 to September 2018 using the Cerner laboratory information system. Results: The first public site saw a reduction from an average of 6.5 to 2.2 urine cultures per month (66% reduction), while the second site showed a similar decrease from 21.0 to 11.3 cultures per month (54% reduction). Similarly, there was a 60% reduction in urine cultures observed at 6 months across all private LTC sites, with a retained decrease of 50% noted at 12 months post-education. In comparison, the public LTC sites as a whole did not see a noticeable difference in urine cultures collected during the same 32-month period. Conclusions: Both a nursing-led UTI Medical Directive and targeted educational efforts resulted in a marked reduction in urine cultures sent for lab testing from LTC facilities. Facilities not receiving either of these two interventions did not see a change. Future analysis will include studying the potential impact on antibiotic microbial use and resistance.
Evaluating the Impact of Prospective Audit and Feedback on the use of Clindamycin and Quinolones in Medicine Clinical Teaching Units

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Background: Antimicrobial usage of quinolones and clindamycin was noted to be greater on the general medicine units of a large academic healthcare institution. The Antimicrobial Stewardship Program (ASP) implemented a prospective audit and feedback (PAF) strategy to optimize prescribing of these agents given their propensity to cause Clostridium difficile infection (CDI). This study evaluated the impact of PAF interventions on quinolone and clindamycin use and the incidence of CDI on clinical teaching units (CTU). Methods: A PAF strategy was introduced in April 2015 at a large two-site academic healthcare institution housing six Clinical Teaching Units for general medicine patients. Using a face-to-face PAF model with medical teams (senior medical resident and team pharmacist), the ASP conducted twice daily reviews of all patients receiving antimicrobials. Clindamycin and quinolone utilization were compared using defined daily doses (DDD) per 1000 patient days pre and post-intervention. CDI rates were also monitored. Results: There was an overall reduction in quinolone use by 68.2% and 75.4% at Site 1 and Site 2, respectively. Clindamycin use decreased in the first year at both sites by 50.5% and 30.8%, respectively. As the use of both antimicrobial classes decreased, the corresponding CDI rates at both sites also decreased.

Table 1: Antimicrobial Consumption and CDI Rates on CTU

<table>
<thead>
<tr>
<th>Site</th>
<th>Antimicrobial Use (DDD/1000 Patient Days)</th>
<th>CDI Rate/1000 Patient Days</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>Clindamycin</td>
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<td>Ciprofloxacin</td>
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<td>Site</td>
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<td>Clindamycin</td>
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<td>1</td>
<td>Pre-PAF (2014-15)</td>
<td>129.80</td>
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<td></td>
<td>Year 1 PAF (2015-16)</td>
<td>64.22</td>
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<td>Year 2 PAF (2017-18)</td>
<td>73.31</td>
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<td>2</td>
<td>Pre-PAF (2014-15)</td>
<td>68.37</td>
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<td>Year 1 PAF (2015-16)</td>
<td>508.66</td>
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<td>Year 2 PAF</td>
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<td>(2017-18)</td>
<td>46.18</td>
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**Conclusion:** The implementation of targeted PAF interventions successfully reduced usage of clindamycin and quinolones, with resultant decreases in CDI incidence.
Provision of Antibiotic Prescribing Feedback to High-Volume Primary Care Physicians: Design and Implementation of a Randomized Controlled Trial

KI Schwartz1,2,3, N Ivers4, B Langford1, V Leung1, KA Brown1, N Daneman5, M Silverman6, S Elsayed6, J Wu1, E Shing1, J Leis5, G Garber1

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Objectives: We partnered with provincial health system organizations to conduct a pragmatic randomized controlled trial, mailing letters to the highest antibiotic-prescribing primary care physicians across Ontario, Canada. Herein, we describe the methodology and present early findings on implementation and acceptability of the intervention. Methods: We used the IQVIA Xponent™ database to identify the top 3500 (27%) of 13,102 Ontario primary care physicians prescribing the highest number of antibiotics by volume dispensed. These physicians were randomized 3:3:1 to letter 1, letter 2, and control (no letter). The letters incorporated persuasive communication and provided normative social comparisons and change ideas for appropriate antibiotic initiation for acute respiratory infections (letter 1) or recommended treatment durations for uncomplicated infections (letter 2). The letters were drafted with extensive stakeholder engagement. Waiver of consent was granted by the ethics research board and all physicians, including controls, will receive an additional letter with a debrief after one year. An email address was provided within the letter for those wishing to ask questions or provide feedback. These responses were organized into common themes. Results: A total of 3000 letters were sent in December 2018. Participants prescribed more than 442 (average=1031) antibiotics in the prior year. We received 31 (1%) responses within one month. The most common themes were i) concerns regarding lack of case-mix adjustment in the measurement of performance (n=30) and ii) interest in ongoing reflection about antibiotic prescribing (n=10). Only three (0.1%) physicians opted out. Conclusions: Provision of unsolicited antibiotic prescribing feedback to primary care physicians is feasible and inexpensive particularly for jurisdictions that have antibiotic use data. Adjusting for patient volume may enhance acceptance of feedback. Changes in antibiotic prescribing rate and proportion of prolonged treatment durations will be evaluated as trial outcomes at 6, 12, and 24 months. NCT03776383.
The 2018 Global point prevalence Survey of antimicrobial usage (AMU) and resistance in 42 Canadian Hospitals

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Objectives: The Global Point Prevalence Survey (PPS) is a well-established initiative for monitoring AMU and resistance. We report the results of a survey conducted in 42 hospitals in 2018. Methods: The electronic PPS questionnaire was completed by each site for all inpatients receiving antimicrobials on a selected day between January and December 2018. Data collected included ward type, demographics, antimicrobial prescribed, indication(s), local guideline compliance, and antimicrobial-resistant organisms. A web-based application was used for data entry and reporting (www.global-pps.com). Results: Canadian survey participation increased by 200% from 2017. Of the 42 hospitals, 25 were teaching institutions, including 14 tertiary care centres. The survey screened 11,748 patients on 702 wards. One-third of patients (n=3924) received at least one antimicrobial, and 31% were on at least one antibiotic (AB). Of the 4779 antibiotic courses, 49% were for community-acquired infections, 30% for hospital-acquired infections, 11% for surgical prophylaxis (SP), and 7.3% for medical prophylaxis. The most commonly treated infection was respiratory (27%). The 5 most frequently prescribed antibiotics were piperacillin/tazobactam (15%), cefazolin (12%), ceftriaxone (10%), vancomycin (8.4%), and ciprofloxacin (7%). Carbapenem use accounted for 5.2%. Of the targeted antibiotic therapies (n=1481) 5.6% were for MRSA, 2.8% for ESBL, 0.74% for VRE, and 0.14% for carbapenemase-producing Enterobacteriaceae. Antibiotic indication and stop date were documented in 60% and 64% of charts, respectively. Guidelines were available for 77% of the therapies with reported compliance of 81%. SP was greater than 24 hours in
29% of instances. **Conclusions:** This type of PPS of AMU is increasingly used in Canadian hospitals and identifies targets for interventions to improve AMU and provide benchmarks for hospitals to compare. Areas for improvement include indication documentation, antimicrobial stop dates, and prolonged SP. Overall the prevalence of treatment for multi-drug resistant organisms in Canada continues to be relatively low.
Direct Vitek 2™ Susceptibility Testing (DST) on Enterobacteriaceae from Blood Culture Samples

D Gregson¹,², W Chan¹,², S Buchan¹, D Doyle¹, J Pitout¹,²

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Purpose: To compare DST testing of Enterobacteriaceae in patients with positive blood cultures (BC) with standard testing using Vitek 2™ gram-negative cards. Methods: BC’s were performed using the BacT/Alert™ system. BC’s positive for gram-negative bacilli on staining were subject to a 1.5 ml sample being lysed and washed for direct MALDI identification. Residual sample was processed for susceptibility testing as per the standard Vitek II protocol. Vitek II susceptibility results of plate based cultures were considered the gold standard. Results were interpreted using CLSI guidelines. Reportable antibiotics for Escherichia, Klebsiella, and Proteus spp. (EKP spp.) in our laboratory are gentamicin (GNT), ceftriaxone (CTRX), piperacillin-tazobactam (PTZ), meropenem, ertapenem, ciprofloxacin (CIP) and cotrimoxazole (SXT). For Enterobacter, Citrobacter, Serratia and Morganella spp (EbCSM spp.) ceftriaxone is replaced with cefepime and PTZ is not reported. Correlation was classified as categorical agreement (CA), minor errors (mE), major errors (ME) and very major errors (VME) according to CLSI guidelines. Results: For 33 EbCSM isolates, there was categorical agreement in all results. Antibiotic resistance in this group was limited to 4 isolates resistant to SXT and 2 resistant to GNT. In the EKP group (n = 492), resistance to GNT/CIP/CTRX/PTZ/SXT occurred in 9/23/16/2/33 % of isolates respectively. There was no carbapenem resistance. VME occurred only in the SXT results (5/161). One ME occurred for all antibiotics reported for a single isolate. For PTZ, mEs occurred in 29 (6%) cases. With the exception of PTZ and SXT, categorical agreement was >99% (95%CI 98.4 - 100%). Results from DST were available approximately 18 hours before standard test results. Conclusion: With the exception of SXT results, DST correlates well with standard testing and can be used to appropriately direct therapy in patients with bacteremia due to these organisms.
I01

**Surveillance for Babesia in Canadian blood donors using the ultra-sensitive Procleix® Babesia Assay (PBA) and secondary laboratory testing methods: July-October 2018.**

S Stramer¹, MC Proctor¹, L Tonnetti¹, V Brès², JM Linnen², F Bernier³, G Delage³, Y Grégoire³, J Labrie³, M Bigham⁴, Sj Drews⁴, G Hawes⁴, S O’Brien⁴, V Scalia⁴, M Fearon⁴

¹American Red Cross, Gaithersburg, MD, USA, ²Grifols Diagnostic Solutions Inc., San Diego, USA, ³Héma-Québec, Ville Saint-Laurent (Québec), Canada, ⁴Canadian Blood Services, Ottawa, ON, Canada

**Background:** Babesia microti is a tick-borne intra-erythrocytic parasite, causing transfusion transmitted infections (TTI), which now threatens the donor blood supply in the Northeastern/upper Midwestern US. A previous limited Canadian seroprevalence study (2013; n=13,993) did not identify B. microti antibodies in Canadian donors Manitoba-eastward. The babesiosis and Lyme disease vector, Ixodes species, is spreading in Canada with an increase in Lyme disease cases reported. Here, we report a follow-up widescale surveillance study of Canadian blood donors using the highly sensitive Procleix® Babesia Assay (PBA) (LOD=1-4 parasites/mL), an investigational nucleic acid test for detection of B. microti, B. divergens, B. duncani, and B. venatorum on the Panther® system. **Methods:** Both randomized and selected EDTA-plasma retention tubes (n=50,586) collected from Canadian blood donors (tick season; July-October 2018) were shipped to the American Red Cross (ARC) for screening by minipool lysates (MPLs; pools of 16) using the PBA. Reactive pools were deconvoluted and resultant donor lysates (IDLs) retested in duplicate. Reactive donations were tested by secondary methods specific for B. microti: ARC IgG immunofluorescence assay [IFA] and IMUGEN PCR (LOD=66 parasites/mL). Another subset of randomly selected PBA-non-reactive samples (Manitoba-eastward, n=14,710) were screened using ARC IFA and if positive, IMUGEN IFA and PCR. **Results:** Of 50,586 donors, one (0.002%) was PBA-reactive with additional ARC IFA-positive (≥1:1024) and PCR-negative test results. Of PBA-non-reactive donors, 3/14,710 (0.02%) were positive by one secondary testing method (ARC IFA [range 1:128-1:512]), while 1/14,710 (0.007%) was positive by more than one secondary testing method (ARC IFA-positive [1:512], IMUGEN IFA-positive (≥1:128)). None of the implicated donors had relevant travel history. **Conclusions:** B. microti is gaining a foothold in the Canadian blood donor population. Future laboratory surveillance of Canadian blood donors using highly sensitive methods for Babesia (including species other than B. microti; current prevalence unknown) is warranted.
Prevalence of Pertactin-Deficient *Bordetella pertussis* Isolates in Ontario, Canada from 2009 – 2017

S Bolotin\(^1,2\), A Marchand-Austin\(^1\), R Tsang\(^3\), M Shuel\(^3\), NS Crowcroft\(^1,2\), K Schwartz\(^1,2\), SL Hughes\(^1\), L Friedman\(^1\), K Cronin\(^4\), J Ma\(^2\), G Van Domselaar\(^3,5\), M Graham\(^3,5\), S Tyler\(^3\), FB Jamieson\(^1,2\)

\(^1\)Public Health Ontario, Toronto, ON, Canada, \(^2\)University of Toronto, Toronto, ON, Canada, \(^3\)National Microbiology Laboratory, Winnipeg, MB, Canada, \(^4\)National Microbiology Laboratory, Toronto, ON, Canada, \(^5\)University of Manitoba, Winnipeg, MB, Canada

**Background:** Despite high vaccine coverage, a resurgence of *Bordetella pertussis* has been observed in recent years, particularly in countries that administer the acellular pertussis vaccine. In many jurisdictions, this resurgence has coincided with the emergence in 2011 of *B. pertussis* strains deficient in pertactin (PRN-N), a virulence factor that is a component of the acellular pertussis vaccine used in Canada and elsewhere. The objective of our study was to measure trends in the prevalence of pertactin-deficient strains in Ontario, from 2009-2017. **Methods:** We characterized all available isolates from 2009-2017 using Western blot analysis performed at the National Microbiology Laboratory and Public Health Ontario laboratory. We performed epidemiological analyses to assess whether there were significant associations in PRN-N status by year, age-group or whole-cell vs. acellular pertussis vaccine program-eligibility. **Results:** Of the 413 isolates available for characterization, 34.6% (143/413) were PRN-N. These first emerged in 2011, reaching a maximum prevalence of 70.8% (34/48) in 2016, decreasing thereafter to 46.2% (30/65) in 2017 (chi2 test for trend p=0.0003). From 2009-2017, the <6 month age-group had the highest PRN-N prevalence at 36/84 (42.9%) (chi2 p=0.29). There was no statistically significant difference in the proportion of PRN-N isolates from individuals eligible for priming doses of whole-cell vs. acellular pertussis vaccine (p=0.95). **Conclusions:** PRN-N strains emerged in Ontario in 2011, coinciding with emergence in other jurisdictions globally; so far, PRN-N in Ontario remains lower in prevalence than is observed in some other jurisdictions. Although no statistical association was observed for PRN-N prevalence by vaccine program-eligibility, this may have been impacted by selection bias of available and archived *B. pertussis* isolates. Future studies should include case vaccination history to elucidate the potential association between PRN-N strains and whole-cell vs. acellular vaccine priming.
Clostridioides difficile Strain Divergence Over Time

Dj Speicher1,2, K Luinstra2, J Maciejewski2, KK Tsang1, AG McArthur 1, M Smieja3,2

1M.G. DeGroote Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, DeGroote School of Medicine, McMaster University, Hamilton, ON, Canada, 2Department of Laboratory Medicine, St. Joseph’s Healthcare Hamilton, Hamilton, ON, Canada, 3Pathology & Molecular Medicine, McMaster University, Hamilton, ON, Canada

Background: Clostridioides difficile infection (CDI) is a serious hospital-associated infection with severe outbreaks caused by the hypervirulent NAP1/MLST-1 strain. Whole genome sequencing has shown that most outbreak strains are clonal whereas non-outbreaks display a wide diversity of strains. To examine strain diversity in clinical settings, a subset of C. difficile isolates from symptomatic CDI from an acute care hospital were compared to isolates from C. difficile colonized (CDC) asymptomatic subjects from the same hospital. Methods: A subset of PCR-positive stool samples from clinically confirmed CDI isolates from 2016 (13/110), 2017 (8/111), and 2018 (13/65), and CDC from 2017 (17/185) were cultured 3-times consecutively on CHROMagar™ C. difficile, sub-cultured on Columbia colistin-nalidixic acid (CNA) media, had DNA isolated, shotgun sequenced, and genome assembled for both MLST typing and genome-wide SNP phylogenetic analysis. Results: Based on MLST profiles, the C. difficile types detected were diverse. Of the presumed binary toxin positive/NAP1 strains (i.e. PCR tcdA/tcdB positive) 7/12 (58%) were NAP1/MLST-1 and 3/12 (25%) were NAP7/MLST-11. NAP1/MLST-1 was not detected in any CDC isolate. NAP4/MLST-2,14 were detected in 2016 (n=4), 2017 (n=2), 2018 (n=1), and in CDC isolates (n=3). MLST-42 was dominant in CDC isolates (5/17; 29%) and decreased in prevalence in CDI isolates over time (2016=4; 2017=0; 2018=1). Conclusion: C. difficile strains amongst both CDI and CDC individuals are highly divergent. Whilst molecular assays are misclassifying 25% of “NAP1” strains, both NAP1 and NAP7 are hypervirulent. The number of MLST-42 CDC isolates is concerning as it has been reported to be the most common strain causing CDI among U.S. adults. This highlights the need for continued genomic surveillance of both CDI and CDC individuals. Genome-wide SNP phylogenetic analysis is currently being performed.
A multi-jurisdictional outbreak of hepatitis A in Ontario, Canada in 2017-2018: The role of genetic sequencing in outbreak detection and response

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1Public Health Ontario, Toronto, ON, Canada, 2Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada, 3Department of Epidemiology and Biostatistics, Schulich School of Medicine and Dentistry, Western University, London, ON, Canada, 4Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada, 5National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB, Canada, 6Department of Medical Microbiology, University of Manitoba, Winnipeg, MB, Canada, 7Toronto Public Health, Toronto, ON, Canada

Objectives: In recent hepatitis A outbreaks in Europe and the United States (US), genetic sequencing has contributed to timely outbreak detection and response. We describe the epidemiology of an ongoing multi-jurisdictional outbreak of hepatitis A in Ontario, Canada, and discuss the role of hepatitis A virus (HAV) genetic sequencing. Methods: Outbreak-confirmed cases were defined as hepatitis A cases with presence of anti-HAV IgM antibody occurring on or after June 1, 2017, in Ontario residents or visitors, with the same HAV genotype (1A) and genetic sequence (VRD_2016_521). Local health units reported epidemiological information in Ontario’s integrated Public Health Information System (iPHIS). Public Health Ontario (PHO) Laboratory referred positive specimens to the National Microbiology Laboratory for sequencing. PHO analyzed iPHIS data. Results: From June 1, 2017 to December 31, 2018, 124 outbreak-confirmed cases of hepatitis A with the HAV genotype 1A, VRD_2016_521 sequence were reported in ten Ontario health units. This strain was circulating in recent HAV outbreaks in Europe and the UK among men who have sex with men (MSM). In Ontario, the median age of cases was 33 years, 59% were male, and 48% were hospitalized. Reported risk factors included illicit drug use (59%), being under-housed (20%), and MSM (12%); most did not travel. In the first affected health unit, sequencing and epidemiological data supported person-to-person transmission among MSM predominantly. However, different health units and groups were affected over time; responses (e.g., targeted promotion of hepatitis A vaccination) focused on populations most at risk locally. Overall, 35% of outbreak cases did not have any risk factor information, i.e., were associated with this outbreak based on genetic sequencing. Conclusions: HAV genetic sequencing and public health surveillance enabled timely outbreak detection and response. Sequencing has helped understand the burden of this ongoing outbreak and inform local responses.
WITHDRAWN
An update of Cryptococcus Molecular Typing results in British Columbia (2011 to 2018)

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¹BCCDC Public Health Laboratory, Vancouver, BC, Canada, ²University of British Columbia, Vancouver, BC, Canada

Objective: C. gattii was previously associated with tropical and subtropical areas until it emerged in 1999 on Vancouver Island, British Columbia (BC) and later spread to the BC Mainland and into the Pacific Northwestern US. In this study we are reporting on the trends of Cryptococcus in BC based on their Restriction Fragment Length Polymorphism (RFLP) patterns to compare the current circulating isolates with previous outbreak strains results. Methods: C. gattii is reportable in BC, with other Cryptococcus species, are referred to the laboratory for subtyping. Cryptococcus isolates (n=251) were recovered using CGB agar from clinical and veterinarian samples between 2011 and 2018. The DNA of isolates was amplified through PCR targeting the URA5 gene. The typing was elucidated from the two sets of restriction enzymes on the amplicons. Results: Approximately 19 C. gattii isolates in average are received annually, with 2012 being the peak year (n=31), while only 8 isolates was received in 2018. Approximately 0.80% (2/251) of the CGB agar results is consistent with the RFLP typing result. This also has been observed in our past surveillance. Seven RFLP types have been identified in the study, 60.16% of them belong to G group (C. gattii) while 39.84% are N group (C. neoformans). The variant G (VG) group is subdivided into VGI-VI, of which VGIIa continues to be predominant in BC. Conclusion(s): Until 2018, the numbers of Cryptococcus isolates were steady except for the peak year in 2012. However, this dropped dramatically in 2018. The VGIIa, the previous dominant outbreak type, continues to be the major RFLP type in BC (84.11% in the C gattii group). All the animal isolates (from bird, cats, horses, dolphin, porpoises, and seals) are all C. gattii which belonged to VGI, VGIIa, and VGIIb type, strains endemic in BC.
ORAL PRESENTATIONS
Saturday, April 7, 2019
10:30 – 12:00 Session J
Room: Governor General I

J01

HCV Screening via Rapid Point of Care Testing in Patients on Opiate Substitution Therapy in Peel Region, Canada

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Background: Chronic Hepatitis C virus (HCV) infection can lead to cirrhosis, liver failure and liver cancer. Recent data has demonstrated that HCV infected patients who are actively injecting drugs or on opiate substitution therapy (OST) have excellent outcomes with new direct-acting antiviral therapy. Barriers to HCV care for OST patients include a) invasive sampling, b) delayed result turnaround, c) lack of physician awareness, d) loss to follow-up. We sought to investigate trends in the standard-of-care blood testing (SOC) vs point-of-care (POC) with respect to diagnosis and linkage-to-care in patients on OST at 3 clinics in Peel Region, Ontario. We hypothesized that patients with a positive HCV-Ab obtained via the POC test will have increased linkage-to-care. Methods: We used a commercially available POC rapid HCV-Ab test (OraQuick®) that has high specificity and sensitivity in detecting HCV-Ab. Subjects were randomized 1:1 to receive SOC or POC test. Results: 40 (100%) oral POC swabs tested negative for HCV-Ab. SOC blood results were received for 7/40 (18%) patients, all HCV-Ab negative. Of 80 patients enrolled, 32% were female; 67% were Canadian-born and 19% were born in India. 62% of patients were unaware of their HCV status, whereas 38% were aware of a previous negative HCV-Ab result. 12/23 (52%) patients on OST enrolled from one clinic had no history of injection drug use. Conclusion(s): The proportion of patients for whom HCV-Ab results were available was greater in POC than SOC. All patients for whom results have been received have tested negative and therefore no linkage opportunity was triggered. It was surprising that in a marginalized population with significant risk factors for HCV infection, no cases were identified; perhaps due to the small sample size, or lower incidence of injection drug use. The study demonstrated that POC testing uptake worked well as a rapid screening method.
Rapid starts to stop Hepatitis C: Same day Hepatitis C Treatment Starts Enhancing Patient Engagement and Follow-up in a Vulnerable, Treatment-naïve Population

S Greenan1, G Carruthers1,2, L Barrett2,3

1Health PEI, Charlottetown, PEI, Canada, 2Dalhousie University, Halifax, NS, Canada, 3Nova Scotia Health Authority, Halifax, NS, Canada

Background: HCV elimination requires alternate care models for key populations. Beyond diagnosis, engaging people in HCV treatment that leads to treatment completion and cure is a large barrier to HCV elimination. Research in the HIV field has demonstrated better health care engagement with rapid, same day treatment starts. Our objective is to determine if rapid access to HCV treatment improves engagement in HCV and non-HCV health care.

Methods: Patients are identified and referred to PEI’s HCV elimination program through public health, community providers, or ‘bring-a-friend’ strategies. Program staff facilitate baseline blood work, do preliminary drug-drug interaction checks, and book a first appointment within 1-2 weeks of blood work. Treatment-naive patients without contraindications are offered glecaprevir/pibrentasvir to start treatment at the first visit. Medication adherence, side effects, SVR12, and attendance at opioid substitution therapy clinics are self-reported.

Results: Patients assessed between February-December 2018 were included. 143 patients were referred and 103 (72%) were seen for initial visits. Of those who attended the first visit, 6 had contraindications to treatment (5 medication interactions and 1 pregnancy). Of the treatment-naïve individuals eligible for treatment, 97 (100%) started treatment. 85 (87.6%) patients started treatment on their first visit, with 5 discontinuations (3 for non-HCV related reasons, 2 due to undetected HCV viral load). 1 patient was lost to follow-up before SVR. 74 (76.2%) have completed treatment with 27 (27.8%) achieving SVR. Importantly, individuals with difficulty attending opioid substitution clinic appointments before HCV treatment had improved attendance at appointments out to the SVR timepoint. Attendance for other medical appointments was variably improved. No significant safety issues were noted.

Conclusions: Rapid treatment start is safe, and has a very high rate of successful HCV and non-HCV care engagement. Same day, first visit HCV treatment start should be explored as an HCV elimination tool.
Burden and clinical impact of non influenza respiratory viral nirv infections among hospitalized adults

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Objectives: The burden and clinical significance of non-influenza respiratory viral (NIRV) infections among hospitalized patients are poorly understood. This study aimed to analyze their characteristics, severity, outcomes, and estimate impacts relative to influenza. Methods: Multiplex PCR-based respiratory viruses surveillance data from two university-affiliated hospitals during the 2014/15–2017/18 seasons were analyzed. All adult (>17 years) hospitalized patients with acute respiratory illnesses tested positive for 1 (or more) of the 18 virus targets using Luminex RVP/RPP assays (FLU=influenza viruses; NIRV=RSV, parainfluenza viruses, rhinoviruses/enteroviruses, coronaviruses, human metapneumovirus and adenovirus) were included. Prospective data in infection control surveillance programs was extracted and electronic records were reviewed. Interim analysis results are reported. Results: Among the 1364 infections analyzed, half (51.6%, 42.7%–56.5%) were caused by NIRVs. RSV (13.2%) and rhinoviruses/enteroviruses (13.0%) were the commonest. NIRV (n=704) and FLU (n=660) patients differed in their characteristics: age (62.4±20.1 vs 67.8±18.2 years, P<0.001), immunocompromised (36.4% vs 27.0%, P=0.002), hospital-acquired (17.9% vs 13.5%, P=0.032), diagnosed by LRT samples (9.0% vs 6.1%, P=0.051). Clinical severity/outcomes were not significantly different: ICU admission (22.3% vs 19.9%), ICU length-of-stay (14.6±18.3 vs 14.8±21.7 days); assisted ventilation (24.4% vs 18.8%); lower respiratory and cardiovascular complications (60.6% vs 60.9%); probable bacterial superinfections (5.3% vs 3.2%); weighted ordinal outcome score (2.0±3.5 vs 1.9±3.2); 30-day mortality (9.0% vs 7.4%). Immunocompromised state independently predicted higher mortality (Cox-regression aHR 1.9, 95%CI 1.2–2.9, P=0.005) [Figure]. Conclusions: NIRVs may cause severe illness and high mortality similar to influenza among the hospitalized adults. Burden of disease is substantial. The unmet need for antiviral therapy and vaccination against NIRVs in adults should be promptly addressed.
Kaplan-meier curves showing probability of survival of hospitalized adults diagnosed with non-influenza respiratory virus infections (NIRVs) and influenza (FLU) using multiplex PCR assays. Adjust survival function (for age, gender, immunocompromised state) showed insignificant difference between:
(a) NIRV vs FLU [aHR 1.3, 95%CI 0.8-2.0, P=0.24], and (b) individual viruses [P=0.52]
WITHDRAWN
Decline in Yield of Acute HIV Infections Detected Using Pooled Nucleic Acid Testing Following Implementation of 4th Generation Screening

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Background: HIV RNA nucleic acid tests (NAT) have a shorter window period (i.e., the time from infection to laboratory-based HIV detection) compared to HIV screen tests which detect antibodies alone (1st to 3rd generation tests). With the introduction of 4th generation screening tests, which detect both HIV antibodies and p24 antigen, many acute HIV infections (AHI) are detected earlier than by 3rd generation screening, thus reducing the impact of pooled NAT testing. Methods: We examined the AHI yield of pooled NAT for three time periods: 1) May 2013 to May 2015: 3rd generation screening; 2) May 2015 to May 2017: 4th generation; and 3) May 2017 to Aug 2018: 4th generation. Screen test negative samples from individuals at high risk of HIV infection were combined into pools of 24 and tested for HIV RNA. AHI was defined as screen test negative, and HIV RNA positive; early HIV was defined as screen test positive, immunoblot negative or indeterminate, and HIV RNA positive. We compared the AHI and early HIV case yields by time period. Results: For the three periods, 598,269, 765,477 and 502,863 specimens respectively were screened, and 834, 969 and 869 pools were RNA NAT tested. Case yields were: 1) 30 AHI; 54 early HIV; 2) 7 AHI; 77 early HIV; and 3) 2 AHI; 29 early HIV. AHI case yields based on pools tested declined from 3.6% to 0.72% and 0.23%, respectively (period 1 vs. 2: p<0.0002). Conclusions: AHI cases diagnosed solely by pooled NAT declined significantly after introduction of 4th generation screening. The decline has continued into the most recent period, even as the number of tested pools increased over time. Pooled NAT adds considerably to program screening costs, and further studies are required to determine whether this approach to AHI detection remains cost-effective.
Sequence-Based Typing of Enteroviruses from Clinical Specimens, 2017-2018

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Objectives: Enteroviruses cause a wide range of human infections, ranging from mild respiratory tract infections, to severe central nervous system infections. Many enterovirus strains are associated with specific clinical syndromes. Surveillance of circulating enteroviruses within a population has important implications for public health. Historically, isolates of enteroviruses were characterized into 71 serotypes. More recently, sequence-based typing has led to the identification of many more genotypes than were previously recognized. Methods: Over a 19 month period (June 2017 to December 2018), specimens positive by PCR for enterovirus/rhinovirus were sequenced. Subtyping of the specimens was performed by partial Sanger sequencing of either the 5’ untranslated region (5’-UTR) or the viral capsid protein (VP1). VP1 is better correlated with the serotype than is 5’-UTR, due to the capsid protein corresponding to the neutralization domains. Results: 110 specimens were sequenced (2017 n=32, 2018 n=78), 32 by 5’-UTR and 78 by VP1. Specimen types included CSF (25), superficial lesions (63), upper respiratory tract (15), stool (5) and blood (2). Sequences that yielded enough data for typing were obtained from 80 specimens; 30 specimens could not be subtyped. Genotypes identified included Coxsackie A2 (1), Coxsackie A6 (54), Coxsackie A9 (1), Coxsackie A16 (4), Coxsackie B5 (1), Coxsackie B9 (5), Echovirus 9 (1), Echovirus 30 (3), human Enterovirus 71 (4), Rhinovirus A (3) and Rhinovirus C (2). Conclusions: Coxsackie A6 viruses were detected most frequently from skin lesions, with 90% of typeable skin lesions positive for Coxsackie A6 virus during this period. CSF samples yielded a variety of enterovirus genotypes. Sequence-based typing of enteroviruses was possible from 70% specimens, and yielded useful information about circulating enteroviruses.
Optimization of a Next Generation Sequencing Assay for HBV Drug Resistance Testing

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Background: Next-generation sequencing (NGS) for Hepatitis B (HBV) resistance testing is a highly sensitive method, able to detect low-level mutant subpopulations. Our clinical virology laboratory transitioned from the GS Junior System (Roche 454) to the MiSeq (Illumina), but identified that MiSeq sequencing of low diversity amplicon libraries containing multiple samples was challenging due to sample mis-assignment and low-quality reads. Our study investigates the validation of the MiSeq for HBV resistance testing and troubleshooting of sequencing errors to enable clinical reporting of low-level mutations.

Methods: We performed amplicon sequencing of the hepatitis B RT gene on the MiSeq Reagent Nano Kit v2. HBV ATCC® 45020D™ was utilized to determine error rates for base calling. Several modifications were made to improve sample read assignments and base calling accuracy: unique dual indexes for each patient sample, PhiX concentration was increased to 33%, cluster density was reduced from 800 to 400 K/mm², Q-score trimming (Q30), and primers with staggered 1-4 base pair barcodes. A total of 56 patient samples were tested on both the GS Junior and MiSeq.

Results: Initial MiSeq results using a dual index PCR method with the recommended PhiX concentration of 12%, resulted in unacceptable levels of error rates for codon calling of up to 7%. After the above modifications were made, the error rates were less than 0.2%. There was a high agreement rate for patient samples between the GS Junior and MiSeq, with regards to total drug resistance mutations and patient sample agreement, 74/79 (94%) and 51/56 (91%), respectively. HBV genotype results were concordant for 56/56 samples.

Conclusions: HBV resistance testing with the MiSeq required significant modifications to decrease sample mis-assignments and base calling errors. With these modifications, accuracy was improved, and mutations could be reported with confidence for subpopulation levels as low as 1%.
Evaluation of a Target Hybridization-Based Next-Generation Sequencing Assay for Diagnosis of Acute Respiratory Tract Infections

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Objective: The ONETest™ (Fusion Genomics Corp., Canada) is a next-generation sequencing (NGS) assay utilizing target hybridization that identifies 48 viral and bacterial respiratory pathogens. In this retrospective pilot study, we evaluated the performance of the ONETest™ to detect respiratory pathogens in patients diagnosed with acute respiratory tract infections. Methods: We selected 36 archived nasopharyngeal swabs collected from patients who were admitted to the Sunnybrook Health Sciences Centre (Toronto, ON) in 2018. Mid-turbinate swabs from patients with respiratory symptoms were tested using the NxTAG Respiratory Pathogen Panel (RPP, Luminex Corp.) as per protocol. RNA extracted from a representative subset of the swabs (19 positive and 17 negative as per the RPP) was tested using the ONETest™. NGS library preparation and probe-based target hybridization were conducted following the ONETest™ proprietary protocol; the target-enriched libraries were sequenced on an Illumina HiSeq; the NGS data were analyzed using the FusionCloud pipeline. The output includes pathogen identity, type/subtype, estimated pathogen load (normalized read count), target gene sequences, and mutations. Results: The ONETest™ showed a high agreement rate with the RPP; it detected either the pathogens found by the RPP (and/or pathogens missed by the RPP) or no pathogen (that is, negative by both assays) in 32 cases (~89%). In 8 cases (~22%), the ONETest™ identified pathogens not detected by the RPP, and these consisted mainly of human coronaviruses. In one of the RPP-negative cases, the ONETest™ detected two co-infecting pathogens, a human parainfluenza virus and a human metapneumovirus. Conclusions: The ONETest™ is an accurate technology for diagnosis of acute respiratory tract infections, with a favorable agreement rate with the RPP and a capacity to detect co-infections missed by the RPP. Furthermore, the ONETest™ yields additional genomic and quantitative data not available using conventional methods.
Laboratory Diagnosis of Vertical HIV Transmission: Test Ordering Practices for Infants in Alberta

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Objectives: Human immunodeficiency virus (HIV) infection in infants is associated with severe disease and high mortality; therefore, accurate and timely diagnosis is crucial. The World Health Organization recommends virologic testing 0–2 days and 4–6 weeks after birth to diagnose in utero and perinatal transmission, respectively. No particular test type is endorsed in any pediatric guidelines, therefore clinical practice can differ in the use of nucleic acid tests (NATs) detecting viral genomic RNA or integrated proviral DNA (pvDNA). We evaluated virologic test selection and appropriateness of testing for infants across Alberta.

Methods: All HIV NATs ordered in Alberta between 2015–2018 were reviewed (n=16,706). Tests for patients <1-week and 1-month-old were considered appropriate for diagnosis of in utero and perinatal transmission, respectively. Results: Of all HIV NATs performed in Alberta, 5% were for infants <18 months; of those, 68% were ordered at urban health centres. Of the infants tested, 58% received a NAT at either recommended diagnosis window (i.e. <1-week or at 1-month-old). Overall, 60% of NATs were RNA and 40% were pvDNA; however, the two urban centres preferred different test types. Finally, we examined turnaround time from specimen collection to results: RNA and pvDNA tests took an average of 5 and 17 days, respectively, highlighting a practical difference between tests that reflects outsourcing the pvDNA test.

Conclusions: This work reveals differences in HIV NAT preferences for infants, ordering practices between regions, and turnaround times. Further research is needed to determine which test is most sensitive for infants, specifically, before optimizing testing to deliver the best possible care for HIV-exposed infants. Because delayed results impact timely treatment in infants with perinatally-acquired HIV, new approaches to reduce pvDNA turnaround time—e.g. offering tests in-house for patients <1-week-old—could improve management of this vulnerable population.
**Adherence to Palivizumab Dosing Schedule – Manitoba Experience**

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**Background:** Respiratory Syncytial Virus (RSV) infection is a major cause for infant hospitalization. Passive immunization with palivizumab (Synagis®) is given as 5 monthly doses over the RSV season to high-risk infants to reduce RSV related hospitalizations. Adherence to dosing schedule optimizes its effectiveness. **Objectives:** Assess whether location of palivizumab administration is associated with difference in adherence to administration schedule, specifically, whether administration outside of urban centers might impact adherence. **Methods:** Patient age, sex, prematurity status, eligibility risk factor, birth weight and location/dose dates were collected from a pre-existing database of Manitoba RSV program (MBRSVP) participants from 2007-2018. Primary analysis included all children who received their first 3 doses at the same outpatient clinic comparing adherence (defined as receiving subsequent doses on schedule) based on location (Urban vs Non-urban). Our secondary analyses looked at children who received all 5 doses in the same location, those who received an initial dose in hospital followed by 3 doses at the same outpatient clinic, and finally, a subgroup analysis for adherence in urban vs rural vs northern patients from the primary analysis. **Results:** Adherence was higher in children receiving palivizumab in urban vs rural locations (89% vs 53% respectively). Using a chi-squared test we found that location was associated with adherence ($X^2=158.68$, $p<2.2e-16$). Using logistic regression analysis, controlling for location and other potential confounders, demonstrated a statistically significant relationship between location and adherence. Secondary analysis showed similar results. Subgroup analysis revealed differences in adherence of 89% vs 73% vs 40% for the urban, rural and northern groups respectively with $X^2=224.66$ and $p < 2.2e-16$. **Conclusions:** Manitoban patients who receive palivizumab doses in urban centers are more likely to be adherent to their dosing schedule. This data suggests that additional strategies and resources are required to improve adherence in rural and northern communities.
Study of Carriage of *Haemophilus influenzae* Type A among Children

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**Background:** Over the last two decades, *Haemophilus influenzae* type a (Hia) has emerged as an important cause of invasive disease mainly affecting young Indigenous children. Hia carriage in the upper respiratory tract is both pre-requisite for invasive disease and reservoir for transmission. To identify target populations for immunization with a new Hia vaccine under development, we initiated a multi-center study of nasopharyngeal carriage among Canadian children. **Methods:** With prior parental consent, we collected used nasopharyngeal anaesthetic tubes from healthy children <5 years of age who underwent routine dental surgery under general anaesthesia in a regional hospital of Northern Ontario (NO) and another dental clinic in Saskatoon (SA). In NO, all children were First Nations; in SA, children came from various ethnic groups. Detection of *H. influenzae* and serotype characterization were performed using PCR amplification of capsular polysaccharide synthesis genes. Multilocus sequence typing was done via amplification and sequencing of 7 housekeeping enzyme genes; assignment of sequence types was done through the *H. influenzae* MLST website. **Results:** By January 2019, 295 nasopharyngeal specimens were collected and analyzed, 198 in NO, and 97 in SA. Hia was identified in 17 (8.5%) and 5 (5%), respectively. In SA, 4 out of 5 children with Hia carriage were First Nations. **Conclusions:** The carriage rates of Hia in healthy children <5 years of age in NO and SA are comparable to *H. influenzae* type b (Hib) carriage among Alaska Native children in the pre-Hib vaccine era. To prevent invasive Hia disease it will be essential to decrease pathogen transmission. Pediatric conjugate Hia vaccines have the potential to decrease carriage of Hia and thus decrease transmission and disease among susceptible populations.
Clinical response and outcomes in patients with recurrent *Clostridium difficile* treated with frozen-and-thawed fecal microbiota transplant

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**Objectives:** Frozen-and-thawed fecal microbiota transplant (FMT) is as effective as fresh FMT for the treatment of recurrent or refractory *Clostridium difficile* infection (CDI). Frozen FMT provides several advantages over fresh FMT including a reduction in the frequency of donor recruitment and screening, and more convenient access. The objective of this study is to assess clinical response and long term outcomes in patients enrolled in an open-label trial of frozen-and-thawed FMT for recurrent CDI. **Methods:** Eligible participants with recurrent CDI enrolled at our centre received frozen-and-thawed FMT from eligible donors as per our open-label trial protocol. A chart review and telephone survey was conducted for participants enrolled between June 2015 and December 2017. Patients with a minimum time of six months of reliable follow-up were included. **Results:** Median time from first FMT to follow-up was 17 months. Ninety-three percent (53/57) of patients achieved cure with repeat FMT. Forty-nine percent (26/53) of patients who achieved cure received one FMT, 28% (15/53) of patients who achieved cure received two treatments, 13% (7/53) of patients who achieved cure received three treatments, and 9% (5/53) of patients who achieved cure received 4-6 treatments. Ninety-one percent (48/53) of patients who achieved cure had a sustained response with no recurrent CDI at follow-up. Of those with recurrent CDI, 60% (3/5) occurred following use of antibiotics for other conditions. **Conclusions:** Frozen-and-thawed FMT is effective for the treatment of recurrent CDI and often requires repeat treatments to achieve clinical cure. With a median follow up time of 17 months, 91% of patients with CDI had a durable cure. Patients with recurrent CDI were often provoked via antibiotic use.
Verification of Three Multiplex Carbapenemase Nucleic Acid Amplification Tests (NAAT) using Species-Diverse Carbapenem-resistant Gram-Negative Bacilli

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Objectives: Rapid detection of carbapenemase-producing organisms (CPO) is important. Data suggest direct-from-specimen NAAT is more sensitive than culture. We evaluated three multiplex carbapenemase NAAT targeting KPC/NDM/OXA48-like/VIM/IMP genes [BDMax Checkpoints CPO (BD), Allplex Entero-DR (Seegene), and Easyplex® SuperBug CRE Assay Version C (Amplex Diagnostics)] using 150 well-characterized (phenotypic and PCR/sequencing) GNB.

Methods: 150 GNB including 122 CPO (116 targeted-CPO: 88 KPC/8 NDM/5 OXA/5 NDM+OXA/7 VIM/3 IMP; 6 non-targeted CPO: 1 GES/4 SME/1 NMC), and 28 non-CPO were tested comprising 145 Enterobacteriaceae/5 non-Enterobactericeae GNB. Isolates were recovered from 80°C under ertapenem-selective pressure. Limit of detection (LOD) was calculated in triplicate using four QC strains following manufacturer direct-from-specimen-protocols using 10E4/10E5/10E6/10E7/10E8 cfu/L concentrations in ESwab transport medium with results from Xpert® Carba-R (Cepheid) as reference. Colony counts confirmed concentrations and average LOD was calculated. Accuracy was determined using ≥10-fold-higher concentrations than calculated LODs. Discrepancies were repeated. Results: LOD (cfu/L) are shown (Figure). The most sensitive to least sensitive assay was Seegene, BD, Cepheid, then Amplex. All 34 non-targeted-CPO/non-CPO were negative by all assays. 1 KPC/1 NDM/3 KPC were initially missed by BD/Seegene/Amplex, respectively but were positive on repeat testing of fresh subcultures suggesting initial lost plasmids. 2 IMP were reproducibly missed by BD and Amplex. Final CPO-detection sensitivities/specificities were 100% for all non-IMP targets; respective 95%CI were: KPC 95.0-100/87.6-100; NDM 73.4-100/95.9-100; OXA48-like 68.0-100/96.0-100; VIM 59.6-100/96.1-100. Sensitivities/specificities for IMP were 100%(38.2-100)/100%(96.2-100)(Seegene) and 33%(5.6-79.8)/100%(96.2-100)(BD&Amplex).
Conclusions: All three assays were highly-accurate (100% sensitive/specific) for detection for KPC, NDM, OXA48-like and VIM CPO. IMP was more challenging for BD and Amplex. LOD was variable but not substantially different between assays. These results along with workflow, turn-around-time, footprint, interfaceability, cost, and laboratory needs can be used to determine suitability for different laboratories.
Evaluation of Commercial Screening Agars for the Detection of Carbapenemase Producing Enterobacteriaceae

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Objective: Carbapenemase producing enterobacteriaceae (CPE) are emerging around the world, including Canada, and are associated with case fatality rates as high as 50%. Gastrointestinal carriage of CPE may serve as the reservoir for cross-contamination in the healthcare setting, thus active surveillance is important for effective containment and outbreak prevention. In this study we evaluate commercially available screening agars for the detection of CPE using a panel of CPE, non-CPE carbapenem resistant and carbapenem susceptible strains. Methods: A panel of strains was assembled including clinical strains from our laboratory and highly characterized strains selected from the CDC-FDA Antibiotic Resistance Isolate Bank as indicated in Table 1.

Table 1. Carbapenemase Types in the test Panel

<table>
<thead>
<tr>
<th>No. of Strains</th>
<th>Carbapenemase Enzyme Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>33</td>
<td>KPC</td>
</tr>
<tr>
<td>34</td>
<td>NDM</td>
</tr>
<tr>
<td>11</td>
<td>OXA-48/OXA-48 like</td>
</tr>
<tr>
<td>10</td>
<td>VIM</td>
</tr>
<tr>
<td>5</td>
<td>IMP</td>
</tr>
<tr>
<td>79</td>
<td>None</td>
</tr>
</tbody>
</table>

Two commercial agars for detection of carbapenemase producing enterobacteriaceae were compared including CHROMID™ Carba Smart (CCS) and Colorex™ SuperCARBA (CSC). Two different inocula were used: 10⁵CFU (high) and 10²CFU (low). All media were incubated in accordance with the manufacturer’s recommendations. Strain viability was confirmed by concurrently planting dilutions to a non-selective blood agar plate and carbapenemase production was confirmed present or absent from all strains by PCR. Results: Sensitivities for the high inocula were 89% and 93% while the low inocula was 40% and 75% for CCS and CSC respectively. The specificities were 75% and 59% for CCS and CSC respectively. Both plates failed to recover four strains including K. pneumoniae IMP-4, K. oxytoeca KPC-3, P. mirabilis KPC-6 and P. mirabilis KPC-2. Interestingly, CCS failed to recover two OXA-48 like strains, including K. pneumoniae OXA-232 and K. pneumoniae OXA-181, even at the high inocula. Conclusions: CSC displayed better sensitivity, at high inocula and particularly at low inocula. Although CCS had higher specificity, overall, CSC had superior performance.
Activity of ceftobiprole against Canadian bacterial pathogens from the CANWARD study

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Activity of ceftobiprole against Canadian bacterial pathogens from the CANWARD study. **Objectives:** Ceftobiprole is a recently re-released 5th generation cephalosporin, currently available on the Canadian and European markets. It demonstrates *in vitro* activity against *Staphylococcus aureus* (methylcillin-susceptible [MSSA] and methylcillin-resistant [MRSA] isolates), *Streptococcus pneumoniae*, ESBL-negative Enterobacteriaceae, and *Pseudomonas aeruginosa*. It also has improved activity against AmpC-positive Enterobacteriaceae relative to ceftriaxone and ceftazidime. Related to its broad spectrum of activity, ceftobiprole may offer a monotherapeutic option for the treatment of complicated skin and soft tissue infections and community-acquired and nosocomial pneumonia. The purpose of this study was to evaluate the *in vitro* activity of ceftobiprole against a contemporary collection of isolates from the CANWARD study. **Methods:** Isolates were collected from the ongoing CANWARD study between 2008-2010 and 2015-2017. Antimicrobial susceptibility testing was performed using broth microdilution panels following CLSI recommendations (M07, 11th edition). Minimum inhibitory concentrations were interpreted using Health Canada breakpoints (ceftobiprole) or CLSI breakpoints (ceftazidime comparator). Where no breakpoints were available for ceftobiprole, the pharmacokinetic/pharmacodynamic breakpoint of 4mg/L was used. **Results:**
Conclusion: Ceftobiprole is active in vitro against S. aureus (MRSA and MSSA) and Enterobacteriaceae. It is more active in vitro than ceftazidime against Acinetobacter baumannii and species with chromosomal AmpC beta-lactamases while it is less active against Klebsiella oxytoca/Raoultella spp., suggestive that its chromosomal β-lactamase (OXY) is more active against ceftopiprole than ceftazidime. While ceftobiprole appears to have anti-Pseudomonas activity, no Pseudomonas-specific breakpoints exist and PK/PD breakpoints were derived using only one dosing recommendation (500mg IV q8h). Further studies in ceftobiprole dose, interval or infusion time may reveal that a higher species-specific breakpoint for Pseudomonas could be considered, concurrent with alternative dosing recommendations. Activity is poor against Enterococcus faecium and Stenotrophomonas maltophilia.
Antimicrobial Susceptibility Testing of bacteria directly from positive blood culture bottles using serum separator tubes

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Objective: Early targeted antimicrobial treatment can effectively reduce the mortality rate caused by bloodstream infections (BSI) and also enhance antimicrobial stewardship efforts in reducing the use of broad spectrum antibiotics. In addition to the Vitek MS® direct from blood culture bacterial identification currently practiced at our center, the ability to perform direct susceptibility testing using the serum separator tubes (SST) has the potential to significantly reduce current turnaround time (TAT) for susceptibility results from positive blood cultures. Method: Positive monomicrobial BACT/ALERT® blood culture bottles received in the microbiology lab between October 3 and December 31, 2018 were included. Ten milliliters of broth was aspirated from a positive blood culture bottle and injected into two 5 ml SST. The SSTs were centrifuged at 3900 RPM for 5 minutes. The supernatant was discarded and a small amount of the remaining pellet containing the bacteria was used to make a suspension equivalent to 0.5 McFarland in 0.45 % saline. Vitek 2® Susceptibility results from the pellet were compared to those performed routinely on isolates after 18hr incubation on agar plates.

Results: 100 positive blood cultures including common Gram negative and positive organisms were evaluated. All reportable antibiotics had 100% essential and categorical agreement. There was one very major error for TMP-SMX for S. aureus and 70% essential agreement but 100% categorical agreement on Nitrofurantoin for K. pneumoniae. Overall essential and categorical agreements were above the acceptable value of 90% with major and minor errors below acceptable value of 10%. Conclusions: Based on the results of this pilot, direct from blood culture bacterial susceptibility testing using the SST provides accurate results for all of the reportable antimicrobials and significantly decreases TAT.
Transient Carriage of Extended-spectrum Beta-lactamase (ESBL) Producing
*Klebsiella pneumoniae* Among Healthy Fecal Microbiota Transplant Stool Donors

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**Background:** MTOP is a fecal microbiota transplantation program. Only healthy stool donors with no personal/family history of chronic illness are accepted. Negative microbiology screens including stool antimicrobial-resistant organism (ARO) cultures are required. Donors are routinely monitored and excluded if their health changes or they travel. Repeat screening is completed prior to release of donations. One donor was unexpectedly positive on repeat screening for an ESBL-producing *Klebsiella pneumoniae*. The purpose of this study was to determine the rate of ARO carriage among healthy stool donors. **Methods:** All active MTOP stool donors between March 2017 and August 2018 were included. Stool aliquots stored at -80°C from each donation were thawed and tested for ARO [methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), ESBL, and carbapenemase-producing organisms (CPO)] by planting onto Oxoid Denim Blue agar, Oxoid Brilliance VRE agar, and Oxoid MacConkey/cefpidixime agar, respectively following clinical laboratory operating procedures. **Results:** Four donors actively donated during the study period. The duration of time each participated varied from 3 months (Donors 1 and 2) to 13-14 months (Donor 3 and 4, respectively). Eighty donations were provided (3 each from Donors 1 and 2; 33 and 41 donations from Donors 3 and 4, respectively). All donors passed initial ARO screening and were well with no antimicrobial use nor travel history. Of the 80 donations, all were negative for MRSA, VRE, and CPO carriage but 3 (3.75%) were positive for ESBL *Klebsiella pneumoniae* [2 (6.1%) from Donor 3 and 1 (2.4%) from Donor 4]. The two positive results from Donor 3 were separated by 10 months. **Conclusion:** Transient carriage of ESBLs in healthy pre-screened donors without illness, antimicrobial exposure, nor travel history suggests local transmission, possibly through food/water sources. Programs should consider screening all donations for ARO prior to acceptance into donor stool programs.
Introduction: Recent cohort studies have identified international travel as an important risk factor for colonization with extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-PE), a multidrug resistant organism of public health concern. Antimicrobial use during travel likely amplifies this risk, but to what extent, and whether this risk varies by antimicrobial class, has not been well studied. A systematic review was conducted to estimate these associations. Methods: Eligible studies were prospective cohort studies which reported on both receipt of systemic antimicrobials during travel versus none, as well as ESBL-PE isolated from stool or rectum acquired during travel. We carried out electronic searches in electronic databases. Studies were selected for full text review and included if eligible. We carried out a random effects meta-analysis. Results: After removing duplicates, we reviewed 3430 citations from electronic databases. Fifteen studies met inclusion criteria. The study population included mainly female travellers from high income countries recruited primarily from travel and vaccination clinics. Asia and Africa were the most common regions travelled to. A median 10% of study participants reported systemic antimicrobial usage. We observed a combined odds ratio (OR) for ESBL-PE acquisition during travel of 2.37 among those who used antimicrobials compared to those who did not (95% confidence interval [CI], 1.69 to 3.33); there was substantial heterogeneity between studies. Fluoroquinolones were associated with the highest combined OR of ESBL-PE acquisition, at 5.55, compared to no antimicrobial use (95% CI, 2.68 to 11.5). Conclusions: The odds of acquiring ESBL-PE during travel are increased substantially with exposure to antimicrobials, especially fluoroquinolones during travel. Further studies should be directed towards identifying mechanisms whereby antimicrobials affect an increased risk of ESBL-PE acquisition to identify potential protective factors. Public health efforts are warranted to decrease inappropriate antimicrobial usage during travel, including antimicrobial use for prevention or treatment of mild-to-moderate traveller’s diarrhea.
Impact of Storage Conditions of Stool and Fecal Filtrate on Microbiome Composition – Implications for Microbiota Researchers and Fecal Microbiota Transplantations

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Objectives: Stool storage is key to researching the association between gastrointestinal dysbiosis and disease states. Fecal microbiota transplantation using frozen filtrate is used for patients with recurrent Clostridioides difficile infection. This study determined the impact of storing stool and frozen filtrate on microbiome composition. Methods: Fresh stool was obtained from a high-diversity (HD) and low-diversity (LD) donor. Aliquots were stored at room temperature (RT), 5°C, and at -20°C for 24 and 48 hours, or processed immediately. Fresh stool was also homogenized with both 0.9N-sterile saline and 0.9N-sterile saline containing 10%-glycerol. Resulting filtrate aliquots were frozen at -20°C and at -80°C. At baseline and after 7, 9, 12, 18 and 24M storage, gDNA was isolated using the MO BIO PowerSoil® DNA Isolation Kit. 16s rRNA gene amplicon sequencing targeting the V4 hypervariable region was performed on the Illumina MiSeq. Low abundant OTUs were excluded. Results: Differences in microbiota profiles were observed in both HD and LD stool when stored immediately at -20°C, more so with the LD stool. Differences were also noted for LD stool stored at room temperature and less so at 5°C. Storage at RT or 5°C had no impact for the HD stool. Long-term filtrate storage of the HD stool filtrate at -80°C with 10%-glycerol best preserved the bacterial microbiota profile followed by -20°C with 10%-glycerol then -80°C and -20°C without 10%-glycerol. Differences were also observed in the LD stool filtrate when stored in any conditions, with the least impact being -80°C with glycerol. Conclusions: To preserve microbiota profiles, storing stool at 5°C until received in the laboratory is optimal. For researchers assessing microbiota correlations with disease states, immediate gDNA extraction from stool upon receipt is ideal. For those using frozen filtrate from healthy donors for fecal transplants, long-term storage is best at -80°C with 10%-glycerol.


**Chlamydia trachomatis and Neisseria gonorrhoeae Infections among Gay, Bisexual, and other Men who have Sex with Men: Extragenital Infections are More Prevalent than Urogenital Infections**

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**Objectives:** A recent review by Chan et al. reported that urogenital testing alone misses a significant percentage of Chlamydia trachomatis (CT) and Neisseria gonorrhoeae (NG) infections among men who have sex with men (MSM): 14-85% of rectal and pharyngeal infections can be missed. We provide estimates of CT/NG prevalence among gay, bisexual, and other MSM (gbMSM) by site in an urban center in Quebec.

**Method:** From February 2017 to June 2018, sexually-active gbMSM ≥16 years were recruited via respondent-driven sampling (RDS). Pharyngeal samples were collected by trained nurses; urine and rectal samples by participants. All samples were analyzed using the cobas 4800 CT/NG assay (Roche Diagnostics). Prevalence proportions (95% CI) were RDS-adjusted.

**Results:** Among the 1177 participants, mainly asymptomatic, CT infection (at least one positive sample) was found in 2.7% (1.3-4.2) and NG infection in 5.9% (3.1-8.7). Proportions for CT by site: 0.3% (0.1-0.4) urine samples, 2.3% (0.9-3.8) rectal samples, and 0.2% (0.0-0.5) pharyngeal samples. For NG, these were 0.3% (0.5-1.0), 2.9% (1.2-4.7) and 3.7% (1.3-6.1), respectively. All three sites were sampled in 1145 participants (Figure). If only urine had been tested, 35/44 (79.6%) CT infections and 72/77 (93.5%) NG infections would have been missed.

**Conclusions:** In our study, 88% (105/121) CT/NG infections would have been missed if only urine was tested. This represents a higher proportion than found in the literature, and higher than data from provincial notifiable diseases (which also includes cases among heterosexual men and cases detected though consultation for symptoms): in 2017, 1568/9656 (16%) CT cases and 2735/4676 (58%) NG cases in men were detected only from pharyngeal or rectal sites. Sampling all sites is crucial for screening and should be promoted, especially in gbMSM.

Number of positive samples for CT or NG among 1145 participants for whom all three sites were tested
Patient-initiated Testing Strategies for Sexually Transmitted Infections (STIs) in Men Who Have Sex with Men (MSM): A Scoping Study

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Background: Men who have sex with men (MSM) are disproportionately affected by sexually transmitted infections (STIs) including chlamydia, gonorrhea, syphilis and HIV. In addition, many men remain undiagnosed and untreated with asymptomatic infections facilitating onward transmission. Barriers to traditional STI testing include healthcare-level stigma and homophobia, lack of confidentiality, long wait-times and limited access to testing sites. Patient-initiated strategies such as self-collection and self-testing have been proposed as alternatives to increase screening and treatment. We conducted a scoping study to summarize successful testing programs, as well as demographics of MSM who benefited, to help guide the creation of a local program. Methods: A literature search was conducted using controlled vocabulary (e.g., “Sexually Transmitted Diseases”, “Mass Screening”, “Internet”) and keywords (e.g., “STI”, “screening”, “self-initiated”). The authors reviewed extracted articles and included them in the study based on title and abstract content. Included articles addressed self-sampling or self-testing methods for sexually transmitted infections in men who have sex with men in developed countries. Results: Forty-one articles were included. Testing was either conducted through downloaded laboratory forms at traditional collection sites, mail-in specimen collection kits or rapid self-testing devices. These strategies especially benefited older men, those with partners, and those unable to access traditional testing. They decreased concerns regarding stigma and homophobia. Barriers to accessing patient-initiated testing were person or care-specific, pertaining to fear of positive tests, concerns over confidentiality, and understanding test results. Some worried their testing would get lost. Care-specific concerns included the missed opportunities for assessment and counselling when performed remotely. Conclusions: Although traditional testing methods remain the standard of care, patient-initiated testing may bridge the gap in detection of STIs in MSM. A successful program may combine both self-collection and printed requisitions, with linkage to established clinics or telehealth. Continuity of care is paramount for program success.
Prevalence of *Trichomonas vaginalis* detection in Urine Specimens and Vaginal and Endocervical Swabs by Molecular Testing in a large Community-Based Population in Ontario

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Over recent years there has been a dramatic shift in the diagnostic testing methods available to identify *Trichomonas vaginalis*, from the lower sensitivity microscopic examination of a wet mount preparation of vaginal secretions, to highly sensitive molecular assays performed on vaginal and cervical swabs, as well as urine samples. Since there are no current surveillance or reporting programs in place, and low sensitivity microscopy is still widely used for the diagnosis of *T.vaginalis*, the true prevalence of infection is unknown. Based on extensive literature review, the prevalence of *T.vaginalis* however, is known to vary greatly between geographic areas and among different risk groups.

**Objective:** To establish epidemiological prevalence data for *T.vaginalis* in a large community based population. **Methods:** Analysis of positivity rates of *T.vaginalis* at two large laboratories over a nine month period to determine the prevalence of infection in the communities serviced by these laboratories. Both laboratories utilized molecular testing on the BD Viper XTR platform for the detection of *T.vaginalis* in urine specimens and vaginal and endocervical swabs. **Results:** Over the nine month period of analysis, a total of 42722 endocervical and vaginal swabs were submitted, and 483 of these tested positive for *T.vaginalis* by molecular testing resulting in a 1.13% positivity rate. The positivity rate for the 30080 urine specimens tested for T.vaginalis was 1.87%. **Conclusion:** Compared to available prevalence estimates in the literature in various geographical regions and across risk groups, the positivity rates of *Trichomonas vaginalis* are lower in the community-based population analyzed in this study.
Disseminated Gonorrhea Infections in Manitoba, Canada: 2013-2018

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Background: Gonorrhea is a sexually transmitted infection caused by Neisseria gonorrhoeae. Infection is usually limited to mucosal surfaces (e.g., urogenital tract, rectum, throat, eyes) but disseminated infections with systemic manifestations can occur. In Manitoba, Canada, the incidence of Gonorrhea increased from 96 cases/100,000 population in 2013 to ≈250/100,000 in 2018. Objective: To review the incidence and features of disseminated Gonorrhea infections. Methods: In Manitoba, screening and reference testing for sexually transmitted infections is centralized at Cadham Provincial Laboratory (CPL). Antimicrobial susceptibility testing and NG-MAST genotyping of cultured N. gonorrhoeae isolates is performed at the National Microbiology Laboratory. Disseminated infections were identified by querying the CPL laboratory information system (LabWare LIMS) for specimens that 1) tested positive for N. gonorrhoeae and 2) had a non-mucosal source (e.g., blood, joint fluid). Cases were reviewed to determine if screening for coinfections was performed at the time of diagnosis. Results: Between January 1, 2013 and December 31, 2018, 34 cases of disseminated Gonorrhea infection were identified. Incidence increased from 2-3 cases/year during 2013-2016, to 9 in 2017 and 15 in 2018. Diagnostic specimens included blood (11 cases), joint fluid (19 cases), CSF (1 case), and multiple sources (3 cases). Nineteen (56%) cases also submitted urine samples for Gonorrhea and Chlamydia screening. Eleven were N. gonorrhoeae positive (including four co-infected with Chlamydia) and eight were N. gonorrhoeae negative (including two positive only for Chlamydia). HIV and Syphilis screening was performed for thirty (88%) and twenty-eight (82%) cases, respectively. None were positive. Isolates from twenty-eight cases were available for susceptibility testing and genotyping. All isolates were susceptible to Azithromycin, Cefixime and Ceftriaxone. Nineteen (68%) were NG-MAST genotype ST-3671. Conclusions: The increasing incidence of Gonorrhea in Manitoba, Canada has been accompanied by an increase in cases of disseminated infection. The majority of cases involved ST-3671 strains.
Comparison of Two Commercial Amplification Assays, SpeeDx Resistance Plus MG and Seeplex STD6 ACE Detection, Performed on Self-Obtained Vaginal and Urine Specimens for the Diagnosis of *Mycoplasma genitalium* Infections

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**Objective:** Few commercial assays for *Mycoplasma genitalium* (MG) are approved in Canada and data is limited with self-obtained samples. The objective was to compare 2 commercial assays on self-obtained vaginal swabs (SOVS) and first-void urine (FVU) from 300 sexually active young women. **Methods:** Employing a research ethics-approved protocol, 171 consecutive women attending a clinic in Toronto, Canada collected a FVU and 3 SOVS. All patient samples were tested in a blinded fashion in a SpeeDx Resistance Plus MG assay (SpeeDx Pty Ltd) in m2000sp (Abbott) and ABI 7500 (ThermoFisher) instruments, and the Seeplex STD6 ACE assay (Seegene Canada Inc) with EasyMag extraction and gel electrophoresis. Discordant samples were arbitrated with an Aptima MG assay (Hologic Inc) on a Panther instrument. Sensitivity (Sens), specificity (Spec), positive (PPV) and negative (NPV) predictive values were calculated. SpeeDx also provided identification of 5 mutations commonly associated with macrolide resistance. **Results:** In this interim analysis, 141 women were negative in SpeeDx and Seeplex in all samples and 30 were positive in at least one sample type by the 2 comparative tests. Aptima confirmed 25 true positives. The percent Sens, Spec, PPV and NPV estimates, respectively, were as follows: SpeeDx-SOVS 96, 100, 100, 97.9; SpeeDx-FVU 64, 100, 100, 94.2; Seeplex-SOVS 44, 97.3, 73.3, 91; Seeplex-FVU 20, 97.9, 62.5, 97.9. SpeeDx determined that 56% (14/25) of infections possessed mutations associated with macrolide resistance. **Conclusions:** The SpeeDx Resistance Plus MG assay demonstrated high accuracy in identifying MG-infected women by testing SOVS, which proved to be a more reliable sample than FVU. Providing simultaneous macrolide resistance testing in SpeeDx provided real-time value for treatment. The results from the Seeplex STD6 ACE assay may be a reflection of level of detection, cross reactions or the subjective nature of identifying bands in a gel.
Mycoplasma genitalium and Macrolide Resistance Mutations in Vaginal Swabs of Canadian Women tested with Commercial Molecular Assays

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Objective: Sexually active women may be infected with Mycoplasma genitalium (MG) with macrolide resistant mutations (MRM). Commercial assays measuring both the presence of MG and MRM have been developed and require clinical evaluation. The objective was to compare Allplex™ MG and AziR assays (Seegene Canada Inc.) to the SpeeDx Resistance Plus MG assay (SpeeDx Pty Ltd) on vaginal swabs. Methods: Two vaginal swabs (VS) in transport media specific for each assay were collected from 190 women. Multiplex assays were performed following the manufacturers’ instructions. Both Allplex STD4 assay which detects MG plus 3 other pathogens and the Allplex MG AziR assay which detects MG and 6 MRM extracted VS on a Microlab STARlet IVD (Hamilton) with subsequent PCR amplification on a CFX96 (Bio-Rad). The SpeeDx assay which detects MG and 5 MRM performed extraction on an m2000sp (Abbott) and PCR in an ABi 7500 instrument (ThermoFisher). Agreement and Kappa statistic compared positive and negative results for the detection of MG. Wild-type (WT) and MRM were also compared for the 2 assays. Results: Allplex assays recorded 27 MG-positives and 163 negatives compared to 25 and 165 in SpeeDx. Agreement of positives was 85.7% and negatives 97.6%. Overall agreement was very good (97.89%), Kappa 0.911 (95% CI 0.825-.997). Each MRM assay recorded 58.3% (14/24) of the samples to be resistant (R) with 8 discordants: MG AziR R and SpeeDx WT (n=4); SpeeDx R (n=4) and MG AziR (3 WT and 1 negative). Allplex assay MRM were A2058G (n=13), A2058T (n=1) and A2059G (n=4). Conclusions: All assays demonstrated very good agreement for the detection of MG in vaginal samples, and were easy to perform. MG detection and MRM results can be provided at the same time. R and WT discordancy was not due to the extra A2059T mutation included in the Allplex assay.
Use of whole genome sequencing data to detect and investigate a community-based outbreak of carbapenemase-producing *Escherichia coli*

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**Objective:** A pipeline of epidemiological, laboratory, and genomic investigation was used for real-time detection and investigation of a cluster of carbapenemase-producing organisms (CPO) in a community setting.

**Methods:** Three patients at an acute care facility tested positive for carbapenemase-producing *E. coli* over a short period of time. Infection prevention and control (IPC) followed up on the cases to identify risk factors for CPO acquisition. Their whole genome sequence data was cross-referenced against a database of CPOs identified in BC since 2008, using core genome SNP-based dendograms to visualize isolate relatedness. MinION long-read plasmid sequencing data were used to supplement MiSeq data to generate a genomics-based case definition, which was used to confirm subsequent cases suspected by IPC to be part of the cluster. **Results:** IPC follow-up initially identified none of the usual CPO risk factors. The isolates were *E. coli* whole-genome MLST type 405, and carried a novel NDM-1-producing plasmid, previously unseen in BC. On a dendogram, these isolates, along with two additional clinical isolates from a community laboratory, clustered within 4 SNPs. In-depth epidemiological investigation revealed shared exposure to two private retirement facilities in the community. The novel plasmid was an IncI1-alpha plasmid. This genomic case definition was used to confirm case inclusion in the ensuing outbreak investigation. It also allowed the identification of two additional cases, not previously known to be related, without known ties to the retirement facilities or the acute care facility. All identified cases clustered very closely by core genome (mean SNVs = 5.61). **Conclusion:** Using WGS to support epidemiological investigation allowed early detection of a community-based cluster, and provided hypotheses for transmission mechanisms. While little is known about the epidemiology of CPO in the community, the close clustering of cases in this outbreak suggested clonal transmission from a point source.

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**Objective:** Increasing antimicrobial resistance (AMR) is a growing concern as it limits the ability to treat infections. Canadian Antibiotic Resistance Alliance (CARA) data from 14 tertiary care hospitals reported an increase % non-susceptibility for ciprofloxacin and ceftriaxone from 2016 to 2017 (about 650 isolates per year). We compare two years of standardized *E. coli* antibiogram data from CNISP sentinel hospitals across Canada. **Methods:** Hospitals participating in the Canadian Nosocomial Infection Surveillance Program (CNISP) were asked to submit annual antibiogram data for all *E. coli* isolates in a standardized format for the years 2016 and 2017. Percent (%) non-susceptibility was calculated for reported antibiotics. **Results:** Fifty (50) hospitals from 9 provinces submitted data for 2016, and 63 hospitals from 8 provinces submitted for 2017. The highest number of isolates were tested for ampicillin (51,965 in 2016 and 58,362 in 2017). From 2016 to 2017 a significant decrease in % non-susceptibility was evident for: ampicillin 44 & 41.9%; ceftriaxone 9 & 8.3%; and cotrimoxazole 23 & 21%; whereas, ciprofloxacin 18.8 & 19%; amoxicillin/clavulanic acid 16.7 & 16.4%; piperacillin-tazobactam 4.7 & 4.5%; and meropenem 0.2 and 0.1% remained stable. Comparing regional to national rates for 2017, Central Canada (Ontario and Quebec) had the highest non-susceptibility rates for amoxicillin/clavulanic acid (23%), ceftriaxone (9.4%), ciprofloxacin (20.3%), and cotrimoxazole (24.1%). Eastern Canada had a significantly higher piperacillin-tazobactam non-susceptibility (6%), but at the same time, the lower non-susceptibility for amoxicillin/clavulanic acid (11.7%), ceftriaxone (6.2%), ciprofloxacin (12.7%) and cotrimoxazole (16.3%). **Conclusions:** Based on CNISP data, no concerning changes in AMR for *E. coli* in Canada were observed between 2016 and
2017. One limitation is allowing either “urine isolates” (typically 90% of all) or “all isolates” submissions interchangeably. This was a robust AMR surveillance project and is likely to increase in organisms tested and subpopulations including blood cultures.
Retrospective Evaluation of the Effectiveness of Fecal Microbiota Transplantation on Antibiotic-Resistant Organism Clearance – A Pilot Study

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Background: Antibiotic resistance is a growing concern. Preliminary data suggests fecal microbiota transplantation (FMT) may help decolonize gastrointestinal antimicrobial resistant organisms (AROs) through competition with susceptible organisms. The objective of this study was to evaluate the effectiveness of FMT by enema to eradicate ARO rectal colonization. Methods: 12 patients treated with FMT by enema for recurrent Clostridiodes difficile infection (rCDI) and 7 patients treated with FMT from a prior rCDI clinical trial who had pre- and post-FMT stool or rectal swabs were included in this study. Pre- and post-FMT stool aliquots stored at -80°C were thawed and tested for ARO [methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant enterococci (VRE), ESBL, and carbapenemase-producing organisms (CPO)] by planting onto Oxoid Denim Blue agar, Oxoid Brilliance VRE agar, and Oxoid MacConkey/cefpodixime agar, respectively following clinical laboratory operating procedures. Microbiota diversity was determined using 16s rRNA sequencing. Correlation with clinical outcomes was completed. Results: 5/19 patients had AROs detected pre-FMT (VRE n=2; ESBL n=2; VRE and ESBL n=1). 2/5 (40%) [95%CI: 0.12-0.77] of patients had complete ARO clearance post-FMT. 2/3 (67%) [95%CI: 0.20-0.94] of ESBL colonized patients and 1/3 (33%) [95%CI: 0.06-0.80] of VRE colonized patients had ARO clearance post-FMT. 2/3 (67%) [95%CI: 0.20-0.94] of patients whose rCDI symptoms were cleared, had ARO clearance. 2/2 (100%) [95%CI: 0.29-1.00] of patients with sustained uptake of diverse donor microbiota, eradicated their AROs post-FMT. Conclusions: FMT is a promising ARO eradication treatment with an estimated efficacy of 100% [95%CI: 0.29-1.00] in patients with sustained uptake of diverse donor microbiota. A prospective evaluation of FMT on ARO eradication is ongoing.

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Background: The development of Canadian healthcare associated infections (HAI) and infection prevention and control (IPC) guidelines facilitates a national approach for responding to public health emergencies and maintaining safe healthcare delivery. The objective of this poster is to describe the role of the National Advisory Committee on Infection Prevention and Control (NAC-IPC) which informs national infection control guidelines. Methods: The NAC-IPC is composed of members with various expertise, including infectious disease, medical microbiology, and infection prevention and control. They lead individual task groups in the development of IPC guidelines. Topic selection for evidence based guideline development is based on a number of criteria including public health response to emerging issues, epidemiology and research findings, changes in practice and impact upon the health of Canadians. Guidelines are developed using a standardized process involving systematic reviews or environmental scans, and evidence grading where applicable. Results: Some examples of documents developed by the NAC-IPC are shown in Table 1. Recommendations are informed by evidence and collective expert opinion where evidence is sparse.

Table 1: Types of documents produced by the NAC-IPC

<table>
<thead>
<tr>
<th>Type of Document</th>
<th>Example</th>
<th>Methodology</th>
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<tbody>
<tr>
<td>Comprehensive</td>
<td>Routine Practices and Additional Precautions for Preventing the Transmission of Infection in Healthcare Settings</td>
<td>Systematic Review</td>
</tr>
<tr>
<td>Targeted</td>
<td>Canadian Tuberculosis Standards 7th Edition; Chapter 15-Prevention and Control of Tuberculosis Transmission in Health Care and Other Settings</td>
<td>Systematic Review</td>
</tr>
<tr>
<td>Peer-Reviewed Publication</td>
<td><em>Mycobacterium chimaera</em> infections in post-operative patients exposed to</td>
<td>Literature Review</td>
</tr>
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heater-cooler devices: An overview

**Conclusions:** The NAC-IPC is well-positioned to facilitate development of national guidelines for HAIs and emerging pathogens; inform federal-provincial-territorial public health networks; and provide opportunities for international collaboration, knowledge exchange and mobilization.
Epidemiology of Carbapenemase-Producing Enterobacteriaceae (CPE) in South-Central Ontario

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Background: CPE are a rapidly evolving problem. This study aims to describe the epidemiology of CPE in south-central Ontario to inform CPE control programs. Methods: The Toronto Invasive Bacterial Diseases Network performs population-based surveillance for CPE colonization/infection in Toronto/Peel. Microbiology laboratories report all CPE isolates to the study; annual audits are conducted. Incidence calculations use first isolates as numerator; population estimates are from Statistics Canada. Results: CPE incidence has increased from 0 in 2006 to 1.5/100,000 in 2016-2018 (Figure). Bacteremia incidence has increased to 0.36 per 100,000 in 2018. Among 783 incident cases, median age is 70y (IQR 57-79yrs); 450 (57%) are male. Most common species are E coli (n=345; 43%), K. pneumoniae (319; 39%) and Enterobacter spp. (79; 10%); most common genes are blaNDM (±OXA, 432; 53%); blaKPC (143; 18%), blaOXA-48-like (186; 23%) and blaVIM (34; 4%). Among 345 patients with only rectal colonization when first identified, 40 (12%) have had a subsequent clinical isolate (6 blood, 7 other sterile, 26 non-sterile sites). Among 646 persons with documented history of hospitalization and travel in the year prior to identification, 199 (31%) had been hospitalized in the Indian subcontinent, 77 (12%) hospitalized elsewhere outside Canada, 83 (13%) had travelled to the Indian subcontinent without hospitalization, 217 (34%) had been hospitalized in Canada without hospitalization elsewhere or travel to the Indian subcontinent, 77 (12%) had travelled to countries outside North America and Northern Europe, and 30 (5%) had no travel or hospitalization history. Among 34 non-hospitalized, non-Indian subcontinent travelers, 7 (all OXA) had travelled to Egypt (5) or other Eastern Mediterranean countries. Conclusions: CPE are increasing in incidence in Ontario. More than one-third of cases appear to be acquired in Canadian hospitals. Travel to some non-Indian subcontinent countries without hospitalization may pose an exposure risk.
Utility of a Multiplex Molecular Gastrointestinal Panel in Rapid Identification and Control of a Norovirus Outbreak in a Pediatric Tertiary Care Centre

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Background: Norovirus is one of the most common viral pathogens implicated in gastroenteritis outbreaks in community and health care settings. Short incubation period and high attack rate allow rapid spread through inpatient wards to patients, staff and visitors. Early identification and implementation of infection prevention and control measures is essential to interrupt transmission. Methods: Our centre is a 250-bed tertiary care Pediatric and Women’s hospital serving the Maritimes. We describe a norovirus outbreak in our 24-bed, single room Pediatric Medical Unit.

Hospital-acquired norovirus definition:

Patients admitted ≥48hrs with lab-confirmed norovirus AND ≥1 of:

Acute onset diarrhea.

OR

≥2 of: nausea, vomiting, abdominal pain, fever, or headache.

In 2017 FilmArray Gastrointestinal (GI) Panel was introduced in our Microbiology Laboratory. Since then, stool samples sent for viral, bacterial, or parasitic testing are evaluated by PCR. The panel tests for 22 GI analytes, with a 2-hr turnaround time. Previously, in-house stool viral testing was limited to adeno- and rotavirus antigen. Patient characteristics were collected and analyzed. Results: Patient 1 had new-onset diarrhea and vomiting on day 0; Patients 2 and 3 became symptomatic on day 1. Patient 3’s parents were previously symptomatic and had used the ward kitchen. Two care-givers of Patient 2, and 1 staff were symptomatic over days 0 to 2. Outbreak was over on day 6. Patients 1, 2 and 3 all tested norovirus positive in stool on day 1. On days 2-3, 6 additional patients with diarrhea tested norovirus negative. Symptomatic patients were immediately placed on contact precautions, ward cleaning frequency increased, and hand hygiene was reinforced. Common areas were closed until the outbreak was over. All patients with diarrhea were tested during the outbreak. Conclusion: FilmArrayGI panel enabled same-day identification of norovirus in this single-ward outbreak and permitted real-time identification of the termination of the outbreak.
National Guideline on the Prevention of Transmission of Bloodborne Viruses from Infected Healthcare Workers to Patients in Healthcare Settings

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Background: Certain surgical procedures may pose a risk of exposing patients to the blood of a healthcare worker (HCW). Although rare, HCW-to-patient transmissions of a bloodborne virus (BBV) have been documented. This Guideline was developed to provide a national framework for policies on the management of HCWs infected with BBV(s). Methods: Systematic reviews of the literature (1995-2016) were conducted to inform the transmission risk of hepatitis B (HBV) and C (HCV) and human immunodeficiency (HIV) viruses from infected HCWs to patients. Grey literature informed sections on disclosure of HCW’s serologic status, Expert Review Panels, and lookback investigations. National stakeholder partners were consulted and a Task Group provided technical expertise. Results: Provided HCWs adhere to Routine Practices, the risk of HCW-to-patient BBV transmission is negligible, except during exposure-prone procedures where HCW injury may expose a patient’s open tissues to the HCW's blood. Reported transmission rates were 0-3% (HIV, Table 1), 0.04-3.7% (HCV) and 0.06–11.11% (HBV). Rates vary with source viral load, nature of exposure, and IPC breaches. Current antiviral therapy informed guideline recommendations, with viral load thresholds defining fitness for practice.

Table 1: HIV transmission risks during exposure-prone procedures

<table>
<thead>
<tr>
<th>Author Specialty</th>
<th>Number of patients exposed/tested (%)/number infected</th>
<th>Transmission rate/risk</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bell 1992 Surgery</td>
<td>N/A (modelling)</td>
<td>1/42,000-1/420,000</td>
</tr>
<tr>
<td>Rogers 1993 Surgery</td>
<td>1131/450(40%)/0</td>
<td>No transmission</td>
</tr>
<tr>
<td>Dickinson 1993 Dentistry</td>
<td>1192/900 (70%)/0</td>
<td>≤0.0002%</td>
</tr>
<tr>
<td>Von Reyn 1993 Surgery</td>
<td>2317/1174 (51%)/0</td>
<td>4.37/100,000</td>
</tr>
<tr>
<td>Crawshaw 1994</td>
<td>1217/520 (43%)/0</td>
<td>No transmission</td>
</tr>
</tbody>
</table>
| Obstetrics/gynecology | Hansen 1996  
Invasive radiology | N/A (modelling) | Known HIV status: 0.03/1,000,000 (95% CI, 0-3.8)  
Unknown HIV status: 7.5/1,000,000 (95% CI, 0-15.3) |
|----------------------|----------------|-----------------|-----------------------------------------------|
| Lot 1999  
Surgery | 3004/983 (33%)/1 | 1.02/1000 | |

**Conclusions:** The guideline provides a pan-Canadian approach for managing HCWs infected with a BBV, with recommendations directly impacting clinical practice related to preventing and controlling healthcare-associated infections.
Role of Contact Precautions for Management of ESBL-Positive Patients: An Evidence-Based Review

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Objectives: Infection prevention and control (IPC) guidelines for extended-spectrum beta-lactamase (ESBL)-producing organisms vary across organizations and jurisdictions. The primary objective of this study was to review the published literature about the use of contact precautions for ESBL-positive inpatients in acute care facilities in non-outbreak settings to aid in the development of provincial evidence-based recommendations. Methods: Literature searches were performed in PubMed and EMBASE from beginning to August 2018. A grey literature search was also done to determine current practices, recommendations, and guidelines. The key search words were ‘Extended Spectrum Beta Lactamase’, ‘ESBL’, ‘patient’, ‘contact’, ‘precaution’ and ‘isolation’. Results: After removing duplication, there were 119 relevant articles. Based on the scoping review, there was strong support for continued attention to IPC routine practices, including hand hygiene. There was no evidence that additional contact precautions or patient isolation practices reduce transmission of ESBL organisms among inpatient populations in non-outbreak settings. In addition, there were no differences in recommendations for high-risk patient populations such as burns, oncology and critical care. Institution and enhancement of antimicrobial stewardship programs and practices was strongly supported. Conclusion: We recommend against routine institution of contact precautions for inpatients colonized or infected with ESBL-producing organisms in non-outbreak settings. Rather, there should be a strong focus on IPC routine practices and enhanced institutional support for antimicrobial stewardship programs. As more research becomes available on this topic, meta-analysis will need to be conducted on comparable data.
Surveillance of Methicillin-Resistant Staphylococcus aureus (MRSA) from Blood Culture Isolates in Alberta, 2013-2017

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Objective(s): MRSA has been a pathogen under public health surveillance in Alberta since 2005 and the epidemic clone CMRSA10/USA300 has remained high in community settings. This study focuses on the characterization of all blood MRSA isolates received by the Provincial Laboratory for Public Health (ProvLab) in the last five years in Alberta.

Methods: MRSA blood isolates from first clinical cases were submitted from all laboratories in Alberta to ProvLab from January 1, 2013 to June 30 2017. Clinical information provided on the requisition was recorded. Molecular characterization was performed using PFGE and spa typing and epidemic types were assigned. Results: Of 758 MRSA isolates, 54.9% were designated as CMRSA10/USA300, followed by CMRSA2/USA100/800 (22.2%), CMRSA7/USA400 (12.1%), CMRSA8 (3.8%), and 5.9% were not assigned a Canadian epidemic type. CMRSA1, 3/6, 4, and 5 were at insignificant numbers (1.1% of all MRSA). For demographic distribution, 47.6% of CMRSA2/USA100/800 isolates originated in the Calgary Zone while similar proportions of CMRSA10/USA300 (46.2%) and CMRSA7/USA400 (45.7%) were from the Edmonton Zone. Most isolates submitted (70.2%) originated from inpatient locations, including 69.0% of CMRSA10/USA300 and 70.8% of CMRSA2/USA100/800. For gender distribution of all prototypes, 61.5% were from males. The highest incidence of CMRSA10/USA300 was in the 30-40 year age group (20.2%) while the majority of CMRSA2/USA100/800 and CMRSA8 patients were in the 70-80 year age group. A total of 101 unique spa patterns were observed among the isolates tested, including t008 (CMRSA10/USA300; n=379), as well as 12 novel spa types. Ten CMRSA8 isolates matched novel spa type t6443 (8/10 male; average age of 74.3 years). Conclusion: The majority of the MRSA blood isolates in Alberta are related to the CMRSA10/USA300 epidemic type with a predominant spa type of t008.
Long-Term Sequelae and Health-Related Quality of Life Associated with Lyme disease: A Systematic Review

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Objective: The long-term health burden of Lyme disease (LD) remains poorly characterized. Our objective was to systematically review the long-term sequelae and health-related quality of life (HRQoL) associated with LD. Methods: We performed systematic literature searches in Medline, Embase, Scopus, CINAHL, PsycInfo and Environment Complete up to July 2017 following PRISMA guidelines. The protocol describing study eligibility criteria was published on PROSPERO (CRD42017068765). We included North American and European observational studies measuring attributable health burden: long-term sequelae, HRQoL, and prognostic factors. We excluded studies with unclear LD diagnosis criteria, co-infected patients, or did not have a non-LD control group. Two reviewers independently completed screening, data extraction and quality appraisal. Results: We screened 8,698 articles and included 35 primary studies conducted between 1994 and 2016. Most studies were conducted in the United States (74%), used retrospective cohorts (54%), and used LD diagnosis based on, or adapted from, the CDC case definition (66%). Studies investigated patients with varying LD stages (1 early localized, 9 early disseminated, 2 late disseminated, 11 post-treatment LD syndrome, and 9 mixed). Studies reported sequelae (79%), HRQoL (42%) and prognostic factors (11%). Mortality was not reported. Arthralgia (8.3%), memory impairment (3.3%), facial nerve palsy (2.9%), and sleep difficulty (4.3%) were the most commonly reported physical, cognitive, neurologic, and functional sequelae, respectively. Most HRQoL studies used Short Form-36 (67%) and reported physical and mental component scores. Mean follow-up duration (range, 2.1–15.4 years) and HRQoL varied with LD stage. Approximately half (52%) of the included studies met 80% of their respective quality appraisal criteria. Conclusions: Our review highlights the presence of long-term sequelae and reduced quality of life associated with certain stages of Lyme disease. Outcomes reported can support clinical management and will be useful for future clinical and economic evaluations of interventions targeting LD treatment and prevention.
Health Outcomes Attributable to Carbapenemase-Producing Enterobacteriaceae Infections: A Systematic Review

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Objective: Carbapenemase-producing Enterobacteriaceae (CPE) are a subgroup of carbapenem-resistant bacteria that pose a significant global health threat. We conducted a systematic literature review on the health-related quality of life (HRQoL), health outcomes, and long-term sequelae attributable to CPE infection. Methods: We followed PRISMA reporting guidelines and published our review protocol on PROSPERO (CRD42018097357). We searched four electronic databases: Medline, Embase, CINAHL and the Cochrane Library between January 2008 and May 2018 for concepts related to: CPE, quality-of-life, complications, and mortality. We included primary studies with a carbapenem-susceptible control group, conducted in Organization for Economic Co-operation and Development countries. We excluded studies that were not published in English, used an inappropriate control, or reported inappropriate outcomes. Quality appraisal was completed using Joanna Briggs Institute checklists. We qualitatively summarized the most frequently reported sequelae and conducted a meta-analysis. Results: We identified 8,671 studies of which 17 met the eligibility criteria for inclusion into this review. All studies reported health outcomes, none reported HRQoL. Most studies were conducted in teaching or university-affiliated hospitals (76%), from Europe (65%), and used case-control designs (53%). Mortality was the most commonly reported consequence of CPE-infections, with in-hospital mortality as the most often reported outcome (62%). Our meta-analysis (n=5 studies) estimated a risk difference of the in-hospital mortality rate of 0.25 (95% CI, 0.17 – 0.32). Duration of antibiotic therapy (range, 4-29.7 days vs. 1-23.6 days) and length of hospital stay (range, 21-87 days vs. 15-43 days) were relatively higher for CPE-infected patients compared to carbapenem susceptible patients. Overall, most studies (82%) met over 80% of their respective quality appraisal criteria. Conclusions: Health outcome studies associated with CPE infection are focused on short-term (e.g. in-hospital) outcomes; long-term sequelae and quality-of-life are not well studied. Future opportunities exist for longer follow-up to assess the clinical outlook for CPE infections.
Review of Clostridioides difficile - related deaths in an Alberta tertiary care hospital over a two-year period

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Objectives: Identify causes and confounding factors associated with Clostridioides difficile deaths over a two-year period in a large, tertiary care, teaching hospital. Methods: Retrospective chart review of deaths directly related to C. difficile or in which C. difficile was a contributing factor at the Royal Alexandra Hospital (RAH) in Edmonton, Alberta, from 01 January 2017 to 31 December 2018. Results: There were 19 deaths due to laboratory-confirmed C. difficile identified during the study period (male, 10/19; mean age, 78.9 years). Initial diagnosis was ‘severe’ in 7 and 16 cases by 2010 and 2018 Infectious Diseases Society of America classification, respectively. All were primary episodes, 15/19 were hospital-acquired to RAH. Recent antibiotic exposure was identified in 16 cases (indication sepsis, 8/16; pneumonia, 7/16) with 12 patients receiving at least two antibiotic classes. Initial management was guideline concordant in 14 cases (by either 2010 or 2018 classification). Pre-printed care order sets were utilized in 8 cases; initially 5/8 were guideline concordant with 2 corrected upon recognition of severity (7/8). Sixteen patients had treatment escalation within 72 hours; 8 were guideline discordant due to inappropriate escalation of oral vancomycin dose. Delay in symptom recognition (>48hr before testing) occurred in 8 cases, and treatment initiation delay (>24hrs) in 1 case. There was a lack of symptomatic response to treatment in 15 cases (average 2.5 days until death). Renal failure was the most common worsening comorbidity identified as contributing to death (9/19). Conclusions: Mortality from C. difficile is a quality indicator for C. difficile management, and the health care system. Review of local data indicate that deteriorating health states and increasing comorbidities influenced poor outcomes. Lack of adherence to updated guideline-recommended treatment, lower uptake of pre-printed care order sets and improved symptom recognition and timely testing are targets for intervention.
Active Approach to HIV/HCV Mass Screening: A Worthwhile Venture?

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Background: In 2015, 80,000 BC residents are living with HCV with the number of hepatitis related deaths expected to increase by one third by the end of 2022. In 2016, HIV incidence in BC was 5.1/100,000 with highest rates in Vancouver Coastal in the nation. HIV and HCV continue to be recognized as a major public health threat. Method: A data base collected from testing fairs at high risk locations Downtown Vancouver was analyzed. Participants self reported risk factors, history of HIV/HCV infection and current infectious status anonymously before screening. Known positive status were not screened. Positive participants were offered private onsite specialist counselling. Results: Data on 421 participants was collected: 247 male, 53 female and 121 chose not to identify themselves. 58% (244) reported screening >6months ago of which 85% (207) tested positive for either HIV/HCV. 88% (372) indicated a history of recreational drug use, of which 36% (135) had a history of IVDU. 41% (173) engaged in unprotected sex, of those 31% (54) were in a relationship. 8% (34) were newly screened and likely to be male. Participants were asked if they were already known to have any of the following illnesses: HIV, HCV, and HBV. There were 8 self-reported cases of HIV, 67 HCV, and 7 HBV. There were 3 new cases of HIV and 23 new cases of HCV. 4 HIV/HCV co-infected cases, 4 cases of HIV, and 81 cases of HCV were engaged in healthcare. History of IVDU was associated with 6 times more likelihood of being HIV positive. PWID were 15 times more likely to have HCV. Conclusion: An active approach to HIV/HCV screening in high-risk population can be used as an effective tool in decreasing disease incidence and eradication of HCV and HIV in Canada.
Perspectives of Infection Prevention and Control Specialists and Medical Officers of Health towards Patient Movement Restrictions during Gastrointestinal Illness (GI) and Influenza-like Illness (ILI) Outbreaks in Acute Care Settings in Alberta

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Introduction: Restriction of patient movement is an important component in management of hospital GI and ILI outbreaks; however, no standard definitions or practices exist. Objectives: Our objectives were to (1) collect information about outbreak-related unit closure decisions in acute care settings across Alberta from the perspective of Alberta Health Services (AHS) Medical Officers of Health (MOHs) and Infection Prevention and Control (IPC) specialists, and (2) investigate provincial variability in unit closure definitions and practices, with the goal of informing policy. Methods: We designed and performed a novel, cross-sectional, confidential, voluntary survey of AHS MOHs and IPC physicians and operational leads. Unit closure approaches were defined separately for Admissions-Transfer to-Transfer out as “No” – prohibiting movement, “Yes” – allowing movement, and “Selective” – allowing movement according to the delineated criteria. The “more-restrictive-approach” was determined as any combination of “No” and “Selective” approaches. Descriptive statistics, Fisher’s exact test, and chi-square were used. Results: The response rate was 38.2% (n=21; IPC, n=15; MOHs, n=6). The majority (n=8, 38.1%) defined unit closure as No-No-Selective. Seventeen responders reported utilizing a more-restrictive-approach (80.9%; p<0.001). Preference for more-restrictive-approach did not differ among health zones (\(\chi^2(2)=0.103; p=0.949\)). IPC inclined towards prohibiting admission and transfer to the unit in 80.0% and 73.3% of the cases (MOHs in 33.3% and 33.3%), but were more flexible in transferring out (prohibition, 13.3% versus 33.3%). Considering ILI and GI outbreaks separately, there was no difference between proportions of specialists with more-restrictive versus less-restrictive approach (n=17, 80.9% for each; p=1.000). Conclusions: Our findings support similar approaches to unit closure definitions and practices across Alberta; the vast majority of specialists apply restrictions to patient movement during hospital ILI and GI outbreaks. Exploring the effect of various unit closure practices on outbreak outcomes will assist in improving outbreak control policies and processes.
Effectiveness of Ward Closure during Respiratory Virus and Gastrointestinal Illness Outbreaks in Acute Care Settings

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Objectives: This study aimed to (1) review evidence from studies, systematic reviews, and guidelines that designate ward closure as a control measure for both influenza-like illness (ILI) and gastrointestinal illness (GI) outbreaks, (2) determine the effectiveness of ward closure in controlling outbreaks in acute care settings based on the most plausible evidence, and (3) provide practical ward closure implementation recommendations based on the current evidence. Methods: Electronic searches were conducted in PubMed, EMBASE, Google Scholar, and the Cochrane Library. A grey literature search was completed to determine current practices, guidelines, and recommendations. The key search words were ward closure, outbreaks, and effectiveness. Results: The term “ward closure” was used variably with no universal definition across the literature. However, in most instances, it referred to restrictions on patient movements into and out of a ward. The effectiveness of ward closure in controlling ILI and GI outbreaks is unclear, with variable results on outbreak duration and severity. Most studies were observational, and ward closure was usually one of multiple outbreak control measures implemented concurrently. Conclusions: Evaluating effectiveness of ward closure as a sole intervention is difficult as it is usually implemented with other infection prevention and control (IPC) measures. The observational nature of the involved studies did not provide concrete evidence for effectiveness of ward closure. Therefore, we recommend that the current state of practice be maintained; that is, that ward closure be considered as a possible outbreak control measure which may be used based on the IPC risk assessment for a particular ILI or GI outbreak. Accordingly, more controlled research studies are needed to determine the effectiveness of ward closure in managing acute care ILI and GI outbreaks.
Clinical manifestations and health outcomes associated with Zika virus infections in adults: A systematic review

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Background: Prior to the recent outbreak in 2015, Zika virus (ZIKV) infections in adults were considered to be largely asymptomatic, and characterized by a short, febrile illness. Increasing reports of symptomatic neurologic disease amongst infected adults warrant further investigation into the manifestations and long-term outcomes associated with ZIKV in adults. Objective: To synthesize the literature on clinical manifestations and sequelae of ZIKV infection in adults. Methods: We conducted a systematic search of the MEDLINE, Embase, PubMed, CINAHL, LILACS and WHO’s ICTRP clinical trials databases using the search terms “Zika virus” and “Zika infection”. Abstracts and conference proceedings were excluded, along with editorials, letters and news articles. Case series/reports with less than 10 participants and any animal studies were also excluded. Two reviewers followed PRISMA and MOOSE reporting guidelines. We used Joanna Briggs Institute Critical Appraisal tools for quality appraisal. Conflicts were resolved by consensus or consultation with third reviewer. Results: We identified 6248 references in our initial search up to April 30, 2018, of which 38 studies were included [Cross-sectional/descriptive (n=28), case-control (n=5), case reports/series (n=3), cohort (n=2)]. The majority of studies originated from North and South America, with publications from Brazil (n=7), Colombia (n=6), and the USA (n=5) constituting more than half of the data set. The most common outcomes reported were Guillain-Barre syndrome, encephalitis and myelitis. Approximately 37% of the studies reviewed met 80% or more of the quality assessment criteria for their respective study design. We will finalize complete analysis of the data prior to the conference. Conclusion: Based on preliminary results, there is evidence of adverse neurological clinical manifestations and long-term sequelae associated with ZIKV infection in adults. More targeted studies need to be conducted in non-pregnant adults to better understand clinical manifestations and longer term outcomes in this population.
Potential Impact of Routine Use of 13-valent Pneumococcal Conjugate Vaccine on Hospitalizations for Pneumonia among Older Adults in Canada

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Objective: 13-valent pneumococcal conjugate vaccine (PCV13) was licensed in Canada for the prevention of vaccine-type (VT) pneumonia in adults in July 2015. Dramatic reductions in VT-disease have been observed in older adults post implementation of pediatric PCV7 programs. Similar herd effect pattern has been assumed post PCV13-implementation, resulting in lack of age-based adult PCV13 recommendation. Recent surveillance suggests reductions of VT-IPD are significantly lower and have plateaued, leaving a persistent and substantial burden of potentially preventable PCV13-type disease in adults. The purpose of this work is to estimate the impact of a PCV13 immunization program for Canadian adults aged ≥65 years on community-acquired pneumonia (CAP) hospitalization, using current data. Methods: A model was constructed to estimate the number of CAP hospitalizations averted in the Canadian population aged ≥65 years over 5 years, based upon Canada-specific disease incidence and published estimates of PCV13 effectiveness and durability. Model parameters included: i) the size of Canadian population aged ≥65 years, ii) all-cause CAP incidence, iii) proportion of VT-CAP, iv) median length of stay, v) PCV13 effectiveness, and vi) duration of PCV13 protection over a five-year time horizon. Impact on multi-drug resistant CAP was also evaluated. Assumptions included: constant rates of all-cause CAP, proportion of VT-CAP, PCV13 effectiveness and 5% annual all-cause mortality rate for the 5-year period. Results: Based on model assumptions, PCV13 use in Canadian adults aged ≥65 years would lead to 62 (11–77) less hospitalizations per 100,000 persons, per year. This reduction, applied to the entire Canadian population of older adults, would avert an estimated 17,274 (3,037–21,711) hospitalizations and 138,192 (24,298–173,690) hospital days over a 5-year period. Conclusion: Despite herd effects from the routine pediatric program, direct PCV13 immunization of older adults in Canada could result in considerable additional reduction in hospitalizations for pneumonia.
**Sharing is Caring: Sustained HCV Care Engagement is Dependent on Successful Task Shifting**

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**Background:** Hepatitis C virus (HCV) elimination requires a marked, contemporaneous scale-up of both HCV diagnostics and therapeutics. In publicly funded health care systems, finding maximum efficiencies is paramount. In particular, revision of medically complex HCV care models is needed. One strategy is task shifting non-nursing roles to other skilled individuals, such as clerical staff. Our objective is to determine the effect of skilled clerical staff on overall HCV wait times and treatment initiations. **Methods:** A provincial HCV elimination strategy was developed where key elements included: centralized triage and referral, rapid treatment start, inclusion of incarcerated individuals, harm reduction strategies, and patient self-referral. Intrinsic to the low cost business plan is each individual working to full scope of practice. In particular, a medical clerk with advanced skills in database management and telephone based patient engagement was added to the HCV clinical team to complement an experienced nurse and physician. The required amount of time to engage each patient, as well as the wait times before and after engagement were measured. **Results:** We collected data from 3 time periods: pre-clerk (Jan - Dec 2017), clerk (Dec 2017 - Aug 2018), and post-clerk (Oct 2018). Treatment initiations were an average of 2.25, 15.3, and 3 patients per month respectively during each of the periods. Median wait time, in days, for the pre-clerk and clerk period was 140 (IQR 84-235) and 35 (IQR 21-63.75), respectively. First appointment attendance was 54.5%, 82.2%, and 14.3% (p<0.05, clerk vs post clerk period) respectively for the pre-clerk, clerk, and post-clerk time periods. **Conclusions:** Task shifting initial HCV patient engagement from a nurse to skilled clerical personnel is a successful tool to gain rapid scale-up of patient treatment initiation. Models that encourage task shifting need to be supported longitudinally to maintain benefit in HCV elimination.
Pseudomonas aeruginosa Strain Sharing in New-onset Cystic Fibrosis Infection

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Introduction: Sharing of P. aeruginosa (Pa) strains between cystic fibrosis (CF) patients with chronic infection is relatively common. It is unclear how common Pa strain sharing and multiple lineage infection are in new-onset Pa infections occurring earlier in CF, when infections are aggressively treated with antibiotic eradication therapy (AET). We performed whole genome sequencing of Pa isolated from sputum of children prior to initiation of inhaled AET, to determine the frequency of mixed infection and strain sharing, and impact on AET failure. Methods: We sequenced genomes of 342 Pa isolates collected from 65 children with 75 episodes of new-onset Pa between 2012 and 2016. Up to 10 isolates were sequenced per episode. An initial phylogenetic tree was constructed using a mash genome distance based method. Closely related strains were further investigated by mapping genomes to a closely related reference followed by generation of maximum likelihood phylogenetic trees. Strain sharing was inferred based on detection of appropriate topological signal in the trees. Univariate logistic regressions were used to assess associations between mixed infection, strain sharing and AET failure. Results: A large number of patients shared Pa strains (N=25/65, 40%). Mixed infection (two or more strains present in sputum sample concurrently) occurred in 12/75 episodes (16%). Having a mixed infection was significantly associated with sharing of Pa strains (unadjusted OR 10.7, 95% CI 2.2; 53.7, p <0.01) but was not associated with AET failure. Furthermore, strain sharing was not associated with AET failure. Conclusions: A substantial proportion of patients with new-onset Pa infection were infected with a strain shared with other patients. Mixed lineage Pa infections were relatively frequently observed in new-onset episodes and were associated with strain sharing between patients; however, mixed infections and strain sharing were not associated with AET failure in this cohort.
A Case of Fatal Tuberculosis Sepsis in an HIV-Positive Woman

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Objective: Sepsis from tuberculosis in people living with HIV is uncommon in Canada. We present a case of tuberculosis sepsis in an HIV-positive woman in B.C. and examine factors contributing to delay in diagnosis until after her death. Methods: Retrospective chart review of clinical notes and investigations. Results: A 38-year-old HIV-positive woman presented to hospital with two weeks of fevers, back pain, and abdominal pain. She was non-adherent with HIV treatment (CD4+ T-cells of <33 cells/mm³ for the previous 3 years), actively injecting drugs, and was partially treated for tricuspid valve endocarditis one year ago. Imaging demonstrated right lung tree-in-bud nodularity and ground glass opacities, L5-S1 osteomyelitis, and a mediastinal mass adjacent to the distal esophagus. She underwent urgent endoscopy and thoracoscopy for possible esophageal perforation, which showed extensive esophageal candidiasis. Vancomycin, piperacillin-tazobactam, and fluconazole were started. Blood, urine, and sputum cultures were negative. She left against medical advice on day three of admission, re-presenting two days later with ongoing fever and new productive cough with dyspnea. Antimicrobials were restarted. Repeat imaging demonstrated pleural and pericardial effusions, mild ascites, and mediastinal lymphadenopathy. Due to rapid decline in respiratory status, she was transferred to ICU and underwent urgent bronchoscopy with bronchoalveolar lavage specimens sent for bacterial culture. She continued to deteriorate despite maximal interventions. After discussion with family, she was transitioned to comfort care and passed away soon after. One week after her death, mycobacterial blood culture grew Mycobacterium tuberculosis. Bronchoscopy specimens were then sent for mycobacterial culture and found to be 3+ AFB smear positive, eventually also growing M. tuberculosis. Conclusion: Sepsis from TB can be missed due to competing comorbidities and anchoring biases, especially in marginalized populations. A high index of suspicion and low threshold for empiric TB treatment should be maintained, particularly for immune-compromised individuals.
Inherited IL-12Rβ1 Deficiency in a Child with Disseminated Bacillus Calmette-Guérin (BCG) Infections, Chronic Salmonellosis and Vasculitis: A Case Report and Literature Review

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**Background:** Mendelian susceptibility to mycobacterial disease (MSMD) is a rare primary immunodeficiency (PID) disorder caused by impairment of interferon-gamma mediated immunity. It is characterized by predisposition to disease caused by weakly virulent Mycobacteria, such as Bacillus Calmette-Guérin (BCG) vaccine, environmental non-tuberculous mycobacteria (NTM), and Salmonella species. Interleukin 12 receptor β1 (IL-12Rβ1) deficiency is the most common disease of Mendelian susceptibility to mycobacterial disease.

**Objectives:** To highlight the importance of clinical suspicion for early diagnosis and treatment of suspected primary immunodeficiency especially in areas with high rate of consanguineous marriages to optimize the patient’s outcomes.

**Methods:** A case report on Inherited IL-12Rβ1 Deficiency with a literature review on its epidemiology and treatment.

**Results:** We report a 6-year-old boy of consanguineous parents, who presented at 7 months of age with chest infection, generalized lymphadenopathy and inflammation at the Bacille Calmette-Guérin (BCG) inoculation site (BCGitis). Gastric aspirates for Acid Fast Bacilli (AFB) smear, and Polymerase chain reaction (PCR) amplification of M. tuberculosis DNA were positive. Mycobacterial culture and TB genotyping confirmed Mycobacterium bovis (BCG) vaccine strain. The diagnosis of Disseminated Bacillus Calmette-Guérin (BCG) infections were established. Patient were started on anti-TB medications, few months later he presented with recurrent lymphadenopathy; Lymph node biopsy culture revealed *a salmonella non typhi*. Initial immunological workup were normal, however in presence of persistent mycobacterial and salmonella infections genetic analysis was sent which identified a homozygous mutation in IL12RB1 gene, p.R173W (c.517C>T). This mutation leading to complete IL-12Rβ1deficiency. Both parents and sibling are heterozygous for this mutation. The patient still on antimicrobial therapy with good response although he developed generalized skin rash, biopsy revealed vasculitis responded to adding more anti-salmonella therapy.

**Conclusion:** Although the incidence of Inherited IL-12Rβ1 Deficiency is rare, early testing and diagnosis is crucial as well as prolonged effective management of disseminated *Mycobacteria and salmonella* infections.
A biologic-false positive sero-diagnosis of spotted-fever Rickettsial disease

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Objective(s): The mainstay diagnosis of rickettsial disease remains acute and convalescent serologies, with extensive cross-reactivity occurring within the Spotted Fever group (SFG). We report a biologic false positive SFG rickettsial serology case due to an unrelated infection. Methods: A 56-year male with controlled chronic HIV infection presented with three days of left-sided hearing loss, 2-weeks of blurry vision, and generalised macular rash involving his forehead, chest, and back. Ophthalmic examination of the left eye revealed optic disk oedema with retinal exudates, flame haemorrhages, a hemi-macular star, and cotton wool spots. Results: MRI of the brain/orbits revealed hyperintensity of the left optic nerve with no infarcts. A titre of 1:4096 to SFG and negative for Bartonella henselae were reported. Lumbar puncture revealed a pleocytosis of 16 x 10**6/L (83% lymphocytes) and protein 0.63 g/L. A diagnosis of early syphilis with neurologic manifestations (neuroretinitis and otosyphilis) was made. Other markers showed a a high RPR (1:256), positive TPPA. CSF VDRL was negative but FTA-ABS reactive (3+). After 14 days of intravenous penicillin, RPR declined to 1:2 at 4 months. He never received treatment specific for rickettsial disease. Conclusion(s): The elevated SFR-titre was considered a biologic false-positive based on the temporal occurrence of events, lack of tick bite, eschar, and no treatment for rickettsial disease: reports in the literature are rare. Acute syphilis is recognised to cause potential biologic false positives amongst other immunological assays due to the production of a myriad of treponemal and non-treponemal antibodies. We hypothesise that the non-treponemal antibodies (towards the cardiolipin-lecithin-cholesterol antigen), could potentially cross-react with the rickettsial antigen in the IFA assay. The initial manifestations were reasonably suggestive of Rocky Mountain Spotted Fever, however the lack of locally acquired cases in Alberta or tick bite eventually ruled out a serologic diagnosis of RMSF.
A Case of Acute Flaccid Myelitis (AFM) In An Immunocompromised Host In The Context of a US Outbreak of AFM

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Background: AFM (Acute Flaccid Myelitis) is commonly due to viral causes: poliovirus, nonpolio enterovirus, West Nile virus, St. Louis encephalitis virus, Japanese encephalitis virus, and adenovirus. [2, 1] Currently there is an outbreak of Enterovirus D68 causing AFM in 24 states in the US (396 cases since 8/2014 to 10/2018) primarily in children. Methods: We present a case report of AFM in an immunocompromised host that highlights the necessary diagnostic workup for AFM, and potential pitfalls in diagnostic testing in immunocompromised hosts. Results: A 70 female presented with fever, generalized weakness and acute confusion. She had a history of marginal cell lymphoma treated with 5 cycles of Bendamustine and Rituximab since 2016 and received her first maintenance dose of Rituximab 2 weeks prior to her recent admission. LP for viral studies and a paraneoplastic workup: LP 21 cells 87% lymphocytes negative HSV 1 and 2 PCR, negative VZV PCR, negative Enterovirus PCR, negative West Nile (WMV) IgM, and negative for bacterial and fungal culture. BAL negative for virology, and MRI head showed postoperative changes with no evidence of lymphoma recurrence. In the ICU she progressed with declining level of consciousness and developed acute flaccid paralysis. EMG studies supported an acute motor axonal neuropathy with active denervation of muscles (Figure 1). This patient was presenting with seronegative West Nile infection due to effect of Rituximab on B cells, which was subsequently confirmed positive with a stored LP sample sent for WNV PCR on the CSF. Conclusions: Patients with compromised immune systems are more susceptible to viral infections and more likely to develop severe complications. A review of the literature in lymphoma patients highlights the impact of Rituximab on B cell function with susceptibility to viral infections and false negative serological testing.[6]
A Rare Complication of Acute Otitis Media in Adults

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Background: Acute otitis media (AOM) is uncommon in the adult population, and while complications are rare, they can be severe. These complications include infectious seeding to adjacent structures resulting in brain abscess, significant neurological deficits and sinus thrombosis. The objective of this case is to highlight the importance of prompt diagnosis and treatment of AOM in adults to prevent serious complications, as well as to consider oral-pharyngeal organisms when treating brain abscess. Clinical Case: A 50-year-old male presented with a one week history of right-sided vision loss and headache. He reported chronic heavy alcohol use, was a long-standing smoker, had poor dentition, and had a two month history of untreated AOM with purulent otorrhea. Shortly after presenting to hospital, he had a first-episode tonic-clonic seizure. The patient was intubated and transferred to a tertiary care center. A head CT showed a left occipital lesion measuring 5.7cm x 3.3cm. An empiric antibiotic regimen was initiated, including vancomycin, metronidazole and ceftriaxone, and an intraventricular shunt was placed to drain the abscess. A follow-up head MRI showed left external auditory canal thickening and extension of the abscess into the lateral and fourth ventricle. Purulent drainage demonstrated gram negative rods on gram stain and Aggregatibacter aphrophilus was identified using MALDI mass spectrometry. Following drainage and ongoing treatment with ceftriaxone, the patient made a full recovery with no residual neurological deficits. Discussion/Conclusion: This case demonstrates the rare but serious potential sequelae of untreated AOM in the adult population, as well as the importance of prompt diagnosis and treatment. Aggregatibacter aphrophilus is a normal oral-pharyngeal organism that is a rare cause of brain abscess. It is important to consider oral-pharyngeal flora in the differential and empiric treatment for brain abscess.
Persistent renal failure following insertion of an antibiotic-impregnated spacer for treatment of a periprosthetic joint infection

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Objective(s): Management of periprosthetic joint infections (PJIs) may involve a two-stage revision. The first stage involves removing all components and placing an antibiotic-impregnated cement spacer that provides high intra-articular concentrations of antibiotic(s) above the minimum inhibitory concentration of the infecting pathogen. Methods: A 59-year-old female underwent the first stage of a two-stage procedure to treat a late-onset Escherichia coli PJI of the left knee. A custom-made cement spacer containing piperacillin/tazobactam, vancomycin, and tobramycin mixed with commercial methyl methacrylate, and gentamicin co-polymer was inserted. A bone abscess cavity was also filled with tobramycin-containing commercial bone filler. One week later, the patient developed progressive renal dysfunction despite hydration and exclusion of other causes, with a serum peak of 151 umol/L (baseline 75) at two weeks. At this point, the spacer was removed, and a new arthroplasty was implanted. Within ten days, her creatinine returned to baseline. Results: Iatrogenic acute kidney injury secondary to aminoglycoside toxicity due to persistent leeching from the antibiotic-impregnated spacer, and possibly the bone filler. Tobramycin serum levels ranged between 1.5-2.2 mg/L for 3 to 14 days post-operatively. Renal function normalised and aminoglycoside levels became undetectable only after the antibiotic spacer was removed and the second stage of the revision completed. Conclusion(s): Intra-articular spacers containing potentially nephrotoxic agents should be considered carefully when managing PJIs. Adding multiple antibiotics to cement mixtures may prevent proper setting, leading to increased and/or prolonged leaching of antibiotics. In our patient, spacer removal was the only course of action. Data to support better patient outcomes when multiple antibiotics are used with or without an aminoglycoside for synergy in cement spacers is scarce. Future directions include evaluation of cement mixture stability when multiple antibiotics are used, in order to determine their utility in treating PJIs.
Prevalence of *Clostridium difficile* Colonization Amongst Various Patient Populations

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**Objective:** *Clostridium difficile* infection continues to be a challenge for healthcare-associated communities. While testing is done on symptomatic individuals, asymptomatic carriers of *Clostridium difficile* are a potential risk to transmission and symptomatic infection. Identifying at risk populations and methods for detection can help determine the epidemiological importance of asymptomatic individuals and provide potential strategies for interventions. **Methods:** Rectal swabs originally for Methicillin-resistant Staphylococcus aureus (MRSA) surveillance were collected from four units across four acute-care hospital sites. The populations of the units consist of medical, hemodialysis, and pediatric patients. Residual ESwab transport medium from these rectal swabs, was tested with a validated laboratory-developed, loop-mediated amplification (LAMP) assay based on the *tcdC* gene. The specimens that tested positive with the LAMP assay, along with a random sample of negatives were further tested by polymerase chain reaction (PCR) to confirm LAMP test results. **Results:** We used our laboratory-developed LAMP assay to test 288 rectal swab specimens for *C. difficile* colonization. Utilizing an established clinical cut off of <45 minutes, 31 LAMP positives were identified. Prevalence for each unit is as follows; 0% (0/20) to 6.7% (2/30) for the two medical units, 7.9% (9/114) for hemodialysis patients, and 6.5% (8/124) for pediatric patients. Across the four hospitals, there is an overall prevalence of 6.6% (19/288). **Conclusion:** For the four hospital sites, there was a moderate prevalence among the various patients undergoing MRSA screening. Outcome studies will be needed to establish prognosis of asymptomatic carriers and the effect of carriage on hospital transmission. LAMP testing was an efficient method for colonization screening, however studies are needed to further optimize detection.
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WITHDRAWN
Screening for Carbapenemase-Producing Organisms (CPO) Carriage Can Be Initiated at 6 Months after the Initial Diagnosis of Intestinal Colonization

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Introduction: The natural course of intestinal colonization with CPO is unknown, but carriage may persist for years. Standardized re-screening criteria are currently not available. Objectives: We aimed to (1) perform a review of the evidence-based literature; (2) compare proportions of CPO-colonized individuals at various timepoints after the initial diagnosis of intestinal colonization; and (3) estimate a predictive value of remaining colonized at those timepoints. Methods: PubMed, EMBASE, Web of Science, and Cochrane Library (January 2000 to August 2018) were searched. Randomized-control trials, retrospective and prospective cohort, case series and cross-sectional studies were included. The primary outcomes were proportions of patients who remained CPO-colonized at 1, 3, 6, 9 and 12 months. Mean proportions (µ±SD) were compared using t-test. Studies with the most complete and homogeneous data were chosen to calculate the predictive value of remaining CPO-colonized at subsequent timepoints versus baseline. Re-colonized patients were removed from the pool. The missing data were replaced based on the proportions of CPO-colonized to compensate for drop-out. Results: Twenty-five studies were analyzed. As shown in Figure 1, mean proportions of CPO-colonized versus CPO-decolonized individuals differed significantly at 6 (25.0±16.3% vs 75.0±16.3%; p<0.0001) and 12 months (21.3±13.9% vs 78.7±13.9%; p<0.0001). There was no difference between the mean proportions of CPO-colonized individuals at 6 and 12 months (25.0±16.3% vs 21.3±13.9%; p=0.562). Five studies’ results were included in the calculation of the predictive value of remaining CPO-colonized at 6 months versus baseline (16.4%; 95%CI=14.5-18.3%); and at 12 months (13.3%; 95%CI=11.6-15.1%). Conclusions: Study findings suggest similar intestinal colonization rates and predictive values of remaining CPO-colonized at 6 and 12 months. These results will enable the development of an evidence-based and justified rationale to consider CPO re-screening at 6 months, which promises to be a more patient-centered and cost-effective strategy.
Figure 1: Mean proportion of CPO-colonized and decolonized individuals at select timepoints

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<th>6 month</th>
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<td>55.5</td>
<td>75.0</td>
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Banked human milk ingestion and *Bacillus cereus* infection in preterm: Case reports

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**Objective:** Banked human milk (BHM) is commonly used in countries around the world as preferred feeding for preterm infants when mother’s own milk is unavailable. However, BHM could incur some inherent infectious risks, even when pasteurized. Because of the ubiquity of *Bacillus cereus* in the environment and its ability to resist the Holder pasteurization process, there is a concern that BHM might lead to severe *B. cereus* infections. We reviewed observed and published cases to determine the potential causal role of BHM as the source for these infections. **Methods:** Two infants in the province of Quebec (Canada) developed a *B. cereus* neonatal infection, both had received BHM. We conducted bacteriological studies to compare clinical isolates and those found in the involved BHM. **Results:** After extended culture of BHM retention lots, *Bacillus cereus* were found in involved batches in the first case. However, molecular typing showed that the strain found in the BHM was different from the clinical isolate, therefore excluding BHM as the source of contamination. In the second case, a *Brevibacillus spp.* was isolated, a species distinct from the clinical isolate. **Conclusion:** Based on these cases and others reported in the literature there has never been a documented causal link between *B. cereus* contaminated BHM and preterm neonatal infection. Therefore, the risk that BHM can cause this infection remains theoretical. Given the widespread presence of *Bacillus cereus* in the hospital environment and its capacity to resist standard cleaning procedures, it seems likely that airborne or direct/indirect contact are the main sources of most, if not all cases of severe *B. cereus* neonatal infections, even in babies exposed to BHM.
Implementation of the Integrated Neonatal Care Kit to Reduce Neonatal Infection in Rural Pakistan: A Cost-Utility Analysis

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Background: Neonatal mortality accounts for nearly half of all deaths among children under five. With 46 neonatal deaths per 1,000 live births, Pakistan has the highest neonatal mortality rate in the world, bolstering the need for interventions that improve newborn survival. A recent cluster randomized controlled trial (cRCT) estimated the effect of an integrated neonatal care kit (iNCK) on neonatal mortality compared to standard of care in Rahimyar Khan, Pakistan. Objective: To strengthen the evidence-base towards wide-scale implementation of the iNCK, we evaluated the cost-effectiveness of iNCK distribution compared to standard care from the healthcare payer perspective. Methods: We performed a cost-utility analysis using a Markov model based on cRCT trial data and a comprehensive literature review. The base case was either standard care or distribution of the iNCK to pregnant mothers whose infant was followed over a lifetime time horizon. Outcome measures were life years, disability-adjusted life years (DALYs), costs and incremental net monetary benefit (INMB, at a cost-effectiveness threshold of USD 15.50), discounted at 3%. We conducted deterministic sensitivity analysis to assess parameter uncertainty. Results: At a cost-effectiveness threshold of USD 15.50, distribution of the iNCK resulted in lower expected DALYs (28.70 versus 29.54 years) at lower expected cost (USD 72.41 versus 86.11), translating to an INMB of USD 27 per iNCK distributed. These results were sensitive to the baseline risk of infection, cost of the kit and the relative risk of infection associated with iNCK use. Below a relative risk of infection of 0.83 and cost of the iNCK less than USD 32, the iNCK remained cost-effective compared to standard of care. Conclusions: The distribution of the iNCK dominated the current standard of care, i.e., is less costly and more effective, with most of the effectiveness attributable to a reduction in neonatal infection.
Etiology and Outcome of Acute Neonatal Infectious Encephalitis

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Objectives: There are very few studies on acute encephalitis with onset during the neonatal period. The objectives of this study were to investigate the etiology and salient clinical features of neonatal encephalitis. Methods: Neonates with possible infectious encephalitis (IE) were prospectively enrolled. Inclusion criteria included encephalopathy (altered/fluctuating level of consciousness ≥24 hours) plus ≥2 of: fever/temperature instability; seizure(s); focal neurologic findings; CSF pleocytosis; EEG abnormalities consistent with encephalitis; neuroimaging abnormalities consistent with encephalitis. Neonates with a clear diagnosis of post-perinatal asphyxial encephalopathy or culture proven bacterial meningitis were excluded. Results shown as absolute numbers, proportions or medians [interquartile range] as appropriate. Results: Fifty-nine neonates fulfilled the inclusion/exclusion criteria (June 2013 – November 2018). Empiric acyclovir was initiated in 49 (83.1%) cases. An infectious etiology was identified in 25 (42.4%): enteroviruses (n=15), HSV (n=5), HHV6 (n=2), parainfluenza 3 (n=1), influenza A (n=1), CMV (n=1). A non-infectious cause was confirmed in 20 (33.9%): missed hypoxic-ischemic encephalopathy (n=10), genetic/metabolic disorders (n=7), ischemic/hemorrhagic stroke (n=3). No specific etiology was identified in 14 (23.7%). Thirteen (52%) neonates with IE either died (n=7) or suffered neurologic sequelae (n=6). Deaths were attributable to HSV (n=4), enteroviruses (n=2) and HHV6 (n=1). Neurocognitive sequelae were documented in one case each of enterovirus, HSV2, HHV6, CMV, parainfluenza 3 and influenza A. Differences between neonates with and without IE, respectively, included age in days of symptom onset (7 [6, 10] vs. 1 [0, 3]; p<0.001), gestational age (37.0 [36.0, 39.0] vs. 38.6 [37.6, 40.0]; p=0.045), peripheral leukocyte count (10.5 [IQR 5.9, 14.6] vs. 14.3 [IQR 10.7, 21.7]; p=0.008) and CSF glucose (2.80 [IQR 2.3, 3.2] vs. 3.10 [2.8, 3.8]; p=0.003). Conclusion: Enteroviruses and HSV are the predominant causes of neonatal IE. Outcome of neonatal IE is poor with approximately half dying or suffering neurologic sequelae.
Competence Assessment Training and Teaching in a Total Automated Microbiology Laboratory

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Objective: Competence assessment, training and teaching (CATT) are integral in developing knowledgeable competent staff and essential in meeting accreditation requirements for a Microbiology Laboratory. The introduction of WASP™/WASPLab™ automation in our laboratory supports effective methodologies to provide the required consistency in specimen processing, incubation and digital imaging. The objective of this study is to use culture images and gram slides generated by the WASP™/WASPLab™ automation for competence assessment, training and teaching programs.

Methods: WASP™/WASPLab™ automation and automated staining was used to provide competence assessment to 49 Medical Laboratory (ML) Technologists and 13 ML Assistants. ML Technologists analyzed digital images and read WASP™ prepared slides from positive blood cultures stained with an automated stainer. ML Assistants performed maintenance tasks.

Results: Upon direct observation, all 13 MLAs performed the appropriate maintenance tasks on the WASP™ slide prep module as well as demonstrating problem solving skills. Using WASP™/WASPLab™, 5 urine specimens were analyzed by 49 MLTs. There were varied images and a simulated choice of button selection in the screening module. All MLTs were successful in their selections, image analysis and reporting. The same MLTs were given 5 gram slide preparations of positive blood cultures, made by the WASP™ and stained with the automated stainer. All of the MLTs were correct in their blood culture gram reporting.

Conclusions: Laboratory automation provides standardized sample preparation, processing and digital imaging which aligns itself perfectly for competence assessment as well as training and teaching opportunities. Digital imaging is stored and available for viewing over time as assessing staff over a long period of time across different shifts is challenging. Laboratory automation can help to develop highly skilled competent personnel who provide consistent, predictable and high quality results. Stored WASPLab™ images can be used for training new personnel or teaching students and residents.
Antimicrobial Activity of Ceftolozane-Tazobactam Tested against Contemporary (2015-2017) Gram-Negative Isolates from Patients with Pneumonia in US Medical Centers

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Background: Ceftolozane-tazobactam (C-T) has been approved for treating adults with complicated urinary tract infections, acute pyelonephritis, and complicated intra-abdominal infections in combination with metronidazole. In the current study, isolates were collected from US patients hospitalized with pneumonia (PIHP) from 2015-2017. Methods: A total of 4,337 GN isolates, including 2,102 Enterobacteriaceae (ENT) and 1,528 Pseudomonas aeruginosa (PSA) isolates, were collected in 2015-2017 from 30 US hospitals and tested for C-T susceptibility (S) by CLSI broth microdilution at JMI Laboratories. Only 1 isolate per patient per infection episode was included. Other antibiotics tested were amikacin (AMK), cefepime (FEP), ceftazidime (CAZ), colistin (COL), levofloxacin (LVX), meropenem (MEM), and piperacillin-tazobactam (TZP). Resistant (R) phenotypes analyzed were ENT R to doripenem, imipenem, or meropenem (CRE) and extended-spectrum β-lactamase (ESBL, non-CRE). Multidrug-resistant (MDR) isolates were identified as nonsusceptible (NS) to 3 or more antimicrobial classes. PSA phenotypes analyzed were CAZ-NS, MEM-NS, and TZP-NS. Results: Of the 4,337 GN isolates, 3,820 (88.1%) had a C-T MIC ≤ 8 mg/L. The 3 most prevalent GN species isolated from PIHP were PSA (n=1,528; 35.2%), Klebsiella pneumoniae (KPN, n=562; 13.0%), and Escherichia coli (EC, n=434; 10.0%). The %S of C-T and comparators for the top 3 pathogens are shown in the table. C-T showed activity against these isolates with %S of 96.5%, 88.6%, and 97.5% against EC, KPN, and PSA, respectively. Conclusions: C-T demonstrated activity against the most prevalent contemporary GN isolates from PIHP in the US. C-T was the only β-lactam that had >88%S against all 3 species: EC, KPN, and PSA. C-T and COL were the only agents tested that had >95%S for EC and PSA pathogens in PIHP. For PSA, C-T maintained activity against isolates resistant to CAZ, TZP, and MEM. These data suggest that C-T may be a useful treatment for GN infections causing PIHP.
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*CLSI (2018), EUCAST for EC and KPN vs. COL*
P40

WITHDRAWN
Doxycycline and tetracycline disc diffusion for susceptibility testing of *Streptococcus pneumoniae*: unexpected differences

D Whellams\textsuperscript{1,2}, M Imperial\textsuperscript{1,2}, M Kelly\textsuperscript{1,2}, R Liao\textsuperscript{1}, R Reyes\textsuperscript{1,2}

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**Objective:** A discrepancy in susceptibility rates between our laboratory and another prompted a review of historical *Streptococcus pneumoniae* disc diffusion results for tetracycline and doxycycline. **Methods:** Disc diffusion zone sizes for 2680 clinical isolates from 2013 to 2017 were extracted from our lab database. Susceptibility rates were calculated based on CLSI breakpoints and by anatomic site. Zone sizes were plotted to visualize the wild-type distribution of isolates. EUCAST breakpoints were also applied. **Results:** When CLSI breakpoints became available for doxycycline in 2014, our lab switched from tetracycline to doxycycline testing by disc diffusion, resulting in a contradictory increase in resistance to doxycycline. Visualization of zone size distribution suggests that CLSI doxycycline breakpoints distinguish poorly between wild-type and non-wild-type isolates of *Streptococcus pneumoniae*; EUCAST tetracycline breakpoints more accurately distinguish. Sputum isolates of *Streptococcus pneumoniae* demonstrate higher doxycycline resistance than isolates from eyes or other anatomic sites. **Conclusions:** CLSI doxycycline disc diffusion breakpoints appear to fall within the wild-type distribution in our patient population and may account for antibiogram differences between our laboratory and others. An additional study is planned to determine whether MIC testing is preferable. Sputum isolates of *Streptococcus pneumoniae* were more resistant to doxycycline than isolates from other anatomic sites.
Dalbavancin Therapy in a Canadian Tertiary Care Centre: a New Paradigm to Improve Adherence?

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Introduction: Dalbavancin, a second generation lipoglycopeptide with a half-life of 14 days, was recently approved for use in Canada for acute bacterial skin and skin structure infections (SSTIs) caused by susceptible gram-positive organisms. There are limited publications describing its use for other indications such as infective endocarditis, bacteremia, and osteomyelitis/joint infections. Objective: We describe two cases of dalbavancin use through the Special Access Programme (SAP) preceding its formal Notice of Compliance, including treating Bacillus cereus endocarditis and diabetic foot infection with osteomyelitis. Case Presentation: The first patient was a 42 year-old male with a history of opioid substance use disorder and multiple infective endocarditis episodes, including several hospitalizations in one year with Bacillus cereus group bacteremia and mitral valve endocarditis. During admissions he was not compliant with vancomycin therapy and had linezolid treatment failure after discharge with persistently positive blood cultures. After obtaining SAP approval, an initial loading dose of 1,000 mg and then three 500 mg weekly infusions of dalbavancin were administered via an outpatient parenteral therapy clinic. The patient attended all appointments and post-treatment blood cultures were negative. The second patient was a 56 year-old male with schizoaffective disorder and diabetes admitted with acute mania, psychosis, and polymicrobial diabetic foot osteomyelitis of the right great toe with pathogens including methicillin-susceptible Staphylococcus aureus and Group B Streptococcus. He required involuntary psychiatric care and restraints for administration of standard intravenous antibiotic therapy. Oral antibiotics were unsuitable due to drug interactions. SAP approval was granted for four weekly inpatient infusions of dalbavancin, dosed as for the first patient, allowing for conservative osteomyelitis management and limb preservation. Conclusion: Dalbavancin, a long-acting parenteral agent with weekly dosing, is a new antimicrobial in Canada for treating SSTIs. These cases of off-label treatment of endocarditis and osteomyelitis illustrate its successful use in challenging compliance scenarios.
Real World Treatment of Multi-drug Resistant (MDR) or Extensively-drug Resistant (XDR) *P. aeruginosa* Infections with Ceftolozane/Tazobactam (C/T) versus a Polymyxin or Aminoglycoside (Poly/AG) based regimen: A Multicenter Comparative Effectiveness

JM Pogue¹, KS Kaye², M Veve³, A Gerlach⁴, TS Patel⁵, SL Davis⁶, E Chaung⁷, AJ Ray⁷, NBousette⁸, LA Puzniak⁹, RA Bonomo¹⁰, F Perez¹⁰

¹Detroit Medical Center, Wayne State University, Detroit, MI, USA, ²University of Michigan Medical School, Ann Arbor, MI, USA, ³University of Tennessee Health Science Center, College of Pharmacy, Knoxville, TN, USA, ⁴Ohio State University Wexner Medical Center, Columbus, OH, USA, ⁵University of Michigan Health System, Ann Arbor, MI, USA, ⁶Henry Ford Hospital; Wayne State University, Detroit, MI, USA, ⁷University Hospitals Cleveland Medical Center, Cleveland, OH, USA, ⁸Merck Canada Inc., Kirkland, QC, Canada, ⁹Merck & Co., Kenilworth, NJ, USA, ¹⁰Louis Stokes Cleveland VA Medical Center, Cleveland, OH, USA

Objective: The emergence of MDR/XDR *P. aeruginosa* has led to a reliance on suboptimal agents (Poly/AG) for the management of infections due to this pathogen. C/T is a novel agent with excellent *in vitro* activity against resistant *P. aeruginosa* that is indicated for cUTI and cIAI and being reviewed for VABP. The purpose of this study was to assess comparative rates of clinical cure, mortality, and acute kidney injury (AKI) among patients treated with C/T versus a Poly/AG based regimen for *P. aeruginosa* infections. Methods: This was a retrospective, multi-site cohort of adult inpatients with infections due to MDR/XDR Pseudomonas. Patients treated for >/= 48 hours with C/T or Poly/AG-based regimen were eligible for inclusion. Patients with a creatinine clearance < 20 mL/min, or those requiring renal replacement therapy at baseline were excluded. Bivariate comparisons for baseline clinical characteristics and outcomes were assessed. Results: A total of 117 (57 C/T, 60 Poly/AG) patients were included. Baseline characteristics, infection source, severity of illness, and time to appropriate therapy were similar between the treatment groups. The most common infections were ventilator associated (54%) or hospital acquired (17%) pneumonia. Combination therapy was more frequently used in the Poly/AG group (72% vs. 12%; p < 0.001) Treatment with C/T was associated with a higher rate of clinical cure (79% vs. 62%; p = 0.046) and a lower incidence of AKI (7% vs. 33%; p < 0.001) compared to Poly/AG based therapy. In hospital mortality rates were similar (28% vs. 37%; p =0.33). No patients receiving C/T had hypersensitivity reactions, neurological adverse events, or *C. difficile* infections. Conclusion: This multi-center retrospective analysis provides real world data supporting improved outcomes with C/T compared to Poly/AG based regimens for invasive infections due to MDR/XDR *P. aeruginosa*. 

SR Arends¹, D Shortridge¹, M Castanheira¹, N Boussete², JM Streit¹, RK Flamm¹

¹JMI Laboratories, North Liberty, Iowa, USA, ²Merck Canada Inc., Kirkland, QC, Canada

**Background:** Ceftolozane-tazobactam (C-T) is approved by the US Food and Drug Administration and by the European Medicines Agency to treat complicated urinary tract infections, acute pyelonephritis, and complicated intra-abdominal infections. The Program to Assess Ceftolozane-Tazobactam Susceptibility (PACTS) monitors gram-negative (GN) isolates resistant to C-T worldwide. In the current study, isolates were collected from patients hospitalized with bloodstream infections (BSIs) from 2015-2017 within the United States (US).

**Methods:** A total of 3,377 prevalence-based BSI GN isolates, including *Escherichia coli* (EC; 1,422), *Klebsiella pneumoniae* (KPN, 630), and *Pseudomonas aeruginosa* (PSA; 344), were collected during 2015-2017 from 32 PACTS hospitals in the US. Isolates were tested for C-T susceptibility by CLSI broth microdilution method in a central monitoring laboratory (JMI Laboratories). Other antibiotics tested were amikacin (AMK), cefepime (FEP), ceftazidime (CAZ), colistin (COL), levofloxacin (LVX), meropenem (MEM), and piperacillin-tazobactam (TZP). Antibiotic-resistant phenotypes analyzed (CLSI, 2018) for EC and KPN included carbapenem-R (CR) and non-CR extended-spectrum beta-lactamase (ESBL); as well as CAZ-nonsusceptible (CAZ-NS), MEM-NS, and COL-NS PSA.

**Results:** Of the 3,377 BSI GN isolates, 3,219 (95.3%) had a C-T MIC ≤ 4 mg/L. The 3 most prevalent GN species isolated from BSIs were EC (42.1%), KPN (18.7%), and PSA (10.2%). The %S of C-T and comparators for the top 3 pathogens are shown in the table. C-T showed activity against these isolates with %S of ≥96.0% against all 3 species. Of the comparators tested, AMK and COL also had high %S against these isolates.

**Conclusions:** C-T demonstrated activity against the most prevalent contemporary GN isolates from BSIs in the US. C-T was the only beta-lactam that had ≥96%S against all 3 species: EC, KPN, and PSA. For PSA, C-T maintained activity (>90%S) against isolates resistant to CAZ, TZP, and MEM. These data suggest that C-T may be a useful treatment for GN BSI.
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*a CLSI (2018), EUCAST for EC and KPN vs. COL.*
Acquisition of a 16S rRNA Methyltransferase-Producing *Klebsiella pneumoniae* Isolate During Hospitalization in India

P Lagace Wiens\(^1,2\), D Alexander\(^1,3\), A Bharat\(^4\), A Walkty\(^1,2\)

\(^1\)Department of Medical Microbiology and Infectious Diseases, Max Rady College of Medicine, University of Manitoba, Winnipeg, MB, Canada, \(^2\)Shared Health, Winnipeg, MB, Canada, \(^3\)Cadham Provincial Laboratory, Winnipeg, MB, Canada, \(^4\)Public Health Agency of Canada, National Microbiology Laboratory, Winnipeg, MB, Canada

**Introduction:** Plazomicin, a next-generation aminoglycoside, retains *in vitro* activity against *Enterobacteriaceae* possessing common aminoglycoside modifying enzymes. *Enterobacteriaceae* that harbor a 16S rRNA methyltransferase demonstrate phenotypic resistance to plazomicin, but these remain rare in Canada at present. A patient with a 16S rRNA methyltransferase-producing *Klebsiella pneumoniae* isolate recovered on urine culture is described. **Methods:** A 64 year-old previously healthy male was hospitalized in India with obstructive uropathy. He subsequently returned to Canada and was admitted to hospital here for further evaluation. Abdominal imaging demonstrated a large bladder neoplasm. A biopsy was consistent with a high grade carcinoma. Bilateral nephrostomy tubes were inserted, and the patient received 14 days of antimicrobial therapy for a possible urine infection. At the completion of treatment, a follow-up urine specimen for culture was obtained and a pan-aminoglycoside (gentamicin, tobramycin, amikacin) resistant *K. pneumoniae* isolate was recovered. Plazomicin susceptibility testing was performed by broth microdilution, as described by the Clinical and Laboratory Standards Institute. The isolate underwent whole genome sequencing (National Microbiology Laboratory, Winnipeg, Canada) to assess for the presence of a 16S rRNA methyltransferase enzyme. **Results:** The *K. pneumoniae* isolate had a plazomicin MIC of >64 µg/ml (resistant by the US FDA breakpoint). The *rmtF* gene, which encodes a 16S rRNA methyltransferase enzyme, was detected by whole genome sequencing. Molecular testing also demonstrated the presence of a NDM-1 carbapenemase and a CTX-M-15 extended-spectrum beta-lactamase. As the patient described here did not have any symptoms consistent with a urinary tract infection at the time the isolate was identified, antimicrobial therapy was not prescribed. **Conclusions:** Hospitalization outside of Canada is a risk factor for colonization with antimicrobial-resistant bacteria. While much of the literature has focused on acquisition of beta-lactamase producers, isolates with genes conferring resistance to other antimicrobials (including novel agents such as plazomicin) may also be acquired.
**Comparison of *E. coli* Antibiotic Susceptibility in Urinary Isolates in Out-patients and Patients from Long Term Facilities in Ontario**

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*LifeLabs Medical Laboratories, Toronto, Ontario, Canada*

**Background:** *Escherichia coli* causes 80-85% of acute episodes of uncomplicated cystitis. Rates of resistance have undergone considerable variations, and consequently the empirical treatment requires regular updating of the antibiograms for different geographical areas and institutions. **Objective:** To compare susceptibility patterns of *E. coli* urinary isolates in out-patients and long term care (LTC) patients in local health integration networks (LHIN) in Ontario. **Method:** Retrospective data analysis was done on *E. coli* isolates from urine samples in 2016-2017 for out-patients and LTC patients, excluding hospitals. Susceptibility to Ciprofloxacin, Trimethoprim-sulfamethoxazole and Nitrofurantoin and prevalence of Extended Spectrum β lactamase (ESBL) were determined. **Result:** A total of 203,336 from 2017 and 191,748 isolates from 2016 were analyzed. Median overall susceptibility to Ciprofloxacin in Ontario was 69%, Trimethoprim-Sulfamethoxazole 74%, and Nitrofurantoin 97%, ESBL prevalence was 12.5%. For patients in LTC facilities, median susceptibilities were 51%, 67.5%, 93%, respectively and ESBL prevalence was 20.6%. For out-patients, median susceptibility to Ciprofloxacin was 84%, Trimethoprim-Sulfamethoxazole 79% and Nitrofurantoin 97%, ESBL prevalence was 5.5%. Lowest ciprofloxacin susceptibility for out-patients was from Central West LHIN at 79%. For LTC, lowest Ciprofloxacin susceptibility was from Champlain LHIN at 40%. For Trimethoprim–sulfamethoxazole, lowest susceptibility in out-patients was in Central West LHIN at 74%, and for LTC was in Champlain LHIN at 59%. Highest prevalence for ESBL in out-patients was from Central West LHIN at 8.9%, and for LTC was from North West LHIN at 31.3%. Susceptibility results were not significantly different in 2017 compared to 2016. **Conclusion:** *E. coli* isolates from urine have more resistance to antibiotics in patients from LTC compared to patients in the community. Separation of the patient population into community and LTC subgroups is helpful when selecting empiric antibiotic therapy. Resistance to Ciprofloxacin and Trimethoprim–sulfamethoxazole was high, highlighting the importance of relevant, local antibiograms.
A Disk-Diffusion Method for the Detection of Cefazolin Inoculum Effect in Methicillin-Susceptible Staphylococcus aureus.

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Objective(s): Cefazolin has excellent activity against methicillin-susceptible Staphylococcus aureus (MSSA), but some strains show cefazolin inoculum effect (CzIE) which may reduce the clinical effectiveness of this drug. Currently, MSSA strains with CzIE are identified by the micro broth-dilution method (MBDM) using a high inoculum, but this method is cumbersome and cannot be used routinely. This study sought to evaluate a more simple method to identify MSSA with CzIE using standard disk diffusion method (DDM).

Method: 201 non-duplicated MSSA isolated from blood cultures were evaluated. The cefazolin MIC was determined by the MBDM using the standard inoculum $[10^5 \text{ colony forming units (CFU)/mL}]$ and high inoculum $(10^7 \text{ CFU/mL})$. MBDM testing was performed according to CLSI guidelines. S. aureus references strains which exhibit high-inoculum effect or not were used as controls. CzIE was defined as an increase in minimum inhibitory concentration (MIC) to cefazolin $>16 \text{ mg/L}$ when tested with the high inoculum. Zones of inhibition for cefazolin were determined by DDM using a $30\mu\text{g}$ cefazolin disk as per CLSI guidelines.

Results: Of 201 MSSA, 62 isolates had a cefazolin MIC of $\geq 16 \text{ mg/L}$, thus were positive for CzIE. One hundred thirty-nine strains did not show CzIE using MBDM. Using a zone of $\leq 29 \text{ mm}$ as a cut-off, the sensitivity of cefazolin DDM was 91.93% (57/62), but the specificity was low at 77.69% (108/139). Conclusion: This study shows that the DDM of cefazolin is reasonably sensitive for identifying MSSA with CzIE. The method is easy to perform and may identify patients for whom cefazolin may not be an optimal drug. Further analyses are underway to validate the robustness of these conclusions.
Successful transition of Antimicrobial Stewardship (ASP) Rounds from an ASP pharmacist to General Internal Medicine pharmacist led approach

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¹Hamilton Health Sciences Juravinski Hospital, Hamilton, ON, Canada, ²McMaster University, Hamilton, ON, Canada

Objective: To evaluate the impact of weekly antimicrobial stewardship (ASP) rounds for general internal medicine (GIM) patients, first led by an ASP and later general internal medicine (GIM) pharmacists. Methods: Weekly interdisciplinary ASP rounds attended by physicians, trainees and pharmacists from both the ASP and GIM teams were conducted at a tertiary care hospital in Hamilton, ON. All GIM patients on anti-infectives and not followed by the infectious diseases service were reviewed. Rounds were first led by an ASP pharmacist (1-6/2018), and then by the GIM pharmacists (7-11/2019). The ASP pharmacist was available for consultation as needed and occasionally attended rounds. The transition was supported by an 11-module educational ASP credentialing program. Process measures were collected and statistical process control (SPC) was used to evaluate changes in antimicrobial utilization (monthly DDD per 1000 patient days). Results: Process measures captured in detail between 1-8/2018 showed that the non-teaching teams attended 19/26 (73%) and teaching teams attended all scheduled rounds, and 567 patients were discussed. ASP intervened on an average 1 in 4 patients and 143/159 (89.9%) interventions were accepted; the majority focused on duration (n=74; 46.5%) and discontinuation (n=35; 22%). Compared to 2016/2017, there was an 18% reduction in utilization (from 559 in 2016/2017 to 460 DDD/1000 patient days). Five months were below 2 control limits, and the monthly utilization was below the 2016/2017 average in each month since the implementation of ASP rounds meeting SPC criteria as a special cause change (‘significance’). Conclusion: Dedicated interdisciplinary ASP rounds to discuss patients admitted under a GIM service facilitated optimization of anti-infective therapy, and resulted in a significant reduction in antimicrobial utilization. These gains were sustained when GIM pharmacists took over leading the rounds, suggesting this is a feasible sustainability model for antimicrobial reviews.
A Cross-sectional Survey: Attitudes Among Resident and Attending Physicians Regarding Development of an Antimicrobial Stewardship Program

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¹Memorial University, St. John's, NL, Canada, ²University of Manitoba, Winnipeg, MB, Canada

Objectives: Antimicrobial resistance (AMR) is a global health concern. Our health region lacks an antimicrobial stewardship program (ASP), an intervention strongly recommended to curb AMR. We explored perceptions and attitudes towards antimicrobial prescription, resistance, and stewardship and whether these varied by practitioner type; and identified prescriber preferences in developing a local ASP. Methods: A 29 item-questionnaire (19 Likert-scale, 7 multiple-choice and 3 open-text questions), adapted from a published survey was disseminated using online software. 401 invitations were emailed to attending physicians and residents within medical specialties, surgical specialties, family medicine and critical care. The survey was open for 6 weeks. Comparisons between groups were performed by Fisher’s Exact tests.

Results: We received 122 completed responses, a response rate of 30.4%. Most (76.9%) respondents were from medical subspecialties or family medicine. 56.5% of participants were residents. Over 95% of participants agreed that broad spectrum agents contributed to AMR, and that prescription optimization limits its development. While only 7.6% of participants felt they had overprescribed antimicrobials, 48.8% felt these were over-prescribed by clinicians other than themselves. 82% of participants felt that an ASP had potential to improve patient care; this attitude did not vary by resident vs. attending status (p=0.311), between prescribers in academic or community settings (p=0.561), by clinical specialty (p=0.508) or by frequent or infrequent antibiotic prescribers (p=0.650). Most respondents favored audit and feedback from an infectious disease physician.

Conclusion: Surveyed attending and resident physicians acknowledged the importance of antimicrobial optimization in limiting AMR. There may exist a lack of awareness among prescribers regarding over-prescription habits. All prescriber groups exhibited receptiveness towards implementation of a formal ASP and agreed it would benefit patients. In developing a formal program in our region, prospective audit and feedback with communication from infectious disease physicians would likely be viewed favorably.
In Vitro Susceptibility of Urinary Isolates of Escherichia coli to Oral Antimicrobial Agents

MS Bader\textsuperscript{1,2}, N Irfan\textsuperscript{3}, A Brooks\textsuperscript{1,2}

\textsuperscript{1}McMaster University, Hamilton, ON, Canada, \textsuperscript{2}Hamilton Health Sciences, Juravinski Hospital, Hamilton, ON, Canada, \textsuperscript{3}Hamilton Health Sciences, Hamilton General Hospital, Hamilton, ON, Canada

\textbf{Objective:} Managing urinary tract infections (UTIs) caused by antibiotic-resistant \textit{E.coli} is challenging given limited oral therapeutic options. Current guidelines recommend basing empirical treatment of UTIs on local or regional susceptibility data. The aim of this study was to evaluate in vitro susceptibility of urinary isolates of \textit{Escherichia coli} to oral antimicrobial agents in patients at two acute care hospitals in the year 2016.

\textbf{Methods:} Patients aged $\geq 18$ years with positive urine cultures for \textit{E. coli} from January to December 2016 were included. In vitro susceptibility testing of \textit{E. coli} to oral antimicrobial agents under review were tested using the commercial VITEK 2 automated identification/susceptibility testing instrument, and when indicated, by disk diffusion in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Descriptive statistics were used to summarize the result of the study.

\textbf{Results:} A total of 1999 urinary isolates of \textit{E. coli} were included for analysis. The rates of \textit{E. coli} susceptibility to nitrofurantoin, trimethoprim-sulfamethoxazole, and ciprofloxacin were 96.3\%(1925/1999), 73.9\%(1478/1999), and 72.3\%(1446/1999), respectively. The rates of extended spectrum $\beta$-lactamase (ESBL)- and AmpC- $\beta$-lactamase - \textit{E. coli} were 11.6\% (231/1999) and 2.3\%(45/1999), respectively. The rates of susceptibility of ESBL-\textit{E.coli} to nitrofurantoin, trimethoprim-sulfamethoxazole, and ciprofloxacin were 91.3\% (211/231), 30.3\%( 70/231), and16\% (37/231), respectively. The rates of susceptibility of AmpC- $\beta$ -lactamase-\textit{E coli} to nitrofurantoin, trimethoprim-sulfamethoxazole, and ciprofloxacin were 91.1\%(41/45), 71.1\% (32/45), and 68.9\%(31/45), respectively.

\textbf{Conclusions:} Nitrofurantoin is the most active oral agent against urinary isolates of \textit{E. coli} including ESBL- and AmpC- $\beta$ -lactamase-producing strains. Trimethoprim-sulfamethoxazole and ciprofloxacin should not be used as empiric treatment of UTIs, particularly in patients at risk of infections with ESBL- and AmpC- $\beta$ -lactamase- producing \textit{E coli} given resistance rates of \textit{Enterobacteriaceae spp} exceed 20\%. 
Influencing Duration of Antibiotic Therapy: A Behaviour Change Analysis in Long-Term Care

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Objectives: Prolonged antibiotic duration of therapy is common in long-term care (LTC) settings and is associated with increased risk of harm for residents, including the development of antimicrobial resistance. Although there is a growing body of evidence evaluating the factors influencing the initiation of antibiotic therapy, little is known about the influencers of prolonged duration. To identify potential antibiotic stewardship opportunities aimed at prolonged duration of therapy, this study examined barriers and enablers to using shorter courses of antibiotic therapy in the LTC setting. Methods: Semi-structured interviews were conducted with prescribers in LTC home settings. A total of eight LTC clinicians participated in the study (4 physicians and 4 nurse practitioners). Questions and clinical scenarios (addressing urinary tract infection, pneumonia and cellulitis) explored the factors influencing prescribers’ decisions about duration of therapy. Interview data were analysed deductively, using the Theoretical Domains Framework (TDF). The coding structure reflected the 14 domains of the TDF. Two reviewers independently analysed the data and disagreements were resolved with consensus. Results: The most commonly cited domains (and frequency of occurrence) influencing duration of antibiotic therapy in LTC were environmental context and resources (n=84); knowledge (n=32); beliefs about consequences (n=29); social influences (n=21); and behavioural regulation (n=19). Specific concerns described by participants included the perceived lack of evidence to support shorter courses in LTC residents, the misconception that shorter courses could lead to greater rates of resistance, and the strong role of habit and prior experience in selecting antibiotic duration. Conclusions: There are several factors affecting antimicrobial duration prescribing behaviour aside from the clinical scenario itself. Tackling misconceptions and providing educational support may be helpful approaches to address prolonged treatment. These findings provide theory-informed evidence to support the development of antimicrobial stewardship interventions aimed at improving duration of antibiotic therapy.
Impact of New Electronic Medical Record System on Duration of Active Antimicrobials

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Objective(s): In April 2018, Lions Gate Hospital (LGH) transitioned from paper charts to a new electronic medical record system. With the new system, automatic stop dates for antimicrobials were replaced by soft stop dates and soft stop reminders. Antimicrobial utilization data from the legacy and electronic system were analyzed and compared to identify the new system’s impact on the duration of antimicrobial therapy. Methods: An antimicrobial point prevalence survey was conducted at LGH between September to November 2018. The survey included all inpatients admitted at the hospital at 8:00am and receiving antimicrobial therapy within the past 24 hours of the survey dates. The duration of the current active antimicrobial prescription order(s) (orders with the same drug, dose, route, and frequency) was recorded. Previous doses were considered a separate order and excluded from the survey. Results: 220 patients were surveyed of whom 60 patients (26.9%) met the inclusion criteria for a total of 79 antimicrobial prescriptions (average 1.32 antimicrobials per patient receiving antimicrobials). Comparing 2017 to 2018, the number of patients receiving antimicrobials (61 vs. 60) and antimicrobial prescriptions (78 vs. 79) remained consistent; however, the survey identified an increase in average duration of antibiotic prescriptions on the day of survey from 3.0 to 4.9 days. Duration of oral antimicrobials increased from 2.5 to 5.5 days while IV antimicrobials increased from 3.4 to 4.5 days. Conclusion(s): These results suggest that the loss of automatic stop dates for antimicrobials due to implementation of an electronic health record system may have resulted in an increase in antimicrobial prescription duration. This presents future opportunity for improvement with implementation of the new electronic system and antimicrobial stewardship initiatives. Further point prevalence surveys need to be done to assess the impact of these initiatives.
a Multi-Centre Audit of Pre-Operative Antimicrobial Prescribing and Administration

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Objectives: Optimal prescribing of pre-operative antimicrobial prophylaxis is complex and multidisciplinary. Previous audits have identified opportunities for improvement in general surgery and orthopedics, but no data is available for the majority of surgical subspecialties. We wish to investigate pre-operative antibiotic prescribing concordance with administered antibiotics in the OR across all surgical subspecialties and assess guideline concordance of those antibiotics received in the OR. Methods: As part of a larger quality improvement initiative, audits were conducted on patients from each of the 13 surgical subspecialties at a large, urban teaching hospital system. Patients were randomly selected for prospective audit conducted during the OR followed by retrospective review of pre-admission consults and antibiotic prescribing. All administered antibiotics were adjudicated for concordance by comparing administered antibiotics to local best practice guidelines. All analysis was conducted using descriptive statistics. Criteria for concordance assessment were initial choice, dose or timing as well as redose choice, dose or timing. Results: 200 patients were audited during the study period (August to November 2018). Discordance was common between antibiotics prescribed on initial assessment by surgeons prior to the OR and those given in the OR (49%). The most common reasons for discordance were 1) no record of antibiotics prescribed in initial surgical assessment (30%); 2) antimicrobial dose change (27%) and 3) antimicrobial choice change (17%). Of all antibiotics administered in the OR, 39% were guideline discordant. The majority of these (56%) were due to discordant initial antibiotic dose followed by initial antibiotic choice (17%) and redose dose (11%). Conclusions: A high degree of discordance exists between both the prescribed and OR administered antimicrobials administered as well as between OR administered antimicrobials and local practice guidelines. Opportunities for both process and outcome improvements exist and require further investigation.
Daptomycin and Linezolid use at an inner-city tertiary care hospital: A 6-month retrospective review

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Daptomycin and linezolid are indicated by Alberta Health Services (AHS) guidelines for resistant Gram-positive infections. The first-line agent is vancomycin; however, daptomycin and linezolid are frequently used for dosing or administration route convenience.

Objectives: (1) Evaluate the number of guideline concordant prescriptions of daptomycin and linezolid in a 6-month period and (2) investigate reasons for guideline discordant prescriptions. Methods: We conducted a retrospective chart review of all inpatient, emergency, and outpatient antimicrobial therapy (OPAT) clinic prescriptions for daptomycin and linezolid at an inner-city tertiary care hospital in Edmonton, AB, over a 6-month period (July to December 2017). Results: There were 45 courses of daptomycin and 24 courses of linezolid prescribed. 26 of 45 (57.8%) daptomycin prescriptions and 11 of 24 (45.8%) linezolid prescriptions were discordant with AHS guidelines. The Infectious Diseases consult service was involved in the majority of these prescriptions (daptomycin, 40/45, 89%; linezolid, 18/24, 75%). 8/11 discordant linezolid prescriptions were initiated due to lack of or discontinuing intravenous (IV) access due to substance use. 14/26 discordant daptomycin prescriptions were initiated to increase compliance (once daily dosing) or facilitate discharge without the need for home parenteral therapy. Conclusion: There is a high rate of discordance for daptomycin and linezolid when using the AHS formulary guidelines. However, the majority of guideline discordant prescriptions were due to valid extenuating circumstances in this unique patient population that are not included in the AHS guidelines (e.g., need for once daily or oral options) that necessitated the use of daptomycin or linezolid rather than first-line vancomycin (either as an inpatient or via home parenteral therapy). Additionally, use of daptomycin in the OPAT clinic instead of vancomycin in the inpatient setting is a cost-saving and patient-centered measure.
Identifying Antimicrobial Stewardship Opportunities through Point Prevalence Comparison

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Objective(s): Global Point Prevalence Survey (PPS) of Antimicrobial Consumption and Resistance is a project collecting international data to monitor rates of antimicrobial prescribing in hospitalized patients. Antimicrobial utilization data from Fall 2017 and Fall 2018 were compared with the goal of identifying stewardship opportunities. Methods: A point prevalence study was performed according to the Global Point Prevalence Survey. In September-November 2017, data were collected from paper charts while in September-November 2018 they were gathered from the newly implemented electronic medical record system. Via a snapshot of all patients receiving antimicrobial therapy at 0800h on the survey day, this project characterizes the overall antimicrobial use pattern (administration, route, and guideline adherence). Results: In 2017 and 2018, a similar number of patients received antimicrobial therapy on the survey day, 61 (28.8%) and 60 (26.9%), respectively. While only 64.1% (50 prescriptions) of the orders were guideline-compliant in 2017, an improvement was seen in 2018 with 84.8% (67 prescriptions) guideline-compliance. While the percentage of orders with documented stop date increased from 34.7% (25 prescriptions) to 41.8% (33 prescriptions) from 2017 to 2018, the proportion of oral antimicrobials decreased from 46.2% to 35.4%. Conclusion(s): The PPS results reveal that the total usage of antimicrobial agents was similar between two consecutive years. While there seems to be an improvement in guideline adherence, the percentage of orders with documented stop date remains low. As a result, documenting treatment duration and IV to PO stepdown remain two key opportunities for the antimicrobial stewardship program.
Performance of two EIA algorithm for Lyme Disease (LD) in Nova Scotia

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Background: US data suggests that a two EIA algorithm (2EIA) (whole cell (WC) EIA followed by C6 EIA) has improved sensitivity but equivalent specificity to the recommended two tier algorithm (TTA) (EIA followed by Western blot (WB)) for the serologic diagnosis of LD. From 2011 to 2014, the QEII laboratory used a WC EIA for LD serology. Positive or indeterminate results were then tested with the C6 EIA by the National Microbiology Laboratory. Only the sera with positive or equivocal C6 results were tested with IgG and IgM WB, providing the opportunity to evaluate the real world performance of the 2EIA compared to TTA in a Nova Scotian population. Methods: A retrospective chart review was performed on patients testing positive with both WC and C6 (2EIA approach). Patients were classified as having LD if they had 1. a positive TTA result; 2. A negative TTA result but had symptoms consistent with LD; or 3. Evidence of seroconversion between consecutive specimens. Specificity was calculated based on standard 4x4 table. Results: From 2011-2014, 10253 specimens were tested for LD, 9790 were negative. Of the 256/463 positive charts reviewed to date, 213 and 43 specimens were classified as coming from patients with and without LD respectively. The number of 2EIA positive patients without LD (false positive results) was 43. Of the 213 results from patients with LD there were: 119 positive IgG WB; 57 positive IgM WB with negative IgG WB; 17 negative specimens with IgG/IgM WBs. The remaining 20 specimens were IgG WB borderline or negative, with negative/borderline/not tested IgM WB. Calculated specificity is 99.56% (99.41-99.68%). Conclusion: Preliminary analysis suggests the 2EIA has excellent specificity and is more sensitive than the TTA. A further chart review is required to accurately define the sensitivity of 2EIA in our population.
Comparison of culture-based methods for the detection of Shiga toxin-producing E. coli

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Objectives: In 2018 the Canadian Public Health Laboratory Network recommended detecting Shiga toxin (Stx)-producing E. coli (STEC) by one of three methods: nucleic-acid testing, chromogenic agar, and toxin antigen detection after pre-incubation in broth. In this study, the sensitivities of the latter two methods were compared prospectively. Methods: Feces submitted for culture were tested for STEC using the CHROMagar™ STEC. The production of Stx by mauve-coloured colonies was confirmed by SHIGA TOXIN QUIK CHEK™. If the requisition indicated hematochezia, hemolytic uremic syndrome, or a request to rule out STEC, feces were additionally incubated in MacConkey broth, then tested using the SHIGA TOXIN QUIK CHEK™ (brothEIA). Enrichment culture to obtain a STEC isolate from brothEIA-positive-only specimens was performed at the Alberta Provincial Laboratory for Public Health. Isolates were serotyped at the Public Health Agency of Canada-National Microbiology Laboratory. Culturing a STEC isolate from the CHROMagar or on subculture from brothEIA-positive-only specimens was considered the reference standard for a positive result. Results: From June 11 to December 31, 2018, there were 12,882 fecal culture specimens. Of 1599 specimens meeting criteria to be tested by both CHROMagar and the brothEIA methods, 41 positives were detected. For two specimens, the brothEIA was toxin positive but failed to grow on enrichment culture, therefore 39 specimens were included in the sensitivity calculations. Each method had a sensitivity of 87% (95% CI 72.8-94.8): 5 false negatives for each method. The most common serotype was O157 (26%), followed by O26:H11 (10%). No serotype was disproportionately represented in the false negatives for either the plate or the brothEIA method. Conclusions: The CHROMagar and brothEIA each exhibits acceptable sensitivity in our study. While using both methods simultaneously would increase the number of STEC detected, the additional costs may not be justifiable in a cost-benefit analysis.
Variable Performance of the Bruker™ MALDI-TOF Mass Spectrometry MRSA Subtyping Module for the Rapid Detection of Methicillin-Resistant *Staphylococcus aureus* from Selective and Nonselective Media

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**Background:** Rapid identification of methicillin-resistant *Staphylococcus aureus* (MRSA) is important for patient care and infection control. Several studies have evaluated the performance of the Bruker™ MALDI-TOF MRSA Subtyping Module, based on the detection of phenol-soluble modulin (PSM), from routine cultures; however, few have tested selective or chromogenic media. The purpose of this study is to evaluate the subtyper using common MRSA surveillance media. **Methods:** 108 MRSA and 101 methicillin-sensitive *S. aureus* (MSSA) isolates were randomly selected from surveillance cultures. Isolates were subcultured to two chromogenic media (Bio-Rad MRSA Select™ II and Alere Colorex MRSA Agar), mannitol-salt agar (MSA), and blood agar (BA) and were confirmed as MRSA by PBP2a’ latex agglutination. Isolates were spotted on a target plate using the direct transfer method and sequentially run on two MALDI-TOF machines. PSM peak detection was done automatically by the Bruker™ software. **Results:** Performance varied depending on the media. From BA, the sensitivity was 35-38% and specificity was 100%. Sensitivity and specificity from MSA was 81-85% and 36-58%, respectively. Sensitivity from the Alere chromogenic agar was 84% but was 0% from the Bio-Rad chromogenic agar. Specificity was not determined as MSSA are unable to grow on chromogenic media. **Conclusion:** Using nonselective media (BA), the subtyper exhibited limited sensitivity but excellent specificity; however, from selective media (MSA), sensitivity increased but the specificity was poor. This suggests that the rate of false positives can be high depending on the media, an observation that has been underappreciated in the literature. Variable performance was also observed between the two chromogenic plates but suggests that the subtyper can be used to confirm presumptive MRSA colonies from the Alere agar. Taken together, our results show that the Bruker™ MRSA subtyper exhibits media-dependent performance and highlights that extensive validations are needed before adapting rapid identification methods for routine resistance detection.
Antimicrobial Resistance in Pathogens Isolated from Patients in Canadian Hospitals: CANWARD 2018

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Objectives: The CANWARD study assesses the pathogens causing infections in patients affiliated with Canadian hospitals and evaluates the prevalence of antimicrobial resistance in these isolates. Methods: In 2018, twelve tertiary-care centres across Canada submitted clinical isolates from patients attending clinics (C), emergency rooms (ER), medical and surgical wards (W), and intensive care units (ICU). Antimicrobial susceptibility testing was performed using CLSI broth microdilution methods. Results: A total of 2,963 isolates were collected: 40.1%, 39.8%, 10.1%, and 10.0% from blood, respiratory, urine, and wound/IV site specimens, respectively. Patient demographics were as follows: patient gender, 54.1% male and 45.9% female; and patient age, 6.6% ≤17 years, 44.7% 18-64 years, and 48.7% ≥65 years. Isolates were from patients on W 39.3%, ER 24.4%, ICU 19.6%, and C 16.7%. The most common pathogens were S. aureus 21.1% (16.5% MSSA / 4.6% MRSA), E. coli 18.7%, P. aeruginosa 9.7%, K. pneumoniae 6.5%, and S. pneumoniae 4.2%. Resistance rates for E. coli were: 0% for meropenem and tigecycline, 0.5% ertapenem, 3.7% piperacillin/tazobactam, 8.3% gentamicin, 10.2% ceftriaxone, 20.4% ciprofloxacin, and 23.6% trimethoprim/sulfamethoxazole (SXT). For P. aeruginosa, resistance rates were 2.7% colistin, 3.4% ceftolozane/tazobactam, 12.9% gentamicin, 13.1% ciprofloxacin, and 17.0% piperacillin/tazobactam and meropenem. Resistance rates for MRSA were: 0% vancomycin, ceftobiprole, daptomycin, linezolid, and SXT, 7.1% tigecycline, 35.7% clindamycin, 64.3% ciprofloxacin, and 73.8% clarithromycin. Overall, the prevalence of MRSA, vancomycin-resistant enterococci (VRE), and extended-spectrum beta-lactamase (ESBL)-producing E. coli was 21.6%, 13.0%, and 11.3%, respectively. Conclusions: In Canada, resistance rates for E. coli remain lowest for meropenem, tigecycline, ertapenem and piperacillin-tazobactam, while for P. aeruginosa, rates are lowest with colistin, ceftolozane/tazobactam, and gentamicin. No resistance was observed in MRSA with vancomycin, ceftobiprole, daptomycin, linezolid, or SXT.
Evaluation of Solana HSV 1+2/VZV Assay Compared to Viral Culture and Commercial PCR Assay for Cutaneous or Mucocutaneous Specimens

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Background. Herpes simplex virus 1 (HSV-1), HSV-2 and Varicella-Zoster virus (VZV) are responsible for a variety of human diseases, of which cutaneous and mucocutaneous infections are the most common. Differentiation between these viruses based on clinical presentation lacks both sensitivity and specificity. Culturing viruses is a lengthy, insensitive and time-consuming process. This study compares the viral culture and a commercial PCR assay to the Solana HSV 1+2/VZV assay for detection of HSV-1, HSV-2 and VZV in cutaneous or mucocutaneous specimens. Methods. From June to October 2018, 302 cutaneous or mucocutaneous specimens for which HSV-1, HSV-2 or VZV viral culture or PCR detection have been requested were randomly selected and kept at -80°C. The Solana HSV 1+2/VZV assay was performed according to the manufacturer’s instructions. Discrepancies between the results of the culture and the Solana assay were resolved with a commercial PCR assay (RealStar alpha Herpesvirus PCR Kit). Results. Compared to culture (n=247), the Solana assay had a sensitivity of 100% (123/123). The Solana assay detected 27 false negative specimens using culture (4 HSV-1, 11 HSV-2 and 12 VZV) that were confirmed positive by the arbiter PCR assay, conferring a specificity of 100%. Compared to the commercial PCR assay (n=55), the Solana assay had a sensitivity of 93.8% (30/32) and a specificity of 100% (23/23). Conclusions. The Solana HSV 1+2/VZV assay was more sensitive than the viral culture for the detection of HSV-1, HSV-2 and VZV in cutaneous or mucocutaneous specimens. It also performed comparably to a commercial PCR assay. This molecular assay is Health Canada approved for the simultaneous detection of HSV-1, HSV-2 and VZV in the same tube. The Solana assay could be completed in 60 minutes for up to 12 specimens, with approximately 1 minute hands-on time per specimen.
**Bordetella pertussis** Molecular Validation / Verification Using AmpliVue and the BDMax with Open System Reagents to Allow for Timely and Cost-effective Testing for Both Routine and Outbreak Demands.

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**Objective:** In early 2017, a Pertussis outbreak of 50 cases led to a 20-fold increase in testing requests from a baseline of 5 tests a month. Case tracking was hampered by offsite testing delay made worse by poor weather conditions. Our objective was to develop a rapid cost-effective process for both outbreak and routine testing. **Methods:** The Health Canada Approved AmpliVue (Quidel) using Helicase Dependent Amplification in a hand-held cartridge was subjected to an expanded validation of 100 tests (24 from the manufacturer, 15 from a proficiency panel, 46 from a provincial laboratory using a mock universal transport media (UTM), and 15 locally acquired random samples). At the same time, the BDMax (Becton Dickinson) with BioGx reagents on a multiplex PCR platform was verified against a panel of 287 samples (The AmpliVue expanded panel and an additional 182 local samples and 5 additional provincial lab samples. The national microbiology laboratory assisted with discordant results. **Results:** Both platforms were easy to use. The AmpliVue assay had 100% sensitivity, 92% specificity for *B. pertussis* only. The BDMax test demonstrated 100% sensitivity, 100% specificity for *B. pertussis*. *B. parapertussis* showed a sensitivity of 71%, specificity of 100%. Sensitivity and specificity of *B. holmesii* was 100%. There was a 9.0% unresolved rate for *B. pertussis* on the BD Max, which may be due to DNA degradation and sample dilution during the mock UTM preparation. Routine testing turnaround time improved from 5.3 days to 1.5 days after implementation (January to March 2016 vs. 2018). **Conclusions:** Both platforms performed well and are highly complementary by allowing rapid turnaround time, decreased wastage, and confirmatory PCR molecular testing with multiplexing and surge capacity. A *Bordetella spp.* proficiency panel should be provided to Canadian laboratories on a more frequent basis to enhance quality assurance of various testing methods.
Validation and implementation of Colorex™ (CHROMagar™) Strep A agar on WASP™/WASPLab™ for screening for Streptococcus pyogenes using the ESwab™

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Objective: Streptococcus pyogenes (Group A) causes “Strep throat”. The objective of this study was to validate the use of WASP™/ WASPLab™ to seed and analyze Colorex™ Strep A agar (CHROMagar™) to screen for Streptococcus pyogenes in throat specimens. Methods: In this study 159 clinical throat specimens were collected with ESwab™ kits and processed on a WASP™ using Colorex™ Strep A (CHROMagar™) agar plates and incubated in the WASPLab™ for 20 hours in CO2 at which point imaging analysis was performed. Vitek MS (Maldi-ToF) and PathoDx were performed on target and non-target colour colonies isolated. Results were compared to the same samples set up on Blood agar incubated at 35 degrees C anaerobically for 20 hours. The samples had all been tested for S. pyogenes by LAMP PCR. Results: Of the 159 clinical specimens, 120 were positive for S. pyogenes Group A by LAMP PCR. Of those 120 specimens, 116 grew on Colorex™ Strep A agar and 109 showed beta haemolysis on blood agar. 56 target positive colonies were tested with Vitek MS (Maldi-ToF) and all 56 identifies as S. pyogenes. The other 60 target positive colonies were tested with PathoDx using A and C. All 60 tested A positive C negative. White colonies identifies as other Streptococcus species. Colorex™ Strep A agar (CHROMagar™) showed a sensitivity of 96.7% (95%CI 0.92-0.99) and a specificity of 100% (95%CI 0.95-1) as compared to LAMP PCR. Conclusions: Results showed Colorex™ Strep A (CHROMagar™) had a significantly greater sensitivity than Blood agar in isolating S. pyogenes from throat specimens. The use of the WASP for set up provides efficient and consistent processing and WASPLab™imaging allows for high resolution digital imaging analysis. Several images appeared negative until zooming into the image showed few target positive colonies.
Validation of the Seegene RV15 multiplex PCR for the detection of influenza A subtypes and influenza B lineages during national influenza surveillance in hospitalized adults

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Objective(s): The Serious Outcomes Surveillance Network of the Canadian Immunization Research Network (CIRN SOS) has been performing active influenza surveillance since 2009 (ClinicalTrials.gov identifier: NCT01517191). Influenza A and B viruses are identified and characterized using real-time RT-PCR, and on a subset of patients, multiplex testing was performed to identify other respiratory virus etiologies. Since both methods could identify influenza A and B, a direct comparison was performed. Methods: Validated real-time RT-PCRs from the World Health Organization (WHO) to identify influenza A and B viruses, characterize influenza A viruses into the H1N1 or H3N2 subtypes, and to describe influenza B viruses belonging to the Yamagata or Victoria lineages. In a subset of patients, the Seeplex RV15 One-Step ACE Detection assay (RV15) kit was also used for detection of other respiratory viruses. Results: In total, 1111 nasopharyngeal swabs were tested by RV15 and real-time RT-PCRs for influenza A and B identification and characterization. For influenza A, RV15 showed 98.0% sensitivity, 100% specificity, and 99.7% accuracy. Performance characteristics of RV15 were similar for Influenza A subtypes H1N1 and H3N2. For influenza B, RV15 had a 99.2% sensitivity, 100% specificity and 99.8% accuracy, with similar assay performance for both the Yamagata and Victoria lineages. Conclusions: Overall, detection of circulating subtypes of influenza A and lineages of influenza B by RV15 was similar to real-time RT-PCR. Multiplex testing with RV15 allows for a more comprehensive assessment of respiratory virus surveillance in hospitalized adults, without significantly compromising the reliability of influenza A or B virus detection.
Effect of temperature and storage time on the viability and molecular detection of bacterial and viral enteric pathogens stored in Copan FecalSwabs™

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Objective: Rapid molecular multiplex testing has revolutionized enteric diagnostics and timely treatment. Nonetheless, maintaining organism viability in the pre-analytic phase remains necessary for isolation, antimicrobial susceptibility testing and serological typing/identification. The new FecalSwab system (Copan Diagnostics, Brescia, Italy) is a convenient alternative to bulk stool for collecting, transporting, and processing specimens for the diagnosis of enteric pathogens. However, FecalSwab suitability for molecular platforms and maintaining bacterial viability at different temperatures has not been well evaluated. Therefore, we assessed the effect of temperature and time on the performance of the FecalSwab system for culture and molecular detection of enteric pathogens. Methods: A clinical stool specimen previously characterized as positive for one of the bacterial (Salmonella spp., Shigella spp., Yersinia enterocolitica, Campylobacter coli/jejuni and Shiga toxin-producing E. coli) and viral (norovirus, rotavirus, and adenovirus) targets was swabbed according to manufacturer guidelines, and stored at 4⁰C, 22⁰C, or 37⁰C for up to 7 days. Conditions were performed in triplicates for each pathogen. Samples of the FecalSwab transport medium were collected at baseline, 24h, 48h, and 7 days following storage to determine colony counts and assessed for molecular diagnostic suitability with a lab developed multiplex enteric assay run on the BD Max system (BD Diagnostics, Baltimore, MD). Results: Following 7 days of storage at the specified temperatures, each bacterial isolate was recovered from the FecalSwab with the exception of Campylobacter spp. which rapidly lost viability. Evaluation of the FecalSwab system to support molecular diagnostics revealed that the target microorganisms could be detected without a significant loss in sensitivity (≤3.2 cycle threshold) from baseline at all time points. Conclusion: Copan FecalSwab is a suitable device to collect and store stool specimens for molecular diagnostics using the BD Max system, as well as for culturing the majority of the tested bacterial enteric pathogens.
Limit of detection of the cobas® Influenza A/B & RSV compared to a laboratory-developed real-time PCR based on the CDC influenza A/B protocol

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Background: Rapid molecular assays for influenza A/B detection are increasingly being adopted in healthcare facilities. We investigated the limit of detection for the cobas® Influenza A/B&RSV (Roche Molecular Diagnostics) assay using the Liat® system in comparison to our laboratory-developed real-time PCR (LDT). Methods: A comparison of the Liat® to the LDT was performed utilizing two previously positive nasopharyngeal samples (influenza A-H1N1 and influenza B) and purified influenza A/PR/8/34(H1N1) (Advanced Biotechnologies Inc). The patient samples were serially diluted either with blank universal transport media (UTM) or UTM from samples previously testing negative to the expected Ct (35, 38.3, 41.6), while the standard was diluted to 25copies/mL. For the LDT, samples were extracted on the MagNA Pure Compact, and amplified on the LightCycler® 480 Instrument II (Roche Molecular Diagnostics). Primer/probes were based on the CDC influenza A/B protocol. Results: For each dilution of patient sample in blank UTM or negative patient UTM, four replicates were tested (n=96). The LDT recovered all influenza A/B at Ct35 and 38.3, regardless of UTM (16/16 and 16/16 respectively). However, a discrepancy was identified on the Liat based on the diluent at Ct38.3: blank UTM (8/8) and negative patient UTM (3/8). Recovery at Ct41.6 was inconsistent for both methods: LDT blank UTM (3/8), LDT negative patient UTM (2/8), Liat blank UTM (1/8) and Liat negative patient UTM (0/8). Serial dilutions of the purified standard with blank UTM revealed identical results between the Liat® and LDT: 250copies/mL (5/5;5/5), 125copies/mL (4/5;5/5), 62.5copies/mL (6/6;6/6) and 25copies/mL (4/6;4/6). Conclusions: Laboratories validating rapid molecular PCR systems should carefully consider dilution media when assessing limit of detection. We identified a difference of approximately 1log in the detection of virus when directly comparing testing performed using blank UTM as diluent versus UTM from negative patient samples.
Utility of rapid influenza molecular testing in an outpatient hemodialysis unit: A prospective cohort study

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Objective: Early initiation of antiviral therapy for individuals with influenza infection is important for improving outcomes. Rapid molecular influenza assays may reduce diagnostic uncertainty and improve patient outcomes by providing faster results compared to traditional batched real-time PCR. The objective of this study is to determine the utility of implementing a rapid influenza PCR compared to the standard of care in a hemodialysis unit. Methods: From November 1, 2017 to March 31, 2018, we assigned samples collected from a single center, hemodialysis unit to be processed using a rapid influenza PCR (cobas® Influenza A/B & RSV assay) or the standard of care (in-house developed multiplex real-time PCR). Samples were assigned to the rapid PCR if the patient received dialysis treatment in the morning dialysis shift, while the remainder were processed as per standard of care. Study outcomes included the time to result of nasopharyngeal swab, prescription of influenza antiviral therapy, time to receiving prescription, and the need for emergency room visit or hospitalization within two weeks of presentation. Results: During the study period, 44 patients were assessed (14 with the rapid PCR and 30 with the standard of care assay). Rapid PCR significantly reduced time to result (2.3h vs 22.6h, p<0.0001). Individuals who were tested using the rapid PCR had a trend to shorter time to receiving antiviral prescriptions (0.7 days vs 2.1 days, p=0.11), and fewer emergency room visits (7.1% vs 30%, p=0.13) and hospitalizations (14.3% vs 30%, p=0.46) within 2 weeks of testing. Conclusions: Rapid influenza molecular testing in the hemodialysis unit was associated with a shorter time to a reportable result and may be associated with reduced time to prescription of antiviral therapy and fewer hospitalizations/emergency room visits. Further study with a larger cohort is needed to confirm these findings.
Comparison of Xpert Xpress Flu/RSV assay with an in-house RT PCR for the detection of Influenza A/ B and RSV.

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Background: The new Xpert Xpress Flu/RSV (Cepheid Inc.) assay is a rapid, on-demand real-time (RT) PCR assay that detects influenza A/B and respiratory syncytial virus (RSV) using a single-test cartridge system with minimal hand-on-time. We evaluated the performance of the Xpert Xpress Flu/RSV assay in comparison with our in-house influenza A/B and RSV RT PCR. Materials/methods: We selected a panel of convenience, archived nasopharyngeal (NP) swab specimens tested by in-house PCR. We included positive specimens for each target covering a range of PCR Ct values (17 – 35) and known negative specimens. All specimens were tested by the Xpert Flu assay and re-tested in parallel by our in-house RT PCR. For discordant samples BioFire FilmArray Respiratory Panel (FA RP) was the resolving test. Results: We included 89 NP specimens of which 69 were positive (23 Influenza A, 23 Influenza B, 23 RSV) and 20 were negative. For 88 of the 89 specimens a concordant result was obtained (98.8 % agreement). One discordant RSV result (in-house PCR positive [Ct=40]; Xpert Xpress Flu/RSV negative) was observed and was re-tested by the FA RP. The discordant result was resolved in favor of the Xpert assay. One previously negative specimen had a low positive influenza A result by both tests (Xpert assay [Ct=35], re-tested in-house PCR [Ct=36]) and was considered a concordant influenza A positive result. After resolution of one discordant result, the Xpert Flu assay correctly detected all 70 positive specimens and all 19 negative specimens for a positive percent agreement and negative percent agreement of 100 % for all three targets. The Xpert Xpress Flu/RSV assay was able to detected all of the 9 specimens with relatively high Ct values (Ct>32).

Conclusions: The Xpert Xpress Flu/RSV assay offers accurate, rapid, on-demand influenza A/B and RSV testing.
Validation of Roche e602 electrochemiluminescence immunoassay against the Siemens Centaur chemiluminescence immunoassay for syphilis screening

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Objective: To evaluate performance of the Roche Cobas e602 electrochemiluminescence immunoassay against a previously-validated Siemens ADVIA Centaur chemiluminescence immunoassay for syphilis screening. Methods: 98 frozen clinical isolates previously-characterized by the Siemens Centaur assay (with a range of positive, negative, and equivocal values) were tested on the Roche Cobas system (resulting in positive or negative values). Precision and interference studies were also performed. Results: Discrepant results were found in 17 of 98 samples (17.3%), 14 of which (82.4%) tested as equivocal by the Siemens assay but non-reactive by the Roche assay. Using additional testing information (repeat EIA and Treponema pallidum particle agglutination assay (TPPA), a provincial test interpretation algorithm, and expert opinion), 15 of 17 discrepant results were further classified as positive or negative. 2 results were excluded from analysis, one due to a lack of confirmatory testing and another because the patient was recently treated for syphilis. All samples that tested as equivocal by the Siemens assay but non-reactive by the Roche assay were classified as negative. The Roche assay was accurate for 94 of 96 results (97.9%). Within-run, between-run and near-cut-off precision testing was satisfactory and there was no evidence of interference with elevated bilirubin, hemoglobin or lipid levels. Conclusions: The Roche Cobas e602 CLIA assay showed good performance as a syphilis screening test when compared to the Siemens Centaur assay. Limitations of this study include comparison to an existing test method and algorithm rather than the gold standard for all samples tested.
Laboratory evaluation of the performance of the Zeus PEPC10/VlsE ELISA to detect antibodies to members of the European genospecies of *Borrelia burgdorferi sensu lato*

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**Objective:** Lyme disease (LD) is the most prevalent tick-borne infection in parts of Europe and Asia and at least five genospecies within the *Borrelia burgdorferi sensu lato* complex can cause disease in people. A number of laboratories in Canada are now using the Zeus pepC10/VlsE IgG/IgM ELISA (pepC10) as a screening assay for LD serology. To-date, there has not been a comprehensive evaluation of this kit’s ability to detect antibodies to the European genospecies of *B. burgdorferi* nor are these performance characteristics available through the manufacturer. Therefore, we evaluated the performance characteristics of pepC10 as a screening test for European LD.

**Method:** A total of 262 diagnostic samples (LD suspect patients with travel to Europe/Asia) and 64 European external proficiency (EP) samples were tested by Immunetics C6 IgG/IgM (C6) and pepC10 ELISAs. Diagnostic (n=75) or EP (n=36) samples that were equivocal or positive by either ELISA were subsequently tested by EUROIMMUN Anti-Borrelia EUROLENE (*B. afzelii*) IgG and EUROIMUN *B. garinii* IgG Western blot assays. The blot results were considered as the gold standard.

**Results:** The analytical sensitivity of the pepC10 was much higher than that of the C6 on diagnostic samples (93.1% vs 65.5%), while the analytical specificity of both kits was quite poor at around 50%. In contrast, both assays performed extremely well on the external proficiency samples of European origin with 100% sensitivity to pepC10 vs 97.1% for C6. The specificity was 100% and 96.6% for pepC10 and C6, respectively.

**Conclusion:** Based on this evaluation, pepC10 ELISA assay is able to detect antibodies to European genospecies within the *B. burgdorferi* complex. It is comparable, if not superior, in sensitivity and specificity relative to the C6 ELISA. Laboratories in Canada can use this assay for screening patients suspected of LD acquired outside of North America.
Clinical Validation of a Next Generation Sequencing (NGS) – Based Approach for the Diagnosis of Central Nervous System Infections

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Objective(s): Central nervous system (CNS) infections such as meningitis and encephalitis cause significant morbidity and mortality worldwide, but their etiology remains unknown in a large proportion (15-70%) of cases. The diagnosis of CNS infections is challenging because the diversity and number of pathogens that may cause CNS infections greatly outnumber available test methods. In this study, we aimed to develop and validate a metagenomic NGS (mNGS) approach for broad-range detection of pathogens associated with CNS infections. Methods: Cerebrospinal fluid (CSF) specimens (n=3) spiked with control bacterial and viral pathogens at varying concentrations were simultaneously assessed by qPCR and mNGS on an Illumina MiSeq platform to determine the analytical sensitivity of mNGS for pathogen detection. For clinical validation, residual CSF specimens (n=36) from patients with suspected CNS infections previously tested by culture and PCR, were retrospectively analyzed by mNGS. Data were analyzed by using MetaPhlAn2 followed by alignment with the viral genome database using Bowtie2. Results: In simulated specimens, mNGS assay detected all spiked pathogens that were detectable by PCR. In clinical specimens, the observed agreement with conventional methods was 92% (Kappa = 0.816; 95% CI = 0.618-1). Confirmatory PCR results on 3 specimens that gave discrepant results were in favor of mNGS assay. MetaPhlAn2 results were more specific than those obtained by other available bioinformatics tools but MetaPhlAn2 was less sensitive for viral detection compared to other tools. Expert assessment of mNGS results is important to exclude potential contaminants and background noise. Analysis of additional CSF samples is currently underway for further validation of the mNGS approach. Conclusion(s): Application of mNGS may detect pathogens that cannot be identified by the existing methods. However, careful interpretation of mNGS results is necessary to prevent reporting of false positive results.
A comparison of the Quidel Solana HSV 1+2/VZV Assay, the Focus Diagnostics Simplexa HSV 1 & 2 Direct Assay and the Luminex Aries HSV 1&2 Assay for detection of herpes simplex virus 1 and 2 from swab specimens

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Objective: Molecular methods enable more rapid and sensitive detection of herpes simplex virus (HSV) than viral culture. Three commercial molecular methods, all of which detect both HSV-1 and HSV-2, were compared to viral culture for the detection of HSV from swab specimens. Methods: Pediatric and adult patient viral swab specimens were cultured for HSV. Residual swab fluid was frozen at −80°C until tested with the 3 molecular methods: the Quidel Solana HSV 1+2/VZV Assay, the Focus Diagnostics Simplexa HSV 1 & 2 Direct Assay and the Luminex Aries HSV 1&2 Assay. A true positive was defined as positive by culture or positive by ≥ 2/3 molecular methods. Results: 177 specimens were studied. The sensitivity of culture was 81.3% (61/75, 95% CI 70.7-89.4%) and specificity was 100% (102/102, 95% CI 96.4-100%). The sensitivities of both the Solana and Simplexa were 100% (75/75, 95% CI 95.2-100%) and specificities were also both 100% (102/102, 95% CI 96.4-100%). The Aries had a sensitivity of 98.7% (74/75, 95% CI 92.8-99.97%) and specificity 99.0% (101/102, 95% CI 94.7-99.98%). All three molecular methods were significantly more sensitive than culture (p ≤ 0.0005 for Solana and Simplexa and p ≤ 0.0012 for Aries). Conclusion: All the molecular methods studied provided a significantly higher sensitivity than culture. In addition, the molecular methods took 1-2 hours to perform compared to a mean of 2 days for culture results. Use of any of the three molecular methods could lead to improved patient care.
How Modern is your Microbiology Laboratory? – Results of the 2017 Institute of Quality Management in Healthcare Patterns of Practice Survey

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Background: New technologies in the microbiology laboratory have the potential to reduce turn-around-time and improve accuracy, antimicrobial stewardship and patient outcomes. However, there is a paucity of data on their adoption by Canadian laboratories. The objective of our study was to investigate the patterns of practice of adopting new technologies amongst the Institute for Quality Management in Healthcare (IQMH) participant laboratories and summarize post-implementation quality indicators. Methods: In June 2017, a web-based patterns of practice qualitative survey on the adoption of novel technologies was conducted by the IQMH across all 73 microbiology laboratories that participate in the IQMH bacteriology proficiency testing program. Results: 69 of the 73 (94.5%) laboratories responded [8 university hospital (univ-hosp), 50 community hospital (comm-hosp) and 11 non-hospital (non-hosp)]. Only 50% of univ-hosp and 8% of comm-hosp reported having dedicated personnel for methods evaluation compared to 82% of non-hosp. Of all laboratories, 30% reported implementing MALDI-TOF (100% univ-hosp, 18% com-hosp, 36% non-hosp) with improved turn-around-time, time to appropriate treatment, and costs reported as benefits. Automated specimen processors were implemented by 14% (62.5% univ-hosp, 10% comm-hosp, 27% non-hosp), while only 4% had implemented total laboratory automation (12.5% univ-hosp, 2% comm-hosp, 9% non-hosp) with post-implementation reduction in turn-around-time, error rate, and costs cited. Syndromic (either respiratory, gastrointestinal, or meningoencephalitis) multiplex testing had been implemented by 7% (25% univ-hosp, 6% comm-hosp, 0% non-hosp) with improved turn-around-time and diagnostic yield reported post-implementation. Conclusions: There is a wide range of adoption of new technologies among the different laboratory categories. Post-implementation quality indicator data provided may be useful for peer laboratory business case development. The lack of dedicated methods evaluation personnel in comm-hosp and less so in univ-hosp compared to non-hosp laboratories is striking and may be partly responsible for the varying degree of uptake of novel technologies.
Evaluation of NG-Test CARBA 5 in a Low CPO Prevalence Patient Population

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Objectives: Local confirmatory testing for carbapenemase producing organisms (CPO) is optimal when isolated from a patient population where such organisms are infrequently isolated. Presumptive reports of CPO place additional strain on health care facilities operating in overcapacity bed situations and create additional stress for Infection Control and Prevention programs and care providers. Methods: Twenty previously characterised isolates including Enterobacter cloacae (7), Escherichia coli (5), Klebsiella pneumoniae (4), Klebsiella oxytoca (1), Klebsiella variicola (1), Enterobacter(Klebsiella) aerogenes (1), and Citrobacter freundii (1) were included. All isolates were previously molecularly confirmed by BCCDC for carbapenemases. To be eligible, each organism had to be resistant to at least 2 carbapenems by two methods (BD Phoenix and etest). All isolates were also tested using NG-Test CARBA 5. (NGBiotech, France). This kit confirms the presence of K-KPC, O-OXA48, V-VIM, I-IMP, N-NDM using a monoclonal based lateral flow assay in 15 minutes.

Results: Eighteen isolates correlated directly with the PCR result from BCCDC – eight positive for NDM, one positive for KPC, and nine that were negative for all carbapenemases. Regarding the two discrepant results, the Citrobacter freundii isolate tested weak positive for NDM by the NG-Test CARBA 5, but the result from BCCDC was negative. One strain of Enterobacter cloacae was difficult to emulsify and did not flood the column rendering the test invalid. Conclusions: Our health authority has a robust admission CPO screening program. Screening or clinical isolates that initially test as presumptive CPO trigger patient isolation and contact screening. It is desirable to perform confirmatory testing promptly to focus infection prevention efforts appropriately. NG-Test CARBA demonstrated excellent sensitivity and specificity for the confirmation of 5 carbapenemase enzymes in organisms testing resistant to carbapenems.
Geo-temporal Epidemiology of Extended-spectrum Beta-lactamase (ESBL)-producing ST131 *Escherichia coli* isolated from Bloodstream Infections in the Toronto Region

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**Objectives:** ESBL-producing *Enterobacteriaceae* are an increasing threat. We have described the rise in ESBL-producing *E. coli* in the Toronto region. Herein, we describe the associated multi-locus sequence types (MLST) and geo-temporal epidemiology using whole genomic sequencing (WGS) of bloodstream ESBL-producing *E. coli*. **Methods:** All adult inpatients from four tertiary-care hospitals in Toronto with bloodstream ESBL-producing *E. coli* from 2006 through 2012 were included (n=174). Corresponding isolates, one/patient/year, were recovered from -80°C and genomic DNA was extracted using DNeasy Blood and Tissue Kit (Qiagen). WGS was completed on the NextSeq500 with 2x150 base paired-end reads using the Nextera XT DNA Library Prep Kit (Illumina). Genomes were de novo assembled with SPAdes. MLST were determined using the Bacterial Analysis Pipeline with MLST 2.0.1 (Center for Genetic Epidemiology). Linear trend analysis and geo-temporal mapping using the patient’s residential postal code was completed using Tableau. **Results:** There was a significant rise in the total number of bloodstream ESBL-producing *E. coli* between 2006 and 2012 (P=0.0005) with a corresponding rise in the proportion of ESBL-producing *E. coli* from 6.4% to 12.7%. This rise was driven by a significant rise in ST131 (P=0.0002) (Figure), with significant rises noted in three hospitals (P=0.004, 0.02, 0.01) and a non-significant trend in the fourth (P=0.08). The change in non-ST131 *E. coli* was not significant (P=0.09) (Figure). ST131 *E. coli* was first noted in patients residing in Brampton, a city in which 30.6% identify as having East Indian ethnicity (Figure), notable as the proportion of ESBL-producing *E. coli* has been reported as high as 70% in South East Asia. **Conclusions:** There was a significant rise in bloodstream ESBL-producing *E. coli* in the Toronto region between 2006 and 2012 led by the introduction and increase in ST131 *E. coli*. Further characterization of the factors associated with the endemicity of ST131 is ongoing.
Detection of Varicella-Zoster Virus in Clinical Specimens by Real-Time PCR: Comparison of Manual Lab-Developed Assay With a Novel Automated Assay

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Objective: Varicella-zoster virus (VZV) is the cause of chicken pox and shingles. Molecular detection is the diagnostic standard for detection of this important pathogen. Many laboratory-developed tests involve significant manual processing steps. For high volume testing laboratories, introduction of automated, random-access testing platforms offers potential time and cost savings. The purpose of this study was to compare an automated real-time PCR assay using analyte-specific reagents (ASR) for detection of VZV in swabs from lesions with clinical performance of a previously-validated lab-developed test (LDT) routinely used in the laboratory. Methods: Swabs collected in virus transport medium were tested using a PCR LDT and a novel PCR utilizing ASRs for VZV. ASR VZV primer probe recon solution (primers: 0.75 μM, probes: 0.5 μM, potassium chloride: 81.25 mM, magnesium chloride: 5 mM, Tris: 10 mM, water, topped with oil layer), enzyme cartridges (lyophilized enzymes, nucleotides, buffer), and extraction reagent packs were loaded onto a Panther Fusion instrument and amplified using the following thermal cycling conditions: 2 minutes at 95°C; 45 cycles of denaturation at 95°C for 8 seconds, and annealing/extension at 60°C for 25 seconds. MyAccess software was used for data analysis. Results: A novel VZV assay was successfully developed using ASR reagents, with full automation of extraction, amplification, and detection. Of 89 samples tested with both assays, 23 (25%) were positive for VZV by both methods. The overall agreement between the methods was 100%. Conclusions: Based upon preliminary results, the VZV PCR assay on the Panther Fusion instrument has similar performance characteristics to the LDT assay currently in use. An automated instrument with continuous random access offers potential for significant reductions in hands on- and turnaround times. However, further study will be required to confirm these findings and to evaluate potential workflow benefits.
Assessment of the Aptima herpes simplex virus 1 & 2 assay on the Panther system

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Objective(s): The Aptima Herpes Simplex Virus (HSV) 1&2 Assay recently received Health Canada approved for detection and differentiation of HSV-1 and HSV-2 from anogenital sites. This assay uses target capture, transcription mediated amplification (TMA), and real-time detection of messenger RNA (mRNA) produced in host cells during HSV infection. To evaluate its performance, the Aptima assay was compared to another Health Canada approved assay, the BD ProbeTec HSV 1&2 Qx Amplified DNA Assay which used strand displacement amplification (SDA) technology. Methods: As recommended by the manufacturers, the Aptima assay was performed on a Panther system, and the BD Probetec assay was performed on a Viper instrument. Analytical sensitivity and specificity were assessed using 10-fold serial dilution of viruses in viral transport media (VTM), and nucleic acids extracted concentrated from other viruses including all members of the Herpesviridae family. The clinical sensitivity and specificity were assessed prospectively using 158 swabs from oral and anogenital sites collected in VTM. Discrepant results were resolved with real-time PCR using the RealStar HSV 1-2 assay (Altona Diagnostics). Results: Both the Aptima and Viper assays showed excellent clinical and analytical specificity, without any false positive reactions. However, the Aptima HSV assay failed to detect HSV in specimens with low viral loads, resulting in reduced sensitivity for HSV-1 of 85.0% (34/40) and 95.8% (23/24) for HSV-2. The analytical analyses coincided with reduced sensitivity of approximately 10-fold for both HSV-1 and HSV-2 for Aptima compared to the Viper Probetec assay. Conclusions: This study demonstrated that detection of HSV mRNA using the Aptima HSV assay was less sensitive than HSV DNA detection through SDA technology on the Viper system. It is unclear whether this difference is attributed to the methodology itself, or limitations of mRNA-based detection for the diagnosis of infection with DNA viruses like HSV.
**HPV Testing for Triaging Women with Low Grade Squamous Intraepithelial Lesion (LSIL) Cytology in Cervical Cancer Screening: Preliminary Findings from a Canadian Study**

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**Background:** Cervical cancer screening relies on Pap cytology to detect precancerous lesions. A majority of women with abnormal cytology have either atypical squamous cells of undetermined significance (ASCUS) or low-grade squamous intraepithelial lesion (LSIL), and in most, these are not predictive of cancer risk. However, all such cases are followed with repeat cytology or colposcopy because some may have an underlying high-grade disease. ASCUS-HPV triage is recommended to better identify those at increased risk. In this regard, LSIL-HPV triage may also be helpful. We assessed the usefulness of LSIL-HPV triage as part of an ongoing study investigating the application of CINtec PLUS (Roche), a dual-stain biomarker test, in LSIL triage. **Methods:** LSIL cases seen at the colposcopy clinic, Juravinski Hospital, Hamilton were prospectively enrolled with informed consent. Cervical specimens were collected at enrolment in ThinPrep for routine Pap. The remnant from the ThinPrep vials was used for HPV testing utilizing cobas 4800 assay (Roche). Biopsy confirmed cervical intraepithelial neoplasia grade 2 or worse (≥CIN2) served as the clinical endpoint. **Results:** Preliminary analysis was based on 347 patients (target, n=600). Ages ranged from 19-76 (median 33), with 204 (58.8%) >30 years of age. Of the 347, 188 (54.2%) tested HPV+, and 159 (45.8%) HPV-. There were 34 cases of ≥CIN2, and 33 had tested HPV+ (sensitivity, 97.1%). Of 313 without ≥CIN2, 158 tested HPV- (specificity, 50.5%; negative predictive value, 158/159 = 99.4%). Among the 188 testing HPV+, most were positive for high-risk oncopgenic types other than 16 and 18 regardless of biopsy result. **Conclusions:** LSIL-HPV triage may have the potential to safely relegate half of women to routine screening with a very high negative predictive value, while maintaining superb sensitivity to detect ≥CIN2. Longitudinal studies could provide additional clinical data to assess the long term negative predictive value of LSIL-HPV triage.
Received as ‘Unidentifiable’? Beware of Small Gram Negative Coccobacilli!!

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**Background:** A Gram-negative coccobacillus (GNCB) unidentifiable by the sender using by MALDI-TOF/other methods was received at the Special Bacteriology Unit (SBU) on a Thursday in September 2018 for ‘urgent testing’. The isolate had been recovered from pleural fluid of a 62y male residing in eastern Canada and hospitalized with empyema. We describe here significant biosafety issues which arose as a result of this case. **Methods:** SBU’s ‘urgent testing’ protocol dictated that the sender be immediately contacted for additional information. 16S rRNA gene sequencing was initiated directly from growth provided by the sender. Coincidently, subculturing of the sample in the BSC was observed by two new students. Assembly / BLASTing was done by usual NML methods. **Results:** The referring lab had been asked if the patient possibly had tularensis or brucella, based on their description of “tiny” GNCB. These were thought to be highly unlikely due to zero prevalence provincially. On Friday pm, the bacterium was identified as *Francisella tularensis* by 16S sequencing. Materials were sealed and either autoclaved or turned over to the BADD unit for further analysis in CL3, which rapidly identified it as the RL3 agent, *F. tularensis subsp tularensis*. The sender was contacted with results. SBU staff were interviewed by biosafety officers regarding handling practices (for a RL3 agent in a CL2). It was ultimately deemed that the isolate had been processed with minimal hazard to staff. **Conclusions.** Negligible prevalence of tularensis in that province and empyema / pleural fluid as source, contributed to having a minimal suspicion for a RL3 agent. This referral created potential occupational hazardous incidents for staff at the NML and sender sites. *F. tularensis* must be characterized using advanced methods within a CL3 by staff with expertise. Labs must also be aware that ‘standard’ MALDI-TOF libraries cannot ID these taxa.
Candida auris Cases in Canada, 2012 - 2018

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Objective: Candida auris is an emerging yeast that is associated with high rates of antifungal resistance and healthcare-associated outbreaks that can be difficult to control. Our objective was to carry out genomic characterization of all known C. auris cases in Canada to monitor the emergence of this species. Methods: Sixteen isolates of C. auris identified from 2012 - 2018 were submitted to the Canadian Mycology Reference Centre which was established this year by the National Microbiology Laboratory (NML). Isolates from all 16 cases were subjected to whole genome sequencing (WGS) on the Illumina Nextseq platform. Phylogenetic analysis based on single nucleotide variations (SNV) was carried out with the SNVPhyl v1.1 pipeline and assemblies were performed with SPAdes v1.6. Results: The isolates were obtained from axilla/groin (n=5), blood (n=4), ear (n=3), and other sites (n=4). All isolates of C. auris fell within the four known genomic lineages (clades) named after their apparent geographical origin. Isolates from the South Asian clade were identified in British Columbia (n=9) and Manitoba (n=1). C. auris was also identified in Ontario (South American clade; n=4), Quebec (South African clade; n=1), and Alberta (East Asian clade; n=1). The four geographical clades were highly divergent (average 16,000 - 65,000 SNV differences between clades) but Canadian isolates within each clade appeared clonal. Canadian isolates from the South American clade differed by 14-26 SNVs while those from the South Asian clade differed by 1 - 128 SNVs. We identified mutations associated with fluconazole resistance (ERG11 Y143R) and voriconazole resistance (ERG11 Y132F) but not echinocandin resistance (FKS1 hotspot mutations). Conclusions: The 16 cases of C. auris in Canada represent all four known genomic lineages. Isolates tended to be clonal within each clade but high resolution WGS may be helpful in discriminating between patient transmission and separate introductions into a healthcare facility.
Verification of the NG-Test CARBA 5 Immunochromatographic Assay to Simultaneously Detect KPC, NDM, OXA48-like, VIM and IMP Enzymes in Species-Diverse Carbapenem-resistant Gram-Negative Bacilli

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Objectives: Rapid detection of carbapenemase-producing organism (CPO) is essential for containment and patient management. We evaluated the ability of the NG-Test CARBA 5 immunochromatographic assay (NG Biotech, France) to detect five common carbapenemases using well-characterized (phenotypic and PCR/sequencing) Gram-negative bacilli (GNB).

Methods: 297 GNB including 257 CPO (250 targeted-CPO: 127 KPC, 69 NDM, 32 OXA, 11 NDM+OXA, 8 VIM, 3 IMP; 8 non-targeted CPO (3 GES, 3 SME, 1 NMC), and 40 non-CPO were tested comprising 289 Enterobacteriaceae (115 Klebsiella pneumoniae, 79 Escherichia coli, 51 Enterobacter cloacae, 44 other) and 8 non-Enterobacteriaceae GNB (2 Acinetobacter baumannii, 3 Pseudomonas species, 2 Aeromonas hydrophila, and 1 Shewanella putida). Isolates were recovered from -80°C under selective pressure (MacConkey with ertapenem disc) and plated to Oxoid MacConkey-cefodoxime/MacConkey-meropenem CPO screening bi-plates. As directed, a fresh 18hx37°C colony was collected with a loop and suspended in extraction buffer; 100µL was added to the sample well with results read at 15minx21°C. The reader was blinded and discrepancies were repeated. Results: Of 297 tests, results were easy to interpret and all but three (2 OXA, 1 mucoid KPC) were available with in 5 minutes. CARBA 5 initially identified 257/261 (98.5%; 96.0-99.5) targeted CPO-proteins [125/127 (98.4%; 94.1-99.9) KPC; 79/80 (98.7%; 92.6->99.9) KPC; 42/43 (97.7%; 86.8->99.9) OXA, 8/8 (100%; 62.8-100) VIM; 3/3 IMP (100%; 38.0-100%)]. Four (1.5%) targeted-CPO that were initially missed were positive on repeat testing suggesting too low an inoculum was possibly initially used; one had notable poor growth on initial testing. All 48 (100%; 91.1-100) non-targeted-CPO/non-CPO were negative. Final CPO-detection sensitivities/specificities were 100% for all targets; respective 95%CI were: KPC 96.5-100/96.6-100; NDM 94.5-100/97.5-100; OXA48-like 90.2-100/ 96.6-100; VIM 62.8-100/97.9-100; IMP 38.0-100/98.2-100. Conclusions: The NG-Test CARBA 5 was easy to use and provided highly-accurate (100% sensitive/specific) rapid detection for KPC, NDM, OXA48-like, VIM and IMP CPO.
Duration of colonization with Carbapenemase-producing *Enterobacteriaceae* (CPE): a population-based study

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**Objectives:** We aimed to determine the duration of CPE colonization to better inform providers, patients and infection control programs about prognosis.

**Methods:** Participants were recruited from population-based surveillance. Eligible persons were colonized/infected with CPE, had stable housing, and were expected to survive and reside in the area for ≥1 year. Participants were screened (groin & rectal swabs, and urine samples) at 1 and 3 months after identification, then quarterly until ≥3 negative sets of screening specimens were obtained. Specimens were incubated in BHI broth overnight then subjected to direct PCR to identify carbapenemase genes, with culture of PCR positive specimens. Decolonization was defined as occurring when 3 complete sets of swabs were PCR negative, and no later swabs were positive or clinical isolates identified. Time of decolonization was defined as date of first qualifying negative swabs. **Results:** 284 (76%) of 385 eligible persons participated: 87 completed follow-up, 113 are being followed, and 84 have incomplete data (30 died; 54 withdrew/were lost to follow-up). Median age is 70 years, 164 (58%) are male, 182 (64%) have at least one underlying comorbidity, and 99 (35%) initially had a clinical specimen (vs. screen only). Most common organisms were *E. coli* (152, 54%), *Klebsiella* spp. (92, 32%) and *Enterobacter* spp. (25, 9%); most common genes were *bla*~NDM~ (±OXA) (164, 58%), *bla*KPC (24, 8%), and *bla*OXA-48-like (82, 29%). The figure shows time to decolonization. Men (OR 0.53 95%CI 0.34, 0.81), persons colonized/infected with *Klebsiella* spp. versus other bacteria (OR 0.50, 95%CI 0.24, 1.02), those with clinical isolates (OR 0.49, 95%CI 0.29, 0.81), and those with more sites positive at enrolment (OR for 2v1 site 0.30, 95%CI 0.14, 0.67) were less likely to become decolonized. **Conclusions:** Most CPE colonized/infected persons appear to clear their organism over time, although about 1 in 5 remain colonized at 2 years. Individual characteristics significantly affect duration of colonization.
**Failure on Antibiotic Prophylaxis Increases Risk of Surgical Site infection after Cardiac Surgery**

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**Background:** Cardiac surgery is procedure on the valves or septum of heart. It does not include coronary artery bypass graft, surgery on vessels, heart transplantation, or pacemaker implantation. The objective of our study is to answer three questions: a) What is the risk of surgical site infection (SSI) after cardiac surgery? b) What are risk factors for SSI after cardiac surgery? c) What are the effects of antibiotic prophylaxis on SSI risk?

**Methods:** Surveillance data based on NHSN/CDC protocols were collected during five years (2013-2017), from 7 hospitals at Belo Horizonte, Brazil. Outcome: SSI and total length of hospital stay. 23 independent variables were analyzed by univariate and multivariated methods. **Results:** A sample of 3,827 patients submitted to cardiac surgery was analyzed: SSI risk = 2.6% (1.C.95%=2.1%;3.2%). Hospital length of stay in non-infected patients (days): mean=19, median=13, std.dev.=21. Hospital stay in infected patients: mean=32, median=25, std.dev.=36 (p<0.001). Main risk factors for SSI: less than five surgical healthcare professionals at surgery (SSI=3.3%, RR=1.7, p=0.008); preoperative hospital length of stay more than four days (SSI=3.9%, RR=1.8, p=0.003); failure on prophylactic antibiotics (SSI=7.7%, RR=3.5, p<0.001). Patients with preoperative hospital length of stay more than four days that did not receive prophylactic antibiotics have 13.7% SSI (RR=4.4, p<0.001). **Conclusion:** If the length of preoperative hospital stay is less than or equal to four days, the risk of surgical infection in cardiac surgery will be reduced approximately 50%, from 3.9% to 2.1%. To prevent infections is crucial to maintain the length of preoperative hospital stay as short as possible and, most important, do not failure on antibiotic prophylaxis.
Impact of Influenza Vaccination on Healthcare Utilization – A Systematic Review

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**Introduction:** Although a vaccine-preventable disease, influenza causes approximately 3 to 5 million cases of severe illness and about 290,000 to 650,000 deaths worldwide, which occur primarily among people 65 years and older. Nonetheless, prevention of influenza and its complications rely mainly on vaccination. **Objective:** We aimed to systematically evaluate influenza vaccine effectiveness at reducing healthcare utilization in the elderly, defined as the reduction of outpatient visits, ILI and influenza hospitalizations, utilization of antibiotics and cardiovascular events by vaccination status during the influenza season. **Methods:** We searched MEDLINE, EMBASE, CINAHL, Cochrane Library and considered any seasonal influenza vaccine, excluding the pandemic (2009-10 season) vaccine. Reviewers independently assessed data extraction and quality assessment. **Results:** Of the 8,308 citations retrieved, 22 studies were included in the systematic review. Overall, two studies (9%) were deemed at moderate risk of bias, thirteen (59%) at serious risk of bias and seven (32%) at critical risk of bias. For outpatient visits, we found modest evidence of protection by the influenza vaccine. For all-cause hospitalization outcomes, we found a wide range of results, mostly deemed at serious risk of bias. The included studies suggested that the vaccine may protect the elderly against influenza hospitalizations and cardiovascular events. No article meeting our inclusion criteria explored the use of antibiotics and ILI hospitalizations. **Conclusion:** The variability between studies prevented us from drawing a clear conclusion on the effectiveness of the influenza vaccine on healthcare utilization in the elderly. Overall, the data suggests that the vaccine may result in a reduction of healthcare utilization in the elderly population. Further studies of higher quality are necessary.
Whole Genome Sequencing and Penicillin Susceptibility Testing for *Corynebacterium diphtheriae*: Are the 2015 CLSI M-45 Breakpoints Relevant?

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**Background:** *Corynebacterium diphtheriae* can cause significant disease, including wound infections and bacteremia. In 2015, CLSI M-45 susceptibility breakpoints for *Corynebacterium* species and penicillin were lowered (≤1µg/mL to ≤0.12µg/mL). We reviewed the impact of updated breakpoints on *C. diphtheriae* susceptibility at our institution and investigated resistance mechanisms through whole-genome sequencing (WGS). **Methods:** A retrospective review was performed on *C. diphtheriae* clinical isolates recovered from March 2015 – June 2018. Susceptibility testing was conducted using Etest (bioMérieux, Marcy-l’Étoile, France) and interpreted using the CLSI M-45 2\(^{nd}\) (2010) and 3\(^{rd}\) (2015) editions. WGS was performed by next-generation sequencing (MiSeq, Illumina, San Diego, CA). MLST and antimicrobial resistance markers were analyzed from WGS utilizing 5 public databases (ARG-ANNOT, CARD, MEGARes, ResFinder and SRST2-ARG-ANNOT) using ARIBA. **Results:** 56 non-toxigenic *C. diphtheriae* isolates were identified: blood (1), throat (1), and wound (54). MICs were available for 39 patients, and 48 isolates were available for WGS. Using 2010 breakpoints, all isolates (39/39) were considered penicillin susceptible, but all were reported as non-susceptible (intermediate) using 2015 breakpoints. Distribution of penicillin MICs did not change over time. One isolate was resistant to erythromycin and clindamycin, with interpretations unchanged between 2010 and 2015. WGS identified a predominant strain: ST-76 (45/48). Other ST types included ST-05 (1/48), ST-32 (1/48) and 1 novel ST (most similar to ST-444/ST-442/ST-441). No mutations associated with beta-lactam resistance were identified for samples with sufficient sequencing depth (n=37). **Conclusions:** Application of 2015 CLSI interpretive criteria resulted in all *C. diphtheriae* isolates recovered at our institution to be classified as penicillin non-susceptible; conversely, 2010 CLSI criteria would have classified all isolates as penicillin susceptible. WGS did not reveal any molecular basis for penicillin non-susceptibility. Further investigation is required to understand the generalizability of these findings to other strains of *C. diphtheriae*, and more broadly, the potential clinical significance of penicillin susceptibility misclassification.
A Pilot Study of Accelerate Phenotest™ BC Kit Compared to Standard Microbiological Testing on Blood Cultures Positive for Gram-Negative Bacilli

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Objective: Calgary Laboratory Services (CLS) performs MALDI and VITEK directly from positive blood cultures for organism identification (ID) and antimicrobial susceptibility testing (AST). Our objective was to compare the performance of direct MALDI/VITEK to a commercial blood culture ID/AST platform, Accelerate PhenoTest™ BC Kits (AXDX), in the ID/AST of clinical blood cultures positive for Gram-negative bacilli (GNB) and in blood cultures inoculated with multi-drug resistant GNB (MDR GNB). Methods: Blood cultures positive for GNB were collected at CLS and tested using AXDX, direct MALDI/VITEK, and compared to conventional methods (plate incubation followed by MALDI and VITEK). A subset of sterile blood cultures were inoculated with MDR GNB. Discrepancies in very major errors (VME) and major errors (ME) were confirmed with microbroth dilution.

Results: Twenty-eight clinical samples and 30 inoculated samples were analyzed. In the clinical samples, direct MALDI had higher ID failures (31.0%) compared to AXDX (3.4%). Time to ID was 1.5 hours, 6.1 hours, and 22.2 hours for AXDX, direct MALDI and conventional methods, respectively (p<0.001). Time to AST was 6.6 hours, 16.8 hours, and 33.4 hours for AXDX, direct MALDI and conventional methods, respectively (p<0.001). In the clinical samples, AXDX had EA/CA >95%, 0 VME/ME, and 3.7% minE. Direct VITEK had EA/CA >99%, 0 VME/ME, and 0.65% minE. In the inoculated samples, AXDX had EA, CA, VME, ME and minE of 85.6%, 87.9%, 1.6%, 1.4%, and 10.4%, respectively. Direct VITEK had EA, CA, VME, ME and minE of 97.6%, 94.8%, 0.8%, 0%, and 4.6%, respectively.

Conclusions: Direct MALDI/VITEK and AXDX performed well on clinical samples but direct MALDI/VITEK outperformed AXDX when challenged with MDR GNB. AXDX had fewer ID failures and faster results, though its results were not based on real-world settings as was the direct MALDI/VITEK.
Bloodstream Infections in Persons Who Inject Drugs on Treatment for Infective Endocarditis

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Objective: Persons who inject drugs (PWID) being treated for infective endocarditis (IE) remain at risk of bloodstream infections (BSIs) due to ongoing intravenous drug use, often through central catheters inserted for prolonged antimicrobial treatment. We sought to characterize BSIs in this patient population and determine the clinical factors associated with their development.

Methods: We conducted a nested case-control study of episodes of definite IE based on the modified Duke criteria in PWID ≥18 years of age, admitted to tertiary care centres in London, Ontario from March 1 2007 to March 31 2018. We identified and characterized cases of new BSIs among this population, and compared them against episodes of IE without new BSIs. We also compared the incidence of inpatient versus outpatient BSIs. Results: There were 424 episodes of IE among PWID, and 81 (19.1%) were complicated by BSIs. There were 138 BSIs with 280 unique isolates, of which 156 (55.7%) were gram negative bacilli, 75 (26.8%) were fungi and 49 (17.5%) were gram positive cocci. The most common bacteria included ESKAPE organisms associated with nosocomial antibiotic resistance. Factors associated with BSIs included previous IE, right-sided IE, opiate and polysubstance use, ongoing inpatient drug abuse and peripherally inserted central catheter placement. BSIs were more commonly identified in PWID receiving inpatient treatment (9.60 BSIs per 1000 days of intravenous access, 95% CI 7.95–11.5) than outpatient treatment (5.23 BSIs per 1000 days of intravenous access, 95% CI 3.50–7.46). Conclusion: BSIs are a common complication in PWID being treated for IE with parenteral antimicrobials, and empiric therapy should cover resistant gram negative bacteria and fungi. Although detection bias could have decreased outpatient BSI rates, carefully selected PWID with IE may be safely treated with outpatient parenteral antimicrobial therapy, reducing the harms and costs of extended hospitalization.
A comparison of the Quidel Solana GAS assay, the Luminex Aries Group A Strep Assay and the Focus Diagnostics Simplexa Group A Strep Direct assay for detection of group A streptococcus in throat swab specimens

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Objectives: Detection of group A streptococcus (GAS) in pharyngeal swab specimens is important to help prevent acute rheumatic fever (ARF) as well as local suppurative complications. Molecular methods are becoming increasingly popular for GAS detection, as they are considerably faster than culture and have greater sensitivity than rapid antigen detection tests. We therefore compared three commercially available GAS nucleic acid amplification tests with bacterial culture. Methods: The three molecular methods assessed were the Quidel Solana GAS assay, the Luminex Aries Group A Strep assay and the Focus Diagnostics Simplexa Group A Strep Direct assay. We defined a true positive result as one positive by culture or positive by ≥ 2/3 molecular methods. Samples collected were set up for routine bacterial culture and the remainder of the swab fluid (BD E-swab) was frozen at −80°C until molecular testing was performed. Results: 286 throat swabs (206 children, 80 adults) were collected from patients with suspected pharyngitis. The sensitivity of culture was 84.8% (95% CI 77.7-90.3%) with a specificity of 100% (95% CI 97.5-100%). Culture was significantly less sensitive than the true positive definition based on the molecular assays (p = 0.0001). The sensitivity of the Solana assay was 94.2% (95% CI 88.9-97.5%) and the specificity was 98.7% (95% CI 95.2-99.8%). Simplexa assay sensitivity was 99.3% (95% CI 96.0-99.9%) and the specificity was 95.3% (95% CI 90.6-98.1%). For the Aries assay, the sensitivity was 96.4% (95% CI 91.8-98.8%) and the specificity was 98.0% (95% CI 94.2-99.6%). For a single specimen, the Solana assay took approximately 40 minutes to complete, the Simplexa approximately 1.25 hours, and the Aries approximately 2 hours. Conclusions: All three commercial methods were more sensitive and also much more rapid than culture for GAS detection from throat swabs.
Klebsiella oxytoca, a rare cause of antibiotic-associated hemorrhagic diarrhea: A Canadian case report

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Objectives: In the case of antibiotic-associated hemorrhagic diarrhea that is not accounted for by common enteric pathogens, Klebsiella oxytoca is often an overlooked cause. This is a Canadian case presentation of antibiotic-associated hemorrhagic diarrhea caused by K. oxytoca, with a review of the literature providing clearer indications for K. oxytoca testing.

Case presentation: A 57-year old woman was hospitalized for with new-onset bloody diarrhea (up to 25 episodes daily) and mild lower abdominal pain following a three-day course of amoxicillin for gingivitis. Previously, the patient had no significant past medical history and was taking no medications. Throughout admission, the patient was afebrile and her vitals were stable. Laboratory test results demonstrated mildly elevated leucocytes (12.0*10⁹/L) and her abdominal X-ray was negative for signs of thumb-printing or obstruction. The initial stool culture and C. difficile toxin assays were negative; however, repeat stool cultures for K. oxytoca were positive. The patient was treated with metronidazole and improved gradually. She was discharged after four days with follow-up colonoscopy.

Conclusions: Our case report describes a 57-year old woman with antibiotic-associated hemorrhagic diarrhea secondary to K. oxytoca infection. Though a rare cause of hemorrhagic diarrhea, K. oxytoca needs to be considered when traditional stool cultures and C. difficile toxin assays are negative, especially given a history of recent antibiotic use with amoxicillin or other penicillin derivatives.
Prevalence of antimicrobial resistant pathogens amongst blood culture isolates from canadian tertiary care centres canward 2007 2016

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Objectives: Bacteremia is associated with significant morbidity and mortality, particularly given increasing antimicrobial resistance. This Canadian ward surveillance study, CANWARD, assesses (1) the epidemiologic profile of blood culture pathogens and (2) their antimicrobial susceptibility profiles. Methods: Between 2007 and 2016, each participating Canadian tertiary care centre submitted 100 consecutive, clinically-significant isolates of aerobic and facultative bacteria from positive blood cultures. Susceptibility testing was performed by CLSI broth microdilution method. Results: 18686 blood isolates were submitted, of which 57.3% were from males. When categorized by location, 35.9% were from emergency rooms, 33.6% from medical units, 15.9% from intensive care units, 7.8% from surgical units and 6.8% from clinics. The most common pathogens were Escherichia coli (23.2%), Staphylococcus aureus (17.7%) [methylcillin-susceptible (MSSA), 13.9% and methicillin-resistant (MRSA), 3.8%], Klebsiella pneumoniae (7.4%), Streptococcus pneumoniae (4.8%), Enterococcus faecalis (4.2%), Pseudomonas aeruginosa (3.8%) and methicillin-resistant Staphylococcus aureus (MRSA) (3.8%). Of the 3297 S. aureus isolates, 21.3% were MRSA with 32.5% possessing community-acquired genotypes and 63.3% possessing healthcare-acquired genotypes. MRSA rates have decreased over 10 years (P<0.0001), while rates of vancomycin-resistant enterococci (VRE), extended-spectrum beta lactamase-producing (ESBL) E. coli and ESBL K. pneumoniae have increased (P<0.007, <0.0001 and <0.0001 respectively, Cochran-Armitage test for trend). The most active agents against MRSA were ceftobiprole (100% susceptible) linezolid (100%), vancomycin (99.6%) and daptomycin (99.7%). The most active agents against P. aeruginosa were ceftolozane-tazobactam (99.3%), tobramycin (96.6%) and colistin (94.3%). Piperacillin-tazobactam, meropenem and ciprofloxacin susceptibility rates to Pseudomonas aeruginosawere 90.0%, 84.7% and 84.8% respectively. Conclusions: E. coli, S. aureus and K. pneumoniae are consistently the top pathogens isolated from blood culture specimens. Rates of MRSA decreased from 2007 to 2016, while rates of ESBL E. coli and ESBLK. pneumoniae increased. Vancomycin, ceftobiprole, daptomycin and linezolid are the most active agents against Gram-positive cocci. Effective agents against Gram-negative bacilli varied depending on speciation, however carbapenems and piperacillin-tazobactam demonstrated consistent activity.
Prospective Audit and Feedback Reduces Inpatient Fluoroquinolone Use and Improves Appropriateness of Prescribing

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Objective: Fluoroquinolones (FQNs) are broad-spectrum antibiotics with diverse indications. In January 2017, Health Canada warned that FQNs should be used with caution given risks for significant adverse effects including tendinopathy, peripheral neuropathy, and neuropsychiatric disorders. Prospective audit and feedback (PAF) is an effective tool to reduce inappropriate use of antimicrobials. The objective was to study the impact of PAF on inpatient FQN prescriptions.

Methods: A multi-center pre-post quasi-experimental design was used to compare pre-intervention (June to August 2017) and intervention (September 2017 to February 2018) inpatient FQN use. Chart reviews were conducted on all patients prescribed FQNs to gather patient demographics, indication for and appropriateness of prescriptions. The intervention consisted of PAF on all FQN prescriptions, with written and verbal feedback from the Antimicrobial Stewardship team to optimize prescribing. The primary outcome was quantity of FQN use and appropriateness.

Results: 1107 patients (pre-intervention = 425, intervention = 682) were evaluated. PAF resulted in an overall reduction from 4.14 to 2.9 days of therapy/100 patient days and 5.36 to 4.4 defined daily doses/100 patient days (p<0.001). Ciprofloxacin was used primarily for genitourinary or intra-abdominal infections and accounted for two-thirds of FQN prescriptions. Following the intervention, ciprofloxacin use for non-specific symptoms attributed to UTI decreased from 60% to 46% (p=0.049). The primary indication for Levofloxacin was respiratory tract infections with a reduction in median days of therapy from 5 to 4 (p=0.009) following the intervention. The appropriateness of all FQN prescriptions increased from 68% to 88% post-intervention (p<0.001). Fewer patients were prescribed unnecessary therapy (p<0.001) or identified to be at high risk for a FQN-associated adverse event (p<0.001).

Conclusion: PAF can significantly decrease overall inpatient FQN use and improve appropriateness of prescribing, making this a useful tool in light of increasing concerns for FQN associated adverse events.
sCD127 Secretion in Response to IL-7 Influenced by a Single Nucleotide Polymorphism

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Background: IL-7 is a key cytokine in CD8⁺ T-cell survival and proliferation. The IL-7 receptor, CD127, is expressed both membrane-bound (mCD127) and soluble (sCD127). In tuberculosis and sepsis, the level of sCD127 in the plasma has been correlated with disease progression. Two factors are known to affect sCD127 levels. IL-7 induces sCD127 secretion from CD8⁺ cells, while C allele rs6897932 is correlated with higher sCD127 levels. We hypothesized that rs6897932 C-allele is associated with higher sCD127 secretion in response to IL-7. Correspondingly, the response to IL-7 of CD8⁺ T-cells from the genotyped donors was measured. Methods: CD8⁺ cells from the peripheral blood of healthy donors were stimulated with IL-7. mCD127 and sCD127 were measured by flow cytometry, and ELISA respectively. The genotype of donors was determined with a PCR. Results: Of 11 donors, 9 were CC, 3 were CT and 0 were TT genotype. As shown previously, the percentage of CD8⁺ cells expressing mCD127 decreased over time of IL-7 stimulation. In the individuals with the CT genotype, mCD127 levels returned to baseline levels at 72hr of stimulation with 10 ng/mL IL-7. No difference in mCD127 between genotype was detected at 8hr, 24hr or 48hr with either 10ng/mL or 1ng/mL IL-7. As expected, sCD127 secretion increased with time of IL-7 stimulation. No difference between genotypes was seen at any time point with 10ng/mL IL-7. Interestingly, with 1ng/mL IL-7, sCD127 secretion was lower in CT donors compared to CC donors [CC: 2030 pg/mL ±73 vs CT: 1188 pg/mL ±75; mean ±SEM]. Conclusion: The results suggest the presence of a host factor that may predict the response to IL-7 therapy, in the setting of, TB, sepsis or other diseases where sCD127 plays a role.
Measuring up! Benchmarking Antimicrobial Use in Canadian Children’s Hospitals

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Background: Inappropriate antimicrobial use (AU) is recognized as a leading cause of antimicrobial resistance. However, quantifying AU in hospitals is challenging due to variability in information systems. Point prevalence surveys (PPS) provide a means to quantify AU in a cross-sectional manner within and between institutions. The aim of this study was to describe and compare the patterns of AU across Canadian pediatric hospitals. Methods: A PPS of AU for all inpatients (excluding mental health and mother-newborn units) was conducted between November 6-13, 2018 in 13 Canadian pediatric hospitals. Data was entered on a REDCap database including co-morbid conditions, admitting service, antimicrobial(s), reasons for AU and pathogen(s) identified. Results: In total, 1493 patients-days were surveyed. The mean proportion of children receiving at least one antimicrobial was 497/1493 (33.3%) [range 21.4% to 43.6%]. Of 757 antimicrobials prescribed, the three most common were aminopenicillins (15.5%; 117), third generation cephalosporins (12.8%; 97) and antipseudomonal penicillins (10.9%; 83). The proportion used as targeted, empiric or prophylactic therapy was 25% (189), 53.1% (402) and 21.1% (160), respectively. The frequency of carbapenems and vancomycin use was 3.8% (29) and 7.4% (56), respectively. Of the antimicrobials used for targeted or empiric therapy (n = 591), 131 (22.2%) were for pneumonia, 106 (17.9%) for abdominal infections and 111 (18.8%) for fever ‘without source’. Ampicillin was used as the empiric treatment of community-acquired pneumonia (CAP) in 34.1% (41/41) of cases. Conclusions: Approximately 1/3 of children hospitalized in Canadian pediatric hospitals were prescribed at least one antimicrobial in our study. Carbapenems were prescribed infrequently. However, ampicillin was prescribed only for 1/3 of empirically treated CAP. More detailed analysis of the rationale for AU (e.g. lack of adherence to CAP guidelines) is required to fully understand antimicrobial prescribing in pediatric hospitals in order to prioritize measures aimed at optimizing AU.
Lock Solutions of Central Venous Catheters for the Prevention of Catheter-Related Complications: a Systematic Review

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Objective: Heparin is often used as a lock solution for central venous catheters (CVC), but the incidence of catheter-related complications remains high. The purpose of this systematic review was to summarize findings about locks, in particular in the pediatric population, and to compare their characteristics to identify which one should be used in our hospital.

Method: We searched the PubMed database from January 1st, 2007 to December 31st, 2018 for clinical trials, observational studies and review articles discussing prophylactic lock solutions for CVCs. We collected data relative to study type, study time, study population, catheter type, lock solution types, outcomes and biases of the clinical trials. The outcomes recorded were catheter-related infections (CRI), adverse events and catheter-related thrombosis, occlusions and dysfunctions.

Results: We identified 56 clinical trials, 6 observational studies and 23 reviews. Ethanol seemed more effective than heparin in preventing CRIs but was associated with a high risk of catheter malfunction. Taurolidine-citrate-heparin and antibiotics (mostly gentamicin) coupled with heparin seemed to be more effective than heparin alone in preventing CRIs and seemed to have similar antithrombotic effects. No antimicrobial resistance was reported. The 0.9% saline locks were similar to heparin in preventing infections and caused a higher rate of catheter thrombosis or occlusions. Other locks such as 4% tetra-sodium EDTA, minocycline-EDTA and tinzaparin were researched, but the limited number of studies and patients included did not allow for any conclusions to be drawn.

Conclusion: Given the risk of antimicrobial resistance with long-term use of antibiotic locks, taurolidine-citrate based locks seemed to be the most effective lock solution. However, most studies included a small population size, decreasing the ability to draw conclusions. Larger scale, multicenter randomized controlled trials are needed.
Criteria for Screening Close and Unit Contacts of Patients Colonized or Infected with Carbapenemase-Producing Organisms

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Objective: To provide updated evidence for carbapenemase-producing organisms (CPO) contact and unit screening practices to inform the revision of Alberta Health Services (AHS) provincial guidelines. Methods: Literature searches were performed in the PubMed, EMBASE, Google Scholar, and Cochrane Library electronic databases. A grey literature search was also done to determine current practices, guidelines, and recommendations. The key search words were carbapenemase-producing organisms, screening, criteria, close, contacts, unit, and ward. Results: Review of 15 studies revealed that the most common definitions for contacts were shared room or unit (10), shared healthcare provider (6), and household/environmental exposure to a previous or current CPO-positive case (4). Other risk factors were duration of exposure, geographic proximity, concomitant infection, antimicrobial therapy, invasive procedure(s), and mechanical ventilation. A scoring system has been proposed based on these definitions and risk factors to support the risk assessment and decision-making for screening of CPO contacts. Twenty studies regarding unit screening for CPO were reviewed. The two major criteria for unit screening were the presence of a CPO outbreak on the unit, and the presence of a known CPO-positive patient on a high-risk unit (e.g., ICU). Thirteen of the examined studies recommended weekly unit screening; however, studies showed considerable variation and heterogeneity in the criteria to define a unit as free of CPO transmission. Most commonly, either two or three unit-wide negative results were recommended. Conclusions: Screening of close and unit contacts of CPO-positive patients relies on an infection prevention and control risk assessment; however, criteria vary across jurisdictions. Further characterization of risk factors, and development of risk scoring systems, will aid in the decision-making process. Further study is required to determine the number of screens required to conclude a CPO outbreak on a unit.
SP13

WITHDRAWN
SP14

One Health Genomic Investigation of the Rise in Gentamicin Resistance in *Salmonella* Heidelberg from Human and Chicken Sources in Canada, 2014-2017

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**Objective:** Following a poultry industry ban on preventative use of ceftiofur in 2014, increased use of gentamicin and lincomycin-spectinomycin was reported. Simultaneous increases in gentamicin resistance (gen-R) rates in *Salmonella* Heidelberg from human and chicken sources were also observed. Our objective was to carry out a One Health genomic investigation of gen-R in human and chicken isolates of *S.* Heidelberg to determine potential transmission.

**Methods:** The Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) collected *Salmonella* isolates from provincial public health laboratories, as well as broiler chicken farms, abattoirs, retail stores and other sources across Canada. Antimicrobial susceptibility testing was carried out by broth microdilution using the Sensititre™ Complete Automated System (ThermoFisher Scientific) and whole genome sequencing was carried out by Nextseq™ (Illumina). Phylogenetic analyses were carried out with SNVPhyl pipeline v1.1, genomes were assembled with SPAdes v0.5 and resistance genes were identified with the staramr v0.3 tool. **Results:** In human isolates of *S.* Heidelberg (n=5974), the proportion of gen-R increased 3-fold from 2.3% in 2003-2015 to 6.8% in 2016-2017, while in chicken isolates (n=3510) from core CIPARS, CIPARS targeted studies, FoodNet Canada, and other monitoring programs, the proportion of gen-R increased 6-fold from 1.8% in 2003-2015 to 11.9% in 2016-2017. Amongst gen-R *S.* Heidelberg isolates from humans (n=66) and chickens (n=27) collected between 2014-2017, three gen-R resistance genes were found in both sources: *aac(3)-VIa* [81.8% of human isolates and 86.2% of chicken isolates], *aac(3)-IId* [16.7% human and 3.4% chicken], and *ant(2′′)-Ia* [1.5% human and 3.4% chicken], while *aac(6′)-Ib3* was identified in chickens only (6.9%). Phylogenomic analyses showed several related clusters of human and chicken isolates whose genomes differed by only 1-30 nucleotides. **Conclusion:** Gen-R was most commonly attributable to *aac(3)-VIa* and isolates from both humans and chickens were closely related suggesting potential transmission.
An Evaluation of Daptomycin Prescribing and Clinical Outcomes: A Retrospective, Single-Centre Experience

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Objectives: Daptomycin is approved for skin and soft tissue infections due to Staphylococcus and selected Streptococcus spp., and S. aureus bacteremia with or without right-sided, native valve infective endocarditis. Since 2015, daptomycin usage has increased at our institution. The study objectives were to describe prescribing patterns of daptomycin, and to identify the rate and predictors of clinical failure overall and in the vancomycin-resistant Enterococcus (VRE) subgroup. Methods: This was a retrospective cohort study of adults prescribed daptomycin for >48 hours (without exposure in the preceding 3 months) between April 2015 and March 2017. Primary outcomes were the patient, infection, and treatment factors associated with daptomycin prescribing. Secondary outcomes were rate and predictors of clinical failure (a composite of in-hospital mortality, daptomycin discontinuation due to toxicity or lack of efficacy, and readmission for or retreatment of the index infection). Results: Among the 81 patients enrolled, the median age was 60 years and 42.0% of patients had a Charlson Comorbidity Index of ≥5. Of those with bacteremia, 18.4% had a Pitt Bacteremia Score of ≥4 and 52.6% had bacteremia for >4 days. Daptomycin was prescribed off-label in 88.9% of cases. VRE was isolated in 50.6% of patients. The median daptomycin dose was 6.0 mg/kg overall and in the VRE subgroup. The rate of clinical failure was 30/81 (37.0%) overall with 13 deaths, and 19/41 (46.3%) in the VRE subgroup with 9 deaths. Bacteremia for >4 days was associated with an increased risk of clinical failure (OR 6.36, 95%CI 1.34-30.17, p=0.02). Conclusions: Daptomycin was largely prescribed off-label for VRE. The median dose of 6.0 mg/kg was consistent with manufacturer recommendations for S. aureus infections. The rate of clinical failure in the VRE subgroup exceeded that of the overall population, suggesting antimicrobial stewardship opportunities to evaluate formulary restrictions, dosing, and indications for daptomycin.
Trends in Antimicrobial Susceptibilities and Serotype Distribution of Invasive Pneumococcal Isolates Collected from Adults Over the Age of 65 in Canada

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Objectives: Invasive pneumococcal disease (IPD) is a significant source of morbidity and mortality, particularly in children and adults ≥65 years. This study identified changes in serotype distribution and antimicrobial susceptibilities of IPD isolates collected from Canadian adults ≥65 years. Methods: The SAVE study (a collaboration between CARA and NML) collected 9166 IPD isolates from 2011-2017, including 3529 obtained from adults ≥65 years. Serotyping was performed by the Quellung reaction and antimicrobial susceptibility testing was performed using CLSI methods. Multidrug/extensive-drug resistance (MDR/XDR) was defined as resistance to ≥3/≥5 antimicrobial classes, respectively. The Cochran-Armitage trend test was utilized to calculate the significance of changes in susceptibility rates and serotype distribution over time. Results: Overall, the most common serotypes identified within the ≥65-year age group were 22F (11.0%), 3 (8.8%), 19A (7.1%), 7F (5.6%) and 15A (5.4%). The proportion of serotypes 7C, 8, 9N, 19F, 23F, 24F, 31 and 38 demonstrated increasing trends over time, while 6C, 7F and 19A demonstrated decreasing trends (P<0.05). Of note, the trends for vaccine serotypes 7F, 19A and 19F were also identified in patients aged <18 and 18-64 years while the increasing proportion of vaccine serotype 23F was only seen in the ≥65-year age group. Overall susceptibility rates <90% were noted for clarithromycin (75.0%), doxycycline (88.7%) and trimethoprim-sulfamethoxazole (88.5%). No individual antimicrobial demonstrated a significant susceptibility trend from 2011-2017, although clarithromycin susceptibility increased and trimethoprim-sulfamethoxazole susceptibility decreased over time (P=NS). The prevalence of both MDR and XDR IPD decreased over time, although only the XDR trend was statistically significant (P=0.039). Conclusion: Within the ≥65-year age group, key vaccine serotypes decreased in prevalence from 2011-2017, accompanied by a decrease in MDR/XDR isolates. However, the prevalence of other vaccine/non-vaccine serotypes have increased, warranting continued surveillance of IPD in this crucial age group.
Impact of Picosalax and Multiple Fecal Microbiota Transplantations (FMT) by Enema on Microbiome Uptake in Patients with Recurrent *Clostridioides difficile* Infection (rCDI)

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Objectives: FMT is an effective treatment in patients with recurrent rCDI. Less is known regarding how the gut microbiota is influenced by bowel lavage prior to FMT and what impact multiple FMTs may have on the gut microbiota. Methods: Nine rCDI patients undergoing FMT by enema were included in this study. Rectal ESwabs were obtained immediately before and after PICO-SALAX®. Patients received 2-3 FMTs over a week following PICO-SALAX® administration. Rectal ESwabs were obtained prior to the second and third as well as at 1-month following FMT. Rectal ESwabs were stored neat in -80°C. The MO BIO PowerSoil® DNA Isolation Kit was used to isolate gDNA; 16s rRNA gene amplicon sequencing (V4 hypervariable region) was performed on the Illumina MiSeq. Low abundant OTUs (<0.001%) were excluded from the dataset. Microbiota measures were compared using Wilcoxon signed-rank test with Benjamini-Hochberg false discovery rate correction. Results: There were no significant differences in proportion of phyla or genera in the pre- versus post-PICO-SALAX® microbiota but there were significant decreases in richness (ACE, Chao1) and number of observed taxa and increases in the diversity (Simpson and Shannon). Significant differences in the patient’s baseline microbiota (increases in Bacteroidetes and Proteobacteria but decreases in Actinobacteria and Fusobacteria) were observed after three FMT at the 1-month follow-up but not after the first nor second FMT. While changes in alpha diversity were observed post-FMT, none were considered significant. Conclusions: The microbiota was only significantly changed consistently at the 1-month follow-up suggesting the need for multiple FMT when delivering FMT by enema. Bowel lavage with PICO-SALAX® significantly reduced the number of observed taxa and modified diversity indices but did not otherwise have a substantive impact on the microbiota. Whether bowel lavage is needed to improve uptake of donor microbiota requires further evaluation.
Comparison of PCV-10 and PCV-13 Vaccine Coverage across Canadian Geographic Regions, SAVE 2011-2017

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Background: The study aim was to assess the coverage of invasive Streptococcus pneumoniae (SPN) by PCV-10 and -13 across Canadian geographic regions. Methods: As part of a collaboration between CARA and the NML, SPN isolates were collected from jurisdictions across Canada. Serotyping was performed by the Quellung reaction and susceptibility testing was performed in accordance with CLSI methods. Multidrug resistance (MDR) was defined as resistance to ≥3 distinct antimicrobial classes. Results: A total of 9166 isolates were collected as part of the SAVE 2011-17 study. Of the total, 66.6% (n=6110), 21.7% (n=1985) and 11.7% (n=1071) of isolates were obtained from Central, Western, and Eastern regions, respectively. Nationally, PCV-13 provided significantly greater coverage (31.7%, n=2905) than PCV-10 (14.3%, n=1309, P=<0.0001). By region, PCV-13 delivered 33.7% (n=2060), 23% (n=456) and 36.3% (n=389) coverage for Central, Western, and Eastern regions, respectively. For PCV-10, coverage was significantly reduced (P=<0.0001) at 15.4% (n=939), 10.1% (n=201) and 15.8% (n=169) for Central, Western, and Eastern regions, respectively. The most common PCV-10,-13 serotype was 7F, accounting for 8.2% (750/9166, 4th most common) of isolates; however, a significant decreasing trend (P=<0.0001) was observed. The most common PCV-13 serotypes were 3 and 19A, representing 8.5% (781/9166, 2nd most common) and 8.3% (757/9166, 3rd most common) of isolates, respectively. Serotype 19A demonstrated a significant decreasing trend (P=<0.0001), whereas serotype 3 demonstrated a significant increasing trend (P=0.008). PCV-13 provided significantly greater national coverage (53.9%, 280/519) of MDR isolates than PCV-10 (14.8%, 77/519, P=<0.0001). Regional coverages of MDR isolates by PCV-10 and (PCV-13) were: 14.6% (46.4%), 17.2% (73.7%) and 13% (62.3%) for Central, Western, and Eastern regions, respectively. Conclusion: Overall, PCV-13 provided significantly greater national and regional coverage of invasive SPN compared to PCV-10. Notably, PCV-13 provided significantly greater coverage of MDR SPN.
**Recurrent *Staphylococcus lugdunensis* bacteremia identified by MALDI-TOF mass spectrometry**

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**Objective:** We encountered an 85-year-old lady with infective endocarditis possibly due to inadequate duration of therapy for bacteremia. In 2017, she was found to have *Staphylococcus lugdunensis* bacteremia thought to be secondary to a tunneled dialysis catheter. The catheter was exchanged over a guidewire and she received cefazolin for 16 days. Ten months later, blood cultures again grew *S. lugdunensis*. A transthoracic echocardiogram showed presence of a vegetation. Through molecular and matrix assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF MS) typing methods, we aimed to establish whether she had the same strain of *S. lugdunensis* during both admissions.  

**Methods:** Three of patient’s *S. lugdunensis* isolates as well as ten random *S. lugdunensis* clinical isolates from Eastern Ontario from 2017-2018 were compared. MALDI-TOF MS was conducted on Bruker Microflex LT benchtop instrument operated by FlexControl software. Mass spectrum analysis was performed using the BioTyper 2.0. A gel view representation of reference strain spectra was visually examined to identify peaks with variable occurrence among strains. Hierarchical clustering of these profiles was performed using the online software DendroUPGMA. The results were internally validated by comparison with polymerase chain reaction (PCR) primed with OPA-18, OPA-2, RAPD1, ERIC1, and ERIC2. The PCR products were electrophoresed on agarose gel. Hierarchical clustering of DNA banding patterns of the PCR was analyzed using the software PyElph.  

**Results:** Results from both typing methods showed that all three patients’ *S. lugdunensis* isolates were closely related to one another. However, these samples showed similarities with two of the ten random *S. lugdunensis* isolates.  

**Conclusion:** This is a preliminary indication that these closely related isolates are likely identical strains. We need to investigate the possibility of prevalent clone in our region by repeating the study on all *S. lugdunensis* isolates collected in 2014-2018.
Verification of MALDI-TOF MS for the Identification of *Burkholderia cenocepacia* isolates in cystic fibrosis (CF) Patients

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**Background:** Patients with cystic fibrosis (CF) can become chronically infected with species within the *Burkholderia cepacia* complex (BCC), leading to worsening lung function and quality of life and increased mortality. One member of BCC, *B. cenocepacia* causes a severe decline in lung function, which can develop into a life-threatening systemic infection known as 'cepacia syndrome'. Reduction in the prevalence of *B. cenocepacia* has been achieved through social distancing of CF patients and implementation of stringent infection control measures. The identification of *B. cenocepacia* is currently performed by molecular methods at a reference laboratory, with a 7-day turn-around-time. In this study, we evaluated the utility of matrix-assisted laser desorption/ionisation-time of flight mass spectrometry (MALDI-TOF MS) for the rapid identification of *B. cenocepacia* in comparison with molecular identification.

**Methods:** 65 previously characterised *B. cenocepacia* isolates and 12 isolates belonging to other BCC species were retrieved from −80°C stock and passaged twice on blood agar plates. MALDI-TOF MS was undertaken directly from isolated single colonies using a Bruker Microflex LT instrument (Billerica, MA) and spectra analysed using Bruker Biotyper with Compass version 4.1.80 (Billerica, MA). Each isolate was spotted in triplicate. Species-level identification was accepted if the score was ≥2.00. **Results:** 61/65 isolates were concordant and produced a score ≥2.00. 3/65 isolates were discordant (in only one replicate spot). None of the 12 non-*cenocepacia* isolates was mis-identified as *B. cenocepacia*, resulting in an overall accuracy of 96%. **Conclusions:** MALDI-TOF MS showed excellent concordance with reference methods in the identification of *B. cenocepacia*. While preliminary, this work suggests a potential use of MALDI-TOF MS for rapid identification of *B. cenocepacia*. Earlier identification of *B. cenocepacia* will ensure rapid implementation of infection control measures and may prevent additional transmission events.
Revision of Meropenem Zone Diameter Screening Breakpoint Reduces Unnecessary Confirmatory Testing for Carbapenemase Producing Enterobacteriaceae

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Background: In light of the increasing need to detect carbapenemase producing Enterobacteriaceae (CPE) in clinical laboratories, EUCAST recently revised its carbapenem zone diameter breakpoints. Since October 2018, our laboratory discontinued screening by ertapenem disk diffusion and adjusted its meropenem zone diameter screening breakpoint to reflect this change. A retrospective analysis was conducted to estimate the effect these updated breakpoints would have had on CPE detection.

Methods: From September 2015 to September 2018, our laboratory screened isolates for CPE based on the 2013 EUCAST zone diameter screening breakpoint of <25mm for meropenem or ertapenem (10µg disks). Isolates which screened positive were subjected to confirmatory phenotypic and molecular testing. For this study, we re-evaluated these previously screened positive isolates with the updated 2017 EUCAST meropenem screening breakpoint of <28mm, when accompanied by a temocillin 30µg disk zone diameter <11mm, and assessed the impact of discontinuing ertapenem screening on CPE detection.

Results: 877 potential CPE isolates were detected from 417 (48%) screening and 460 (52%) clinical specimens using 2013 EUCAST breakpoints. 111/877 isolates were later confirmed CPEs, producing 766 false positive screens (positive predictive value, PPV 13%). If we defined CPE detection using only an ertapenem zone diameter <25mm, all 111 CPEs would be detected, but at a cost of 757 negative confirmatory tests (PPV 13%). Alternatively, if we defined detection using only a meropenem zone diameter <25mm, we would miss one OXA-48 producer while generating 159 negative confirmatory tests (PPV 41%). When using the 2017 EUCAST meropenem breakpoint coupled with temocillin testing, the missed OXA-48 was detected, and there was no difference in PPV (41%).

Conclusion: Applying the 2017 EUCAST zone diameter screening breakpoints for meropenem and discontinuing ertapenem screening can reduce unnecessary CPE confirmatory testing by up to 80% without otherwise affecting the overall detection of CPEs identified in our laboratory.
Reducing Outpatient Vancomycin Use Without an Outpatient Parenteral Antimicrobial Therapy Program

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Objectives: Delivery of outpatient antimicrobials is complex, particularly for vancomycin which usually requires therapeutic drug monitoring, dose adjustments, slow infusion time, and monitoring of kidney function. In areas without outpatient parenteral antimicrobial therapy programs, safe and appropriate use of vancomycin can be challenging. The purpose of this study is to characterize and compare vancomycin use before and after an audit and feedback based intervention. Methods: This study was an observational study of the barriers to optimal outpatient vancomycin use in a small health authority zone. After identifying these barriers and summarizing outpatient vancomycin use, we performed a quality improvement intervention to address these barriers. The use of vancomycin was compared in the post-intervention period. All patients in the health region prescribed outpatient vancomycin were included in the study. Results: The main barriers for optimal outpatient use were physician knowledge of treatment guidelines and microbiology results and limited outpatient nursing resources. In the post-intervention period, there were 60% less patients (25 vs 63) on outpatient vancomycin. Overall there was a reduction in days of vancomycin therapy per 100 days by 29%. The average vancomycin level was approximately 8 and 10 mg/L before and after the intervention, respectively. Conclusion(s): By identifying the local drivers of excessive outpatient vancomycin prescriptions, we were able to reduce outpatient vancomycin use. Utilizing local data to provide feedback to stakeholders was effective in decreasing vancomycin use in a small health authority zone.
A review of test utilization of *Pneumocystis jirovecii* microscopy in Northern Alberta

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Objective: *Pneumocystis jirovecii* is an opportunistic fungus associated with respiratory infections. It is most strongly associated with an impaired immune response due to HIV infection; however, non-HIV associated immunosuppression such as malignancy or transplant can also predispose to infection. Microscopic examination of GMS-stained slides from respiratory specimens is currently the test method performed in our laboratory. With the future goal of introducing PCR for *P. jirovecii* diagnosis, we sought to review test requests to determine if ordering practices are appropriate. Methods: All requests for *Pneumocystis jirovecii* investigation for January and June 2018 were extracted from the laboratory information system. We reviewed the corresponding requisitions and recorded the following data: the presence of clinical information, the extent of microbiology test requests and the method of specimen collection. Additionally, we reviewed the provincial electronic health record for the presence of qualifying risk factors. Results: During the review period, a total of 233 samples from 184 patients were submitted for examination. *Pneumocystis jirovecii* cysts were identified in 4 specimens. HIV infection was documented in 11 patients (13 specimens). Most specimens were collected during bronchoscopy (95%, n=221) with 56% (n=130) and 39% (n=91) submitted as bronchial wash and bronchial-alveolar lavage samples, respectively. 61% (n=142) of requisitions were devoid of information relating to immunosuppression. In 42% (n=97) of specimens submitted, no risk factors for immunosuppression could be identified from the electronic health record. 57% (n=133) of submitted specimens also had all other listed microbiology tests requested. More than 1 specimen was submitted for 42 patients resulting in an additional 49 (21%) specimens. Conclusions: We conclude that laboratory resources for the identification of *Pneumocystis jirovecii* are not being utilized effectively. Possible strategies to improve test utilization prior to PCR implementation may include audit and feedback, and requisition design to discourage testing without consideration of risk factors.
Antimicrobial Stewardship Targets in an Outborn, Surgical Neonatal Intensive Care Unit

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Objectives: To describe the prescribing practices in an outborn, surgical neonatal intensive care unit (NICU) setting and inform targeted antimicrobial stewardship initiatives toward decreasing the antimicrobial burden. Methods: We performed a retrospective review of all antibiotics prescribed at an outborn level III NICU between November 1, 2017 and August 31, 2018. For all antibiotic courses, a complete electronic chart review was performed to identify the antibiotic indication, microbiological data, days of therapy (DOT), duration and appropriateness of therapy. Results: Antibiotics were prescribed in 173 neonates (57% of all admissions) at a rate of 519 DOT per 1,000 patient-days. The most common indication was empiric therapy for suspected early-onset sepsis (EOS), followed by antibiotic prophylaxis and empiric therapy for suspected late-onset sepsis (LOS) (Figure 1). Antibiotics for EOS were initiated in 94% (83/88) of neonates prior to transfer. Of the 25 patients with CNS symptoms (seizures or hypoxic ischemic encephalopathy) started on empiric antimicrobial therapy, 13 (52%) remained on antimicrobials even after an alternative diagnosis was assigned. Among the 311 DOT (38 courses) prescribed for prophylaxis, 192 (62%) were for surgical prophylaxis. Eighteen courses (72%; 110 DOT) were deemed to be inappropriate because of prolonged use, with a median therapy of 3 antibiotic days (IQR 2-8). General surgery (90 DOT), followed by ENT (73 DOT) and cardiovascular surgery (17 DOT) prescribed the majority of these courses. Conclusion: Prolonged therapy for suspected EOS and surgical prophylaxis are key drivers for antibiotic utilization in the outborn, surgical NICU setting. The decision to initiate these courses is often made by care providers prior to transfer to the receiving neonatal team. Thus, antimicrobial stewardship initiatives should target efforts to discontinue antibiotics by 36 hours of culture incubation, or earlier if a unifying non-infectious diagnosis is confirmed, and to decrease prolonged post-operative antibiotics.
prophylaxis.

Figure 1 - Main indications for antibiotic use stratified by proportion of antibiotic courses and DOT

![Bar chart showing proportions of antibiotic use by indication.

DOT: days of therapy; EOS: early-onset neonatal sepsis; LOS: late-onset neonatal sepsis; NEC: necrotizing enterocolitis]
Bedside Predictions of Sepsis and Pneumonia in ICU: Multivariate Analyses of Risk for Identifying Unexpected Infections

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Background: Sepsis and pneumonia are main causes of unexpected death in ICU. Although the main processes related to these infections are already known, risk prediction models can be used to identify unexpected cases. Methods: Multiple logistic regression models were built to predict central line-associated bloodstream infections (BSI) and ventilator-associated pneumonias (VAP). Independent variables: age, ICU length of stay (STAY), severity scores at admission (APACHE, TISS-28, SOFA), and Braden score for pressure ulcers. BSI and VAP were identified by using NHSN/CDC protocols, collected between Jan-Jun/2018 from one Medical/surgical ICU. Unexpected infections: any infection that is 5% or less likely to occur according to its model that eventually occurs, will be classified as UNEXPECTED. Results: A total of 532 patients were analyzed (16 BSI [3.0%], 48 VAP [9.0%], 34 deaths [6.4%]). Hospital death in patients without BSI was 5% which increased to 63% in infected patients (p<0.001). While mortality rate in patients with VAP was 44%, in non-VAP mortality was only 3% (p<0.001). Only 1% of patients without BSI and VAP died. Logistic model coefficients for BSI: -7.3 (constant); 0.07 TISS-28 (p=0.03); 0.13 SOFA (p=0.01); 0.04 STAY (p=0.01); Area under the ROC Curve = 0.74. From the 16 BSI patients, five were classified as unexpected BSI. VAP logistic model coefficients: -3.7 (constant); 0.03 TISS-28 (p=0.03); 0.05 APACHE (p=0.02); 0.03 STAY (p=0.02); -0.11 BRADEN (p=0.01); Area under the ROC Curve = 0.69. From the 48 VAP patients, just one was classified as an unexpected VAP. Conclusions: The models built allowed us to identify unexpected infections. Those cases were deeply analysed by the London protocol, which showed gaps in the ICU nosocomial infections prevention.
Fetal and neonatal outcomes after Zika virus infection during pregnancy: A systematic review

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Objective: A systematic review of the current literature to determine the fetal and neonatal outcomes of pregnancies infected with Zika virus (ZIKV). Methods: We conducted a systematic review following PRISMA guidelines and Cochrane systematic review methodology. MEDLINE, Embase, PubMed, CINAHL, LILACS, and WHO’s ICTRP clinical trials registries database were searched using terms “Zika virus” and “Zika infection”. Editorials, letters, news articles, and experimental animal studies were excluded. Case reports or series with less than 10 cases were excluded. Two independent reviewers conducted title/abstract screening, full text screening, and data extraction using a pre-specified form. Conflicts were resolved by consensus or consultation with a third reviewer. JBI tools were used to assess quality. Results: The initial search (up to 30/04/2018) identified 7394 references, of which 69 studies met inclusion criteria (92,882 cases of possible ZIKV in pregnancy). There were 47 case series, 7 case-control, 9 cohort and 6 cross-sectional studies. Studies were predominately from Brazil (45), the USA (11) and Colombia (5). There was wide variation in diagnostic criteria for ZIKV exposure due to local availability of serological testing and pre/postnatal neuroimaging. 6.5% (258/3772) of exposed fetuses developed birth defects consistent with ZIKV. Anomalies were most common after first trimester exposure (8.5% vs. 6.3% vs 5.2% per trimester). Microcephaly and intracranial abnormalities predominated, but extracranial CNS, cardiac and growth abnormalities were also frequently present in affected fetuses/infants. The effect of timing of exposure, maternal symptoms, testing approaches and infant follow up duration were analyzed individually. Final analysis will include all publications to 31/12/2018. Conclusion: ZIKV infection during pregnancy leads to intracranial and extracranial abnormalities in affected fetuses and infants. Understanding the nature, timing and frequency of these abnormalities will allow development of screening, diagnostic and clinical guidelines for ZIKV.
A Paediatric Investigators Collaborative Network on Infections in Children (PICNIC) Multi-Centre Canadian Descriptive Analysis of *Haemophilus Influenzae* Bacteremia in Children: Emerging Serotypes in the Era of Efficacious Conjugate Vaccines

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**Objective:** To describe the serotype distribution and clinical spectrum of *Haemophilus influenzae* (Hi) bacteremia in children admitted to 7 PICNIC centres. **Methods:** All cases of Hi bacteremia were identified in children admitted between 2013 and 2017 to participating centres. Disease was defined as complicated if the following occurred: a) ≥ 2 sites were affected, b) surgical intervention was required, c) organ failure, d) ICU admission, e) seizures, f) sensory or motor deficits, g) treatment-related complications, or h) death. **Results:** There were 87 eligible cases of Hi bacteremia. Preliminary analysis was limited to 53 cases from 4 centres with complete clinical and microbiological data. Male to female ratio was 31:20 and median age was 1.0 year (range: 0-15) years. Twenty-three (45%) were infants with median age 6 months (range 0-11 months). Hi serotypes included: a (N=18; 34%), b (N=8; 15%), f (N=7; 13%), c (N=1; 2%), e (N=1; 2%), non-typeable (N=16 cases; 30%) and unknown (N=2; 4%). Clinical foci included: bacteremia without a focus (N=22; 41%), meningitis (N=17; 32%), cellulitis (N=4; 8%), septic arthritis (N=3; 6%), pneumonia (n=3; 6%), epiglottitis or sinusitis (N=2; 4%) and endovascular infection (n=2; 4%). Complicated disease occurred in 19 (36%) cases; there was one (2%) death. Of the 17 cases with serotyping available, complication rates were: 62%, 42%, 13% and 13% for Hia, Hif, Hib and nontypeable Hi, respectively. Factors associated with complicated disease included typeable Hi (p=0.029) and a CNS focus (p<0.001). **Conclusion:** In the era of efficacious conjugate Hib vaccines, serotype a has emerged as the leading cause of typeable Hi disease and is associated with more complicated disease as compared to other serotypes. Strategies for preventing Hi disease should be directed at improving vaccine uptake rates to control Hib disease and developing an effective vaccine for preventing serotype a disease.
Frequency of colonization of therapy dogs with *Staphylococcus pseudintermedius*, *Staphylococcus aureus* and *Escherichia coli*

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**Background:** Visiting therapy dogs are growing in popularity within long term care facilities, psychiatric wards, prisons and hospitals. However, concerns regarding zoonotic disease (particularly MRSA) and infection control often limit the application of the visits. The objective of this study was therefore to determine the frequency of colonization of therapy dogs with zoonoses (*Staphylococcus pseudintermedius*, *S. aureus* and *Escherichia coli*), and the antimicrobial susceptibility of these organisms. **Methodology:** In October and November 2018, pharyngeal and rectal swabs were taken from 38 dogs registered with the St. John’s Ambulance Therapy Dog program. Samples were selectively cultured for each organism using CHROMagar Staph aureus and CHROMagar Orientation, and the antimicrobial MICs were determined by broth microdilution. A survey was administered to handlers to gather metadata regarding therapy dog activities, duties and health status. **Results:** 28 dogs (74%) were colonized with *S. pseudintermedius* of which 3 (10.7%) were MRSP. 13% of dogs were colonized with *S. aureus* none of which were MRSA; all visited hospitals or special care facilities. All dogs were colonized with *E. coli* including 4 carrying ESBL-producers. Penicillin + ampicillin was the most common resistance phenotype identified in 66.7% of *S. pseudintermedius* and 80% of *S. aureus* isolates. 89.7% of *E. coli* isolates were pan-susceptible. The survey revealed that visits to hospitals were common, 13 dogs (34%) reported visiting a hospital in the previous 3 months. Hand hygiene was variably practiced; 31% of handlers reporting using hand sanitizer at every therapy dog visit, 46% sometimes and 23% never. When used, hand sanitizer was most commonly applied both before and after dog contact (70%). **Conclusion:** While therapy dogs carry potential pathogens, the magnitude of the zoonotic risk associated with these animals is ill defined. Although this study had a small sample size, it was encouraging that no MRSA were identified.
Determination of Antibiotic Susceptibilities in *Aerococcus urinae* Urinary Isolates

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**Objectives:** *Aerococcus urinae* is a Gram-positive organism, initially identified in 1992. It is known to cause urinary tract infections (UTIs), bacteremia, and endocarditis in humans. There is limited data regarding the susceptibility of *A. urinae* to first-line antimicrobials indicated for the treatment of UTIs. In 2016, *A. urinae* was isolated in 125 urine samples processed by four hospitals in the study region. The unfamiliarity with this organism and the lack of local antimicrobial susceptibility rates presents a challenge for clinicians and often results in the unnecessary use of broad-spectrum antibiotics. The primary objective of this study was to establish the susceptibility rate of *A. urinae* urinary isolates to cefazolin, ampicillin, nitrofurantoin, fosfomycin, and ciprofloxacin. The secondary objective was to identify demographic characteristics associated with *A. urinae* bacteriuria in our patient population. **Methods:** Urinary samples received by the laboratory from October 2017 to June 2018 underwent routine identification as per physician orders. Samples that grew *A. urinae* were included in this study and subjected to susceptibility testing. Susceptibility testing was conducted via disk diffusion and results were interpreted based on published breakpoints for zone diameters. **Results:** A total of 72 isolates were included. Susceptibility rates for cefazolin, ampicillin, nitrofurantoin, fosfomycin, and ciprofloxacin were 100%, 99%, 99%, 96%, and 65%, respectively. The average age of patients was 79 years, 63.9% were female, 31.9% were recently hospitalized, and 44.4% were residents of a long-term care facility. **Conclusion:** Cefazolin, ampicillin, nitrofurantoin, and fosfomycin demonstrated good *in vitro* activity against *A. urinae*. In contrast, ciprofloxacin demonstrated decreased activity against this organism. Currently recommended first-line agents for the management of uncomplicated UTIs could be utilized to treat this organism. Characteristics of patients with *A. urinae* bacteriuria are consistent with risk factors predisposing to UTIs.
Comparison of INNO-LIA and TPPA treponemal confirmatory testing at ProvLab Northern Alberta (PLNA) as part of a reverse syphilis screening algorithm

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Background: Treponemal and nontreponemal serologies remain the cornerstone of syphilis diagnosis and management. In Alberta, the reverse screening algorithm is utilized with a treponemal enzyme immunoassay (EIA) used as the screening test and the Treponema pallidum Particle Agglutination assay (TPPA) performed as the confirmatory test. If the EIA is positive and the TPPA is indeterminate on repeat testing the clinician can request an INNO-LIA (Innogenetics multiparameter line immunoassay), a type of treponemal pseudo-Western blot which is performed at the National Microbiology Lab (NML). Prior to October 2016, PLNA performed the INNO-LIA in-house as the confirmatory test but, due to prolonged turnaround time (TAT), a high number of indeterminate results and clinician dissatisfaction, it was replaced by the TPPA. In this study, we compare these two methods over similar time periods. Methods: INNO-LIA results from April 2015 to March 2016 and TPPA results from October 2016 to December 2017 were extracted from our laboratory information system and analyzed. Results: Out of 2578 INNO-LIA, 480 (19%) were invalid. From the initiation of TPPA, there were 3904 TPPA run, of which 198 (5%) were indeterminate which was significantly less (p<0.0001) than the INNO-LIA. Fourteen (7%) of those tests were arbitrated by INNO-LIA at NML. 13 (93%) INNO-LIA tests were reactive and 1 test was indeterminate. Supply cost for the INNO-LIA was $35.54/test and TPPA was $2.35/test. TAT for the INNO-LIA was 10 days whereas TPPA was 72 hours. Conclusions: We demonstrate that in Alberta confirmatory syphilis testing by TPPA produces significantly less indeterminate results than INNO-LIA, is cost saving and ultimately, improves care and management of patients and their close contacts. The one disadvantage of the TPPA is the poor sensitivity in early and primary syphilis.
Patterns-of-Practice Survey Demonstrates the Need for National Guidelines Regarding the Implementation of Microbiology Point-of-Care Tests Across Canada

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Background: Microbiology point-of-care tests (POCT) are simple-to-use, automated assays performed outside of a laboratory infrastructure that can improve diagnostic accessibility and turnaround times, with potential benefits for antimicrobial stewardship and patient flow. Commercial availability and performance of POCT have rapidly evolved. Accreditation standards for implementing POCT exist for laboratories but if POCT are implemented without laboratory knowledge, these standards may not be followed. The goal of this survey was to describe laboratory awareness and involvement in POCT use. Methods: In January 2018, a web-based patterns-of-practice qualitative survey was conducted by the Institute for Quality Management in Healthcare across all 73 laboratories participating in their bacteriology proficiency testing program. Questions addressed laboratory awareness and involvement in assuring accreditation standards were followed regarding POCT implementation. Results: All 73 participants completed the survey. 12% of respondents reported POCT use within their hospital, while 5% reported adoption across affiliated outpatient settings. Notably, 11% and 18% were unsure, respectively. Of those aware of POCT use, 45% were not involved in the decision to introduce POCT on site, and 40% did not participate in the device selection process. Similarly, 40% of participants were unaware of any verification completed prior to the routine use of the device, and 20% noted the absence of standard operating procedures. 20% of participants noted absence of initial training and 30% were unaware of longitudinal competency assessments. Ongoing device maintenance was lacking in 89% of participating institutions. Additionally, 70% of participants stated that there was no overall monitoring of outcome measures after POCT implementation. Conclusion: Our survey results indicate a low amount of laboratory awareness and involvement with microbiology POCT and a concerning proportions of institutions lacking standard quality management of POCT. In anticipation of the expanding adoption of POCT, establishing national guidelines requiring laboratory oversight of POCT should be a priority.
Evaluating the effect of standardized ICU bedside reporting of infections on antimicrobial prescribing decision-making.

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Objectives: To describe antimicrobial prescribing decision-making by ICU clinicians before and after implementation of Stewardship at Bedside Rounds (SABeR).

Methods: Assessment of antimicrobial decision-making was conducted in a 24-bed tertiary care ICU using a standardized audit tool before and after implementation of the intervention. The audit tool captured discussion of antimicrobial decision-making using a framework developed by the antimicrobial stewardship (AMS) program consisting of eight antimicrobial prescribing decision nodes. The intervention consisted of transitioning the ICU inter-professional team from thrice-weekly AMS team-led rounds to standardized infection reporting and review during daily bedside rounds. This included introducing “infection” (temperature, white blood cell count, and antimicrobial therapy) as a body system by nurses during head to toe patient report. ICU physicians and pharmacists were educated to expect inclusion of infection as a separate system as an AMS intervention, and to move stewardship discussions to the bedside. All outcomes were assessed using descriptive statistics. Results: Ninety-five (95) pre-intervention observations occurred between May and October 2017 and 217 post-implementation observations occurred between October 2017 and August 2018. Table 1 illustrates the difference in antimicrobial decision-making discussion of patients prescribed antimicrobials. Discussion of all decision-making nodes increased post-implementation except tailoring of therapy.

Table 1: Antimicrobial Therapy Discussion Pre- and Post-Implementation

<table>
<thead>
<tr>
<th>Decision Making Framework Node</th>
<th>Pre-Intervention</th>
<th>Post-Intervention</th>
</tr>
</thead>
<tbody>
<tr>
<td>Evidence of Infection</td>
<td>7%</td>
<td>73%</td>
</tr>
<tr>
<td>Focus of Infection</td>
<td>18%</td>
<td>73%</td>
</tr>
<tr>
<td>Likely Pathogens of Infection</td>
<td>17%</td>
<td>71%</td>
</tr>
<tr>
<td>Discussion about Intention of Therapy</td>
<td>17%</td>
<td>76%</td>
</tr>
<tr>
<td>Current Day of Antimicrobial Therapy</td>
<td>21%</td>
<td>80%</td>
</tr>
<tr>
<td>Tailoring of Antimicrobial Therapy</td>
<td>69%</td>
<td>52%</td>
</tr>
<tr>
<td>Expectations Adjusted</td>
<td>23%</td>
<td>54%</td>
</tr>
<tr>
<td>Planned Duration</td>
<td>54%</td>
<td>64%</td>
</tr>
<tr>
<td><strong>Overall</strong></td>
<td><strong>28%</strong></td>
<td><strong>68%</strong></td>
</tr>
</tbody>
</table>

Conclusion: Antimicrobial prescribing decision-making improved after the implementation of SABeR.
**Role of Pseudomonas aeruginosa RpoN in Susceptibility to Tobramycin-Fumarate Combination Treatment**

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**Background:** Patients with cystic fibrosis (CF) suffer from chronic lung infections that frequently involve *Pseudomonas aeruginosa*. Antibiotics cannot eradicate the *P. aeruginosa* lung infection due to the high degree of tolerance displayed by the bacteria. Tobramycin combined with fumarate (TOB-FUM) has been previously shown to promote significant killing of antibiotic tolerant *P. aeruginosa* whereas tobramycin alone is ineffective. TOB-FUM is currently being investigated in clinical trials to treat chronic *P. aeruginosa* infections in CF patients. However, *P. aeruginosa* genes that are required for TOB-FUM susceptibility have not been previously documented. **Objective:** Demonstrate that the *rpoN* gene is required for TOB-FUM killing of *P. aeruginosa*. **Methods:** Antibiotic tolerant cultures of *P. aeruginosa* wild-type and Δ*rpoN* strains were incubated for 4 hours with or without fumarate and increasing concentrations of tobramycin. Bacterial survival was assessed by plate counting. **Results:** Minimal killing of wild-type and Δ*rpoN* cells was observed when cultures were treated with either tobramycin or fumarate alone. Treatment of wild-type cells with TOB-FUM resulted in a 3-log10 decrease in cell viability. In contrast, TOB-FUM treatment was unable to kill Δ*rpoN* cells. This phenotype could be complemented *in trans* with a plasmid-borne copy of *rpoN*. TOB-FUM treatment of mixed wild-type and Δ*rpoN* cultures (as might be observed in a CF lung) led to preferential killing of the wild-type cells while the Δ*rpoN* cells were spared. **Conclusion:** The *rpoN* gene is required for susceptibility to TOB-FUM. Importantly, loss of RpoN function is commonly observed in *P. aeruginosa* CF clinical isolates. Future work will confirm that clinical isolates lacking RpoN function are not susceptible to TOB-FUM. Clinical trials that test TOB-FUM efficacy might need to stratify patients based on the frequency of *rpoN* mutant isolates in their lungs to determine if patients with a lower frequency of *rpoN* mutant isolates benefit more from TOB-FUM than patients with a higher burden of *rpoN* mutants.
Health Outcomes in Post-natally Acquired Pediatric Zika Virus Infection: A Systematic Review

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Background/Objective: The primary focus of pediatric Zika virus (ZIKV) research has been the sequelae of congenital infection. ZIKV acquired post-natally has generally been described as asymptomatic or a self-limited febrile illness; however, there has been minimal research into the clinical course and potential complications. Animal studies suggest that ZIKV acquired in infancy may have neurodevelopmental sequelae. We aim to summarize the literature on health outcomes in post-natally acquired pediatric ZIKV infection using systematic review methodology. Methods: We are conducting a systematic review following PRISMA guidelines and Cochrane systematic review methodology. MEDLINE, Embase, PubMed, CINAHL, LILACS, and WHO’s ICTRP clinical trials registries database were searched using terms “Zika virus” and “Zika infection”. Editorials, letters, news articles, and experimental animal studies were excluded. Case series required 10 or more cases for inclusion. Two independent reviewers conducted title/abstract screening, full text screening, and data extraction. Conflicts are resolved by consensus or consultation with a third reviewer. Results: Initial search up to April 30, 2018 recovered 7394 references. 9 case series met inclusion criteria and present data from Brazil (N=1), Colombia (N=1), Dominica (N=1), Singapore (N=2), and US (N=4). N ranged from 11-18,576, and age from 1 month-18 years. Laboratory confirmation of ZIKV infection was inconsistent across regions. Overall, there was poor reporting of clinical symptoms. The most common symptoms were fever (71-93%) and rash (94-100%), in part reflective of case definitions. Severe complications were rare (Guillain-Barre Syndrome 0-0.2%; meningitis/encephalitis 0-0.09%; mortality 0-0.05%). No neurodevelopmental outcomes were reported. Literature search will be updated to December 31, 2018 and data analysis completed by the time of the conference. Conclusion: This up-to-date systematic review of health outcomes in post-natally acquired pediatric Zika virus infection will summarize current knowledge and identify research gaps for optimization of clinical care and public health interventions.
SP35

WITHDRAWN
SP36

WITHDRAWN
Prenatal Screening of *Chlamydia trachomatis* and *Neisseria gonorrhoeae* Infections: Sufficiently Reliable to Abrogate Topical Ocular Prophylaxis to Newborns?

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**Objectives:** The Canadian Pediatric Society no longer recommends the use of universal ocular prophylaxis with erythromycin ointment 0.5% to prevent neonatal gonococcal ophthalmia. Instead, screening for *Chlamydia trachomatis* (CT) and *Neisseria gonorrhoeae* (NG) in all pregnant women is considered the most effective way of preventing vertical transmission and neonatal conjunctivitis. The aim of this study was to assess compliance with Quebec pregnancy screening guidelines. **Methods:** The list of all women who delivered at a tertiary care hospital in the province of Quebec, between April 2015 and March 2016, was cross-referenced with the list of samples tested for CT/NG. Maternal medical records were reviewed for demographic, prenatal and diagnostic information. **Results:** Amongst 2688 women, 432 (16%) weren't screened during pregnancy and 38 (1.4%) had an invalid result reported. Among the 2218 (82.5%) women with at least one valid result, infection was detected in 45 (2%): CT (43; 1.9%) and NG (4; 0.2%); two women were co-infected. Prevalence of CT infection was significantly higher among women aged <25 years old (9.3%; 28/301) than among those aged ≥25 yo (0.9%; 17/1926; p<0.001). Of the 2 177 women with an initial negative test result for CT and NG, 8% (170/2177) were retested: 36/272 (13.2%) among women aged <25 yo and 134/1905 (7%; p<0.0001) among those aged ≥ 25 yo. Subsequent infection was detected in four (2.4%) women, three of whom being <25 yo. **Conclusions:** Compliance with CT/NG screening guidelines is insufficient to stop current universal ocular prophylaxis. Repeating universal screening later in pregnancy should be considered: in addition to identifying women who become infected later in pregnancy, this strategy could decrease the number of women who are not screened at all during pregnancy.
Evaluation of the impact of reduced incubation times of Kiestra TLA incubated primary cultures on the outcome of Kirby-Bauer (KB) disk diffusion testing

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Objective: Total laboratory automation (TLA) smart incubators have the potential to reduce incubation times of primary cultures which would also improve time to reporting for susceptibility testing. Our goal was to verify the performance of susceptibility testing by KB from clinical isolates recovered from primary cultures with reduced incubation times. Methods: Inoculum for KB testing of clinical isolates was prepared from cultures incubated for 12 and 15 hours in the Kiestra smart incubators and compared to susceptibility testing performed after 18 hours of incubation. Antibiotic disks were dispensed on inoculated Mueller-Hinton agar and incubated according to CLSI recommendations. Zones of inhibition were measured using the Kiestra zone measurement function. Results: Susceptibility testing was performed on 117 Enterobacteriaceae, 32 non-fermentors, 46 S. aureus, 54 coagulase negative Staphylococcus and 75 Enterococcus species. There was no statistically significant difference in the zone of inhibition for any drug-organism combination when KB was performed from isolates recovered from 12 or 15 hour cultures compared to 18 hours. For Enterobacteriaceae there was 1 very major error (VME) (tobramycin at 12 hours), no major errors (ME) and 43 minor errors (MNE). There were 21, 12 and 11 MNE with isolates recovered from cultures incubated for 12, 15 or 12 and 15 hours respectively. Categorical agreement for all organism-drug combination when performed from 15 hour cultures was higher than if performed from 12 hour cultures (p<0.001). There were 2 MNE among non-fermentors (12 hours) and no discrepancies for the Gram positive organisms. Conclusion: Reducing incubation times of primary cultures did not adversely affect the outcome of KB susceptibility testing. Correlation with 18 hours was better if primary cultures were incubated for 15 hours compared to 12 hours.
Epidemiologic, Microbiologic and Clinical Outcomes of Patients with Intravenous Drug Use-Associated Infective Endocarditis Admitted to X Hospital: A Descriptive Observational Study of Cases Between 2012 and 2017.

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Objective(s): The objectives of this study are to describe the epidemiological, microbiological, clinical, echocardiographic and outcome variables of patients with intravenous drug use-associated infective endocarditis (IVDU-IE) admitted to X hospital, estimate the prevalence of IVDU-IE in X city, and estimate the rates of complications and mortality among patients with IVDU-IE admitted to X hospital. Methods: A retrospective chart review was conducted on patients who met the following three criteria: (1) International Classification of Diseases, Tenth Revision (ICD-10) codes with a discharge diagnosis of IE, (2) IVDU within 3 months of IE, (3) admitted to X Hospital between January 1, 2012 and December 31, 2017. Data was collected on cases meeting these criteria on the following categories: epidemiology, microbiology, clinical signs and symptoms, echocardiography, complications throughout admission, and outcomes. Results: 42 cases were identified that met our inclusion criteria. The majority of patients (72.4%) were male, with opioids being the most common injection drug used (79.3%). The most common clinical sign exhibited by cases was fever (90.5%) and Staphylococcus aureus (61.9%) was the most common microorganism isolated. The tricuspid valve was most commonly affected (58.5%) and 50% of cases had heart failure as a complication throughout admission. 45.2% of cases required a valve replacement, and all patients received antibiotics. 31.0% of patients died during the study period. Conclusion(s): Despite the relatively young age of this patient population, IVDU-IE is a disease associated with significant morbidity and mortality. Implementing effective harm reduction strategies for these patients are always a worthwhile effort. We hope that the information gathered in this study will be used by all healthcare professionals who work with this population to better understand the clinical characteristics and the outcomes of these patients.
SP41

WITHDRAWN
Clinical Course of Patients Following Beta-Lactam-Induced Acute Interstitial Nephritis – A Retrospective Review

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Background: Beta-lactam (BL) antibiotics are considered first-line treatment for a range of infections. Patients who develop acute interstitial nephritis (AIN) secondary to BL exposure are often prescribed less optimal antibiotics or those reserved for resistant organisms to avoid the potential risk of recurrent AIN with other BLs. In the medical literature, therapies used following development of BL-induced AIN have not been well-defined, making it difficult to standardize antibiotic alternatives. Objectives: To describe the management and evaluate the clinical course of patients following BL-induced AIN. Methods: Retrospective cohort study at a tertiary hospital from 2012 to 2017. Patients with AIN were identified using ICD-10 code “N10” for “Acute Tubulo-Interstitial Nephritis,” and search parameters “acute kidney injury,” “acute renal failure”, and “AIN.” Demographics, antibiotic treatment regimens, symptoms, and clinical outcomes were collected. Results: Fourteen patients (male 64%/female 36%) were diagnosed with BL-induced AIN (biopsy-proven 14%, clinically-proven 86%) from 2012 to 2017. Mean increase in serum creatinine was 192 µmol/L secondary to BL-induced AIN, with a mean decrease to 130 µmol/L within 30 days of discontinuation of the BL. Classical symptoms of AIN included rash (14%), fever (57%) and eosinophilia (50%, n=10), however, presenting symptoms varied amongst the population. Carbapenems (36%), fluoroquinolones (21%) and vancomycin (14%) were the three most common alternative antibiotics following development of BL-induced AIN, and no further modifications were made to the initial change in antibiotic. Three patients did not require additional antibiotic therapy. All patients experienced microbiological cure. Conclusion: The incidence of BL-induced AIN appears low. Discontinuation of the offending BL antibiotic improved signs and symptoms of AIN within 30 days. Use of alternative antibiotics, including BLs, did not appear to worsen clinical outcomes, which is suggestive that these antibiotics can be used. Further studies are required to confirm use of alternative BLs in BL-induced AIN.
Initial Vancomycin Treatment for First Episode Non-Severe *Clostridium difficile* Infection Amongst Adult Inpatients

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**Background:** *Clostridium difficile* infection (CDI) is an important cause of nosocomial diarrhea. Previous studies have suggested that metronidazole and vancomycin are equally effective for the treatment of non-severe CDI, however, recent guidelines have recommended the initial use of vancomycin. Our study objective was to identify clinical predictors of adverse outcomes and the impact of first-line vancomycin for treatment of non-severe, inpatient CDI. **Methods:** We conducted a retrospective chart review of all adult inpatients with first episode CDI at our institution from January 2013 to May 2018. CDI was defined as a positive *C. difficile* Loop-mediated isothermal amplification assay, in conjunction with ≥3 Type 5–7 stools on the Bristol stool scale. We abstracted comorbidities, medications, and relevant outcomes (recurrence, relapse, and death). **Results:** A total of 737 cases were included. Patients had a median age of 72.3 years (Q1: 61.2, Q3: 83.3) and 628 (85.2%) were classified as non-severe CDI. Predictors of relapse and all-cause 30-day mortality for the overall cohort were: hospital-acquired infection (OR_adj: 2.08; 95%CI: 1.50–2.89; P<0.001), age ≥65 (OR_adj: 1.98; 95%CI: 1.37–2.88; P<0.001), and white blood cell count >15×10⁹/L (OR_adj: 1.76; 95%CI: 1.26–2.46; P=0.001). Amongst patients with non-severe CDI, relapse, recurrence, and mortality rates were 17.4%, 7.0%, and 11.4% respectively when treated with initial metronidazole, compared to 18.6%, 3.1%, and 7.8% respectively when treated with initial vancomycin. The use of first-line vancomycin for treatment of non-severe CDI was not associated with relapse, recurrence, or 30-day mortality alone. However, in an adjusted analysis, the use of first-line vancomycin for treatment of non-severe CDI was associated with a reduction in the composite outcome of recurrence or 30-day mortality (OR_adj: 0.51; 95%CI: 0.28–0.94; P=0.03). **Conclusions:** First-line vancomycin was associated with reduced recurrence or all-cause 30-day mortality in the treatment of inpatients with non-severe, first episode CDI.
**Epidemiology of Viral Respiratory Infections and Preventative Measures in High Acuity Units in Manitoba [VIRIAC-MB]**

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**Background:** Viral respiratory infections are acute self-limited illnesses; however those with chronic underlying illnesses are at greater risk of morbidity. **Objective:** To understand the epidemiology and usage of preventative measures to help reduce transmission events. **Method:** A retrospective chart review was performed on patients admitted to high-acuity units (MICU, SICU, PICU, NICU) with positive molecular tests from Oct. 1st, 2016-May 30th, 2017 at 7 hospitals in Winnipeg, MB. **Results:** 307 (188 adult [18+y]; 119 pediatric) patients had specimens submitted for multiplex viral testing; at least one virus was detected in 112 (39.4%). Among adults, viruses identified were: influenza (12, 6.4%), parainfluenza (11, 5.9%), rhinovirus (10, 5.3%), coronavirus (7, 3.7%), HMPV (5, 2.7%), RSV (3, 1.6%) other (3, 1.6%). Among children, viruses identified were: RSV (27, 23%), rhinovirus (15, 13%), parainfluenza (6, 5.0%), influenza (4, 3.4%), coronavirus (3, 2.5%), other (6, 5.0%) (distribution P<.001 compared to adults). Overall, 4 (7.8%) of adult infections and 3 (5.1%) of pediatric infections were hospital-acquired. No significant difference in the distribution of viruses was noted based on geographic region or urban vs. rural environments. Influenza vaccination history for the current season was documented in 7.8% of adults and 5, 4.2% of children (p=0.001). 42.3% of patients had documented infection control orders. Among children, 34 (58%) had orders, 31 (92%) meeting infection control guidelines. Among adults, 11 (22%) had orders, 4 (36%) of which met guidelines. **Conclusions:** Viral respiratory tract infections are common in high-acuity units, and causative viruses appear to differ between adult and pediatric patients. Hospital-acquired cases are uncommonly diagnosed. Infection control orders were sub-optimal in both adult and pediatric settings. This study highlights the need for further research into respiratory viral illness in ICUs, as well as barriers with regards to the implementation of infection control measures.
Time from Drawing to Loading of Blood Culture Bottles, and Time to Positivity in the Context of Laboratory Consolidation: a One-Year Retrospective Study.

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Objectives. The Champlain local health integration network offers health services to 1.3 million residents. Within an 18000 sq. km area, 16 community and tertiary care hospitals collect and send blood cultures to the Regional Microbiology Reference Laboratory situated in a tertiary care University hospital. A retrospective audit of blood cultures over a one-year period assessed time from collection to loading of blood cultures bottles in, and time to detection by the BD BACTEC blood culture system for each site.

Methods. A total of 59122 negative blood cultures were reviewed to assess time from collection to loading, and 10535 positive blood cultures were assessed for average time to positivity. For selected sites, hourly distribution of number of samples was compared to daily courier schedules.

Results. Median time to loading for samples originating from within the Ottawa city-limits was 3 hours compared to 7.6 to 22.7 hours for blood cultures collected from client sites outside of the Ottawa City limits. For most sites, 75% of samples reached the laboratory within 20 hours. Average time to positivity for all cultures did not vary significantly between inner-city sites (22.5 hours) and distant sites (25.6 to 31.8 hours). However, there was a trend of decreasing time from loading to positivity for distant sites (13.5 to 16.1 hours) compared to inner-city sites (18.5 hours).

Conclusions. Despite prolonged delayed entry of blood cultures from remote client sites, bacterial growth may have reduced the time to detection of positive cultures by the BD BACTEC blood culture system and mitigated some of the negative impact of delays in transportation. Successful laboratory regionalization may largely depend upon optimization of courier routes. Adequate coordination of courier service with peak collection times may reduce delays.
Factors Associated with Gammaproteobacterial Aerosolization from Intensive Care Unit (ICU) Sinks

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Background: Sink drains are a reservoir of gammaproteobacteria which may be transmitted to patients. We sought to assess factors associated with aerosolization from ICU sinks. Methods: Sink tailpiece and faucet interior surfaces in 7 ICUs were cultured semi-quantitatively by swabbing defined surface areas, inserting swabs into 1ml of neutralizing broth, plating different volumes onto MacConkey3 with crystal violet (Mac3CV), incubating aerobically at 37ºC for 18-24hours, then counting gammaproteobacterial colonies. 850L air samples were collected by impaction onto Mac3CV with the sampler held at a defined location 20cm from faucets, and plates incubated aerobically at 37ºC for 18-24hours before counting colonies. For sinks without electronic controls, air samples were collected first with cold, then hot, water running. Logistic regression with generalized estimating equations was used to assess factors associated with detectable gammaproteobacteria in air.

Results: Of 382 tailpiece swabs, 70 had no growth (NG), 144 growth 1-750cfu/cm², and 168 growth >750cfu/cm². Among air samples, 247 had NG, 126 growth 1-235cfu/1000L, and 9 growth >235cfu/1000L. In multivariable analysis, gammaproteobacteria were more likely to be detected in air if tailpiece surface growth was 1-750cfu/cm² (OR=3.5, 95%CI 1.3-9.5) or >750cfu/cm² (OR 5.5, 95% CI 2.0-15) compared to NG, and in summer (April-September) versus winter (OR 6.0, 95%CI 2.0-18). The probability of detection of gammaproteobacteria in air also differed in different hospitals (growth in air detected in 4.7%-90% of samples, P=0.0002), but was not affected by growth from faucet samples. Of 301 matched air samples with hot and cold running water, 94 (31%) and 67 (22%) had detectable growth, respectively (OR=1.6, 95% CI 1.1-2.3). Conclusions: Gammaproteobacteria are more often detected in air adjacent to sinks when higher concentrations are present in sink tailpieces, when hot versus cold water is running, and in summer. Further data are needed to understand whether such aerosolization creates patient risk.
Evaluating the Educational Experience of Resident Physicians with Antimicrobial Stewardship

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Background: Antimicrobial stewardship (AS) aims to optimize appropriate use of antimicrobials. Education of medical trainees is an important strategy to achieve this goal. Our study assesses resident physicians on their previous educational experiences with AS and subsequent preparedness towards prescribing antimicrobials appropriately. Methods: Resident physicians from all levels in training from all postgraduate residency programs at a Canadian university-affiliated teaching hospital were invited to complete a 16-item online survey (April – October 2018). Results: 127 (20%) of the 630 residents completed the survey. 85% of residents (108/127) are familiar with the term “Antimicrobial Stewardship”. Only 57% (72/127) are familiar with in-hospital strategies employed by AS, including stewardship rounds, local antibiograms and restricted antimicrobial formulary. Even fewer (31%) residents have participated in AS initiatives, most of which were passive activities such as AS lectures and learning modules during undergraduate medical studies or attending in-patient AS rounds. Over 90% of residents believe that AS should be integrated as part of their education during both medical school and residency. However, only 53% and 60% of residents felt their medical school and residency programs have prepared them well with antimicrobial use in practice, respectively. Conclusion: Most residents have an awareness of AS but only a minority report participation in AS endeavours. Residents recognize the importance of formative education on AS principles and appropriate use of antimicrobials. Our survey highlights a perceived need by residents for enhanced education at both the undergraduate and postgraduate levels. Formal integration of AS into the undergraduate curriculum is planned by our AS team to address this.
Imported Malaria in Migrant Children New to Canada: A Retrospective Review to Inform the Value of Pre-Departure Empiric Malaria Treatment

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Background: Malaria is a common illness in people migrating to the West. Hospital care, including intensive care unit stays, can result in significant financial costs. Pre-departure anti-malarial treatment of migrants to Canada from malaria-endemic countries could prevent morbidity and reduce costs to Canada’s universal health care system.

Methods: Health records for children diagnosed with malaria at the Children’s Hospital of Eastern Ontario were retrospectively reviewed from 2010-2017. Patient demographics, details of care, and costs of inpatient and outpatient care related to malaria were determined and compared between migrants (immigrants/refugees) versus children who acquired malaria while traveling to visit friends and relatives.

Results: 24 migrants and 9 VFRs with malaria were identified. 20/24 (83%) migrants and 9/9 (100%) VFRs had Plasmodium falciparum malaria; 18/24 (75%) migrants and 3/9 (33%) VFRs were from East Africa, and 5/24 (21%) and 6/9 (67%) were from West/Central Africa. Migrants were median 12.0 years (IQR 8.8, 14.0) versus VFRs 6.4 years (4.0, 11.0) (p=0.09). Time from arrival to Canada to onset of symptoms was similar between groups (migrants – median 5 days; VFRs – 3 days). Similar proportions of migrants and VFRs were admitted to hospital (80% and 71%) and admitted to intensive care unit (27% and 29%). Total cost of care for migrant malaria over the study period was $174,485 CAD, and for VFRs was $61,656 CAD.

Conclusions: A significant burden of malaria among migrant children was found in this study, shortly after arriving to Canada. Assuming a cost of empiric pre-departure treatment for malaria of $3/person, the cost of treating all newcomers from Africa to Canada in the same 8-year period (194,267) would be ~$582,800 CAD. This is only three times the cost of treating children at a single tertiary care center, indicating an apparent cost benefit to pre-departure treatment.
Evaluation of the Allplex Respiratory Panel Assays 1, 2 and 3 for Detection of Respiratory Viruses

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Background: We compared the Allplex Respiratory Panel (RP) Assays 1, 2, and 3 (Seegene, Republic of Korea), one-step real-time PCR detecting 15 respiratory viruses with influenza A subtyping, against a 12-target multiplex PCR laboratory-developed assay (LDA) used at our institution. Methods: In Jan.-Feb. 2018, 325 nasopharyngeal specimens underwent the routine LDA. Specimens were stored at 4°C and within 24 hours underwent automated nucleic acid extraction using the STARLET system (Hamilton, USA), and Allplex RPs on a CFX96 (Bio-Rad, USA) thermocycler. Another 68 samples tested by the LDA in July-Sept. 2018 containing underrepresented viral targets were stored at -80°C, then tested by Allplex RPs in Sept. 2018. Percent agreements and Cohen’s kappa values were calculated. Discrepant results were examined. Results: Ten samples were excluded for failed extraction or invalid results on the LDA. 207/383 (54.0%) samples yielded positive results by Allplex RPs and 177/383 (46.2%) by the LDA. Positive percentage agreement were between 83.3% to 100%, except for human enterovirus (HEV) and parainfluenza virus (PIV) 2 (66.7% and 58.3%). Negative percentage agreements ranged from 93.1% to 100%. Kappa values ranged from 0.56 to 1, and was lowest for human rhinovirus (HRV). Discordant results were identified in 69 samples. Thirty specimens contained targets only identified by Allplex RPs. Twelve were positive only by the routine assay, of which five were PIV-2 from frozen samples. Twenty-seven samples positive by both assays contained discrepancies, of which the majority were polyviral. Seventeen involved one assay detecting HEV/HRV while the other detected one of the two. Conclusions: In this partially prospective evaluation, the Allplex RPs and our LDA show high percentage agreement and kappa values. Discrepant results mainly involve HEV, HRV and PIV-2, which may result from testing of frozen samples and/or cross-reactivity between picornaviruses, requiring further testing to resolve.
Audit and Feedback Interventions Associated with Lower Mortality in a Retrospective Analysis of Clinical Outcomes from an Antimicrobial Stewardship Program

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\textbf{Objective:} Inappropriate use of antimicrobials results in unnecessary costs, \textit{Clostridium difficile} infections, longer length of hospital stay (LOS), adverse drug events, and antimicrobial resistance. As such, an antimicrobial stewardship program should measure these and other outcomes for quality improvement of patient care. The objective of this study was to assess the feasibility of specific patient-centred outcome measures that would be possible targets for ongoing prospective analysis. \textbf{Methods:} We reviewed the electronic medical records of patients admitted to the internal medicine and family practice services at our tertiary referral centre from June to August 2018. Patients who received audit and feedback interventions were matched to controls by age, gender, antibiotic, and indication. The following outcomes were collected: acceptance of stewardship intervention, ICU admission, represcription, bloodstream infection with any antibiotic-resistant organisms, fungemia, renal toxicity, neutropenia, readmission, and mortality. Linear regression was used for analysis of numerical outcomes and logistic regression was used for analysis of categorical outcomes. \textbf{Results:} The 31 patients in the intervened group and the 31 patients in the control group were similar with respect to their baseline characteristics of age (median 83.5 years, IQR 73.75-90), gender (71% males), Charlson Comorbidity Index (median score 8, IQR 6-10), and pre-intervention LOS (median 2 days, IQR 0-5). Twenty-three interventions (74\%) were accepted. Compared to the control group, the intervened group had significantly lower 30-day mortality (Odds Ratio 0.31, p=0.0485), adjusted for comorbidity score and pre-intervention LOS. Other outcomes were not significantly different between the two groups. \textbf{Conclusions:} Audit and feedback interventions were associated with significantly lower 30-day mortality. Ultimately, mortality represents the most objective clinical outcome measure and is readily extractible from electronic medical records for analysis and inclusion in dashboard metrics and quality improvement cycles.
Drivers of Health Behaviours Among Private Well Users in Ontario: A Cross-Sectional Survey of Awareness, Perception, Attitude and Experience

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Background: Ontario has one of the largest groundwater-reliant populations in Canada, with approximately 1.6 million households utilising private wells. Unlike municipal water supplies, well owners are the primary agents responsible for managing their drinking water, including source maintenance, resource protection, and water testing. A previous Ontarian study found that just 11-12% of well owners complied with provincial water testing guidance during any year between 2008 and 2012. This finding suggests significant gaps in knowledge and/or tools for stewardship, representing a major concern due to the ubiquity of contaminant sources in rural areas (e.g. agricultural run-off, septic tanks, etc.). The current study sought to identify and assess the gaps associated with private well water stewardship; namely, knowledge, attitudes and practices (KAP), to contribute to improved health behaviours among rural Ontarian residents.

Methods: A province-wide online survey was undertaken over the 4-month period May to August 2018. The survey was designed to quantify information among Ontario’s well owners based on their awareness, perceptions and behaviours in relation to their personal source and local sources of contamination.

Results: The survey was completed by 1030 respondents (99% CI 4.02%). Preliminary findings indicate that previous experiences (i.e. residential presence during well construction, previous case(s) of acute gastrointestinal illness within household) significantly influence both owner awareness (p<0.001, p=0.038, respectively) and perception of local groundwater contamination risk (p=0.017, p<0.001, respectively). Additionally, increased awareness (p=0.018) and positive attitudes (p=0.006) towards personal well water supplies were associated with increased likelihoods of testing.

Conclusion: Findings illustrate that experiences influence both respondent awareness and risk perception, with increased levels of awareness and positive attitudes enabling health behaviours. Results will provide public health agencies with a framework for designing strategies and policies for increasing awareness and addressing the drivers of, and barriers to, protective actions among well users in Ontario, and further afield.
Disseminated mycobacterium avium complex in non-HIV infected patients: Three cases and a literature review

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Background: Mycobacterium avium complex (MAC) are a group of ubiquitous non-tuberculous mycobacterium (NTM) known to cause disseminated infection in individuals with impaired cell mediated immunity, such as advanced HIV. Recently, disseminated MAC infection has been reported in otherwise healthy individuals with impaired functioning of the interferon-gamma (IFN-γ) pathway, particularly Asian populations. In patients with anti-IFN-γ autoantibodies, rituximab has been used successfully to treat refractory cases. Case Presentations: Case 1: A 44-year-old Filipina woman presented with five months of constitutional symptoms, lymphadenopathy, elevated liver enzymes and pancytopenia. She was found to have disseminated MAC involving her lungs, liver, bone marrow and lymph nodes. Initial immunodeficiency work-up including HIV-1/2 antibodies was negative. Autoantibodies to IFN-γ and IL-17a were positive. She was treated with daily azithromycin, ethambutol and rifabutin but had clinical and microbiological progression at four months. Rituximab was initiated with immediate symptomatic improvement. Case 2: A 53-year old previously healthy Cambodian woman presented with nausea, vomiting, and abdominal pain, and was found to have disseminated intra-abdominal MAC. Autoantibodies were positive to IFN-γ. She was treated with parenteral azithromycin, rifampin, amikacin and moxifloxacin, but failed to respond. After three months without improvement, rituximab was added with good clinical response. Case 3: A 52-year Filipino man with a history of non-typhoidal salmonella bacteremia presented with cough, back pain and constitutional symptoms, and was found to have disseminated MAC involving the lungs, lymph node and bone. Autoantibodies to IFN-γ were positive. He is currently on azithromycin, ethambutol and rifabutin with clinical response to therapy at five months. Conclusion: We present the first reported cases of disseminated MAC associated with anti-IFN-γ autoantibodies in Canada. Refractory disease was common and improved with rituximab therapy. These cases illustrate the importance of investigating the IFN-γ pathway in otherwise healthy patients with disseminated NTM disease.
SP53

WITHDRAWN
Effect of Repeat Sampling on *Escherichia coli* Detection Rates in Private Well Water in Ontario: 2010-2017

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**Background:** Approximately 1.5 million individuals in Ontario are supplied by private wells. Unlike municipalities, private well water quality remains unregulated; therefore, owners are responsible for testing, treating, and maintaining their own systems. It is estimated that contamination of private wells is responsible for approximately 80,000 cases of acute gastrointestinal illness per year in Canada, highlighting their significant impact of this water source on human health. **Methods:** Well water sample submission data from 2010-2017 were analyzed for *Escherichia coli* (*E. coli*) to study the relationship between sampling frequency and *E. coli* detection rates in Ontarian private wells. Detection rates were further analyzed relative to geological (consolidated and unconsolidated aquifers) setting to determine how hydrogeology impacts *E. coli* detection (via transport). Power curves were used to estimate the number of samples required to achieve a number of sentinel detection rates (e.g. 25%, 50%, 75%). **Results:** Province wide, 897,378 samples were analyzed, with detection rates found to increase in concurrence with sample number per well. Power curves indicate that a 50% detection rate (i.e. *E. coli* present at least once in half of sampled wells) would occur if each well were sampled 12 times. Statistically significant differences were found between detection rates in consolidated and unconsolidated aquifers (p = 0.00023), highlighting geological structure highlighting geological differences and their potential impact on well water contamination. In consolidated aquifers, *E. coli* were detected in 2.1% of wells sampled once and 6.2% of those sampled twice. In unconsolidated aquifers, significantly more samples are required to achieve analogous detection rates. **Conclusions:** A site specific approach is required for private well testing recommendations in Ontario. Current practises (e.g. ≤1 test per annum) put well owners at risk of exposure to waterborne pathogens, likely due to a poor understanding of pathogen occurrence and movement in and to groundwater sources.
Practice Variability of Gram-Negative Bacteremias

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Objective: There has been evolving literature on appropriate duration and step down to oral therapy for treatment of Gram-negative bacteremias. The primary objective of this study was to describe the practice variability in management of uncomplicated Gram-negative bacteremias in patients who did and did not have an infectious diseases (ID) consult. Methods: This was a retrospective cohort study of adult patients admitted to hospital between December 2014–2017 with a bacteremia secondary to non-multiple drug resistant Gram-negative bacteria. Exclusion criteria included death, discharge, or change to palliative status within 48 hours of positive culture. Febrile neutropenia patients were also excluded. In addition to descriptive statistics, chi-square test, Wilcoxon two-sample test, and Student t test were done as appropriate. Results: Sixty-one patients were enrolled, with 24.6% (n=15) having an ID consult. Average age was 68.7±15.3 years, with 45.9% (n=28) being male. Community-acquired bacteremia was most common (61.7%, n=37), followed by hospital (20.0%, n=12) and long-term care (18.3%, n=11) associated infections. The most common microorganism was Escherichia coli (n=31) followed by Klebsiella pneumoniae (n=7), with genitourinary source the most frequent etiology (n=31). Piperacillin/tazobactam was the initial antibiotic in 49.2% (n=30) of patients. Total days of therapy averaged 16.1±5.4 versus 13.3±3.7 in patients with and without an ID consult, respectively (p=0.087). The percent of total therapy provided intravenously was 52.7% in the ID consult group versus 44.5% in those without a consult (p=0.1334). Both mortality in-hospital (p=0.5637) and readmissions to hospital at 30 days (p=0.1763) were not statistically significant between groups. Conclusions: Practice patterns in regards to total duration of therapy and proportion of therapy provided intravenously were similar in patients with uncomplicated Gram-negative bacteremias with and without an ID consult. The majority of patients were treated initially with broad spectrum agents with total durations longer than 7 days.
PBP3 mutations and β-lactam resistance in β-lactamase Negative (BLN) Ampicillin (Amp) Resistant (BLNAR) Haemophilus influenzae (HI) strains from Eastern Ontario: EUCAST Penicillin (Pen) screen for detection PBP3 amino acid substitution

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Objective: Susceptibility testing of HI is problematic and does not correlate well with PBP3 mutations in BLNAR strains. We tested BLN HI strains for the presence of recognized PBP3 mutations and evaluated the EUCAST Penicillin screen test for predicting Amp resistance.

Method: Amplification products of part of the ftsI gene of PBP3 for 120 BL negative HI was sequenced as previously described and compared to the ftsI gene of the parent Rd strain. Screening for PBP3 mutations using the 1U Pen disk was performed as per EUCAST. Broth microdilution by Sensititre (Thermofisher, CA) was performed as per CLSI. Results: There were 57 BLN HI with no amino acid substitution (AAS) in ftsI and for 63 there were 20 AAS patterns organized into 9 groups. The common AAS R517H and N526K were present in 3/40 and 39/40 strains respectively with reduced Amp susceptibility (median MIC 1μg/mL). The sensitivity, specificity and agreement of the Pen screen to predict PBP3 AAS was 95%, 93% 92% respectively. For 32/40 Pen screen positive isolates the Amp MIC was 0.5 – 2.0μg/mL, for 1 >8μg/mL and for 7 ≤0.25μg/mL. Of these 4 (10%) isolates were non-susceptible (intermediate or resistant) to Amp by CLSI or EUCAST interpretations respectively. Conclusion: The Pen screen test was accurate at predicting the presence of one or more AAS. Although isolates with AAS had reduced susceptibility to Amp compared to wild type strains the clinical relevance of these mutations is not clear since 90% of the BLN strains with a PBP3 mutation were susceptible to Amp by broth microdilution. However, the Pen screen test would be a rapid and cost effective approach for screening HI from sterile sites for Amp resistance for further susceptibility testing.
Meningitis after Ventricular Shunt Operations: Multicenter Study to Identify Etiology, Incidence and Risk Factors

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Background: Surgical site infection associated with shunt placement, treatment for hydrocephalus, is the most common complication and cause of morbidity and mortality. The objective is to answer three questions: a) What is the risk of meningitis after ventricular shunt placement? b) What are the risk factors for meningitis? c) What main microorganisms cause meningitis? Methods: Data based on NHSN/CDC protocols were collected between Jul/2015-Jun/2018 from 12 hospitals at Belo Horizonte, Brazil. Outcomes: meningitis, hospital death and total length of hospital stay. We evaluated 26 independent variables by univariate and multivariate analysis. Sample size= 926. Results: 71 cases of meningitis were diagnosed (risk = 7.7% [I.C.95% = 6.1%;9.6%]). Mortality rate in patients, without infection was 10% while hospital death of infected patients was 13% (p=0.544). Hospital length of stay in non-infected patients (days): mean = 21, median = 9, std.dev. = 28; hospital stay in infected patients: mean = 34, median = 27, std. dev. = 37 (p=0.025). Three main risk factors were identified by logistic regression model: age beneath two years (Odds Ratio – OR = 3.20;p<0.001), preoperative hospital length of stay greater than four days (OR = 2.02;p=0.007) and four days post hospital admission, the risk of meningitis is increased from 9% to 18% (p=0.026). From 71 meningitis, in 45 (63%) the etiologic agent was identified: Staphylococcus aureus (33%), Staphylococcus epidermidis (22%), Acinetobacter sp (7%), Enterococcus sp (7%), Escherichia coli (7%), Pseudomonas sp (7%), and other (18%). Conclusion: Two intrinsic risk factors for meningitis post ventricular shunt (under two years old and multiple surgeries), and one extrinsic risk factor, preoperative length of hospital stay, were identified. Incidence of meningitis decreases when patients receive urgent surgical treatment.
**Echinococcus multilocularis** Causing Disseminated Alveolar Echinococcosis in Patient Presenting with Focal Seizures

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**Background:** Alveolar echinococcosis (AE) caused by the tapeworm *Echinococcus multilocularis* is endemic to Canada. While human infection is rare, most cases of AE in humans present in the liver. We describe a rare case of disseminated AE in a patient who presented with focal seizures. **Methods:** A case encountered in clinical practice is presented. **Results:** A 74-year-old woman from Saskatchewan presents with focal seizure involving the right hand and face. There is no history of travel outside of the province. The patient has regular contact with hunting dogs. Brain imaging reveals a multicycstic mass in the left frontal lobe measuring 28 x 12 x 28 mm with surrounding edema (Figure A). The patient undergoes work-up for potential malignancy revealing multiple cystic lesions in the liver, spleen, kidneys, and pancreas. Open biopsy of the brain lesion is reported as meningioma. Three weeks post-biopsy the patient develops worsening right hemiplegia. MRI brain reveals the left frontal lobe mass has tripled in size (Figure B). Near-complete surgical excision is performed. Histopathology initially queries neurocysticercosis; tissue polymerase chain reaction returns positive for *Echinococcus multilocularis*. The patient is placed on long-term albendazole therapy with periodic imaging to monitor residual lesions. **Conclusion:** *Echinococcus multilocularis* is a parasitic infection endemic to Canada. Diagnosis is based on appropriate history and examination in addition to imaging. Definitive diagnosis can be made by histopathology and molecular confirmation. Complete surgical excision (where possible) and medical therapy are essential to halting further progression of disease. Consideration of the diagnosis is essential to guide proper management and avoid improper technique sampling of lesions which can cause worsening of the disease.
A Common IncI1 Plasmid Encoding bla\text{CMY-2} Affects Growth Rates and the Proteome in \textit{Salmonella} Heidelberg

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\textbf{Background:} \textit{Salmonella enterica} serovar Heidelberg is the third most frequently isolated serovar in Canada and is of particular interest due to its resistance to the cephalosporin class of antimicrobials. Through national surveillance of Canadian \textit{S. Heidelberg} isolated from poultry and human infections we previously demonstrated that human and animal derived isolates were genetically similar (ST15), and that structurally similar IncI1 plasmids harbouring the \textit{blaCMY-2} gene were predominantly responsible for cephalosporin-resistance. Here, we focus on the impact of a well-characterized and widely disseminated IncI1 plasmid (p12-2460) on the core-physiology of a \textit{S. Heidelberg} isolated from the Canadian national surveillance.

\textbf{Methods:} The plasmid was transferred via conjugation to a susceptible and previously whole-genome sequenced (WGS) \textit{S. Heidelberg} isolate (N13-01291). Illumina WGS was performed on the parent and transconjugant to monitor genetic alteration introduced during conjugation. Growth curves were conducted in technical triplicate over 24-30 hr periods under various conditions including growth at 37°C, 30°C, or 42°C in Luria-Bertani broth, and growth at 37°C in M9 minimal media. For proteomic analysis, proteins were extracted from mid-log phase cultures (OD\textsubscript{600} ≈ 0.6) and trypsin digested overnight. The peptides were then labeled with tandem mass tags, fractionated, and underwent LC-MS/MS analysis.

\textbf{Results:} WGS analysis revealed that the strain pairs were isogenic except for a threonine to serine change in TrmE in the transconjugant. Plasmid p12-2460 reduced the growth rate and maximum cell density under all growth conditions tested, including minimal media, rich media, and different temperatures. 85 chromosomally-encoded proteins had a 2-fold or greater change in the presence of the plasmid. Upregulated proteins included 3 from the Tol/Pal system which is involved in outer membrane integrity and downregulated proteins included 2 porin proteins.

\textbf{Conclusion:} The p12-2460 plasmid conferred a growth disadvantage in various conditions and caused changes in chromosomally-encoded protein expression of the host.
Incidence and Outcome of Community Onset Staphylococcus aureus Bloodstream Infections Between Residents of Tertiary and Non-Tertiary Care Areas

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Objectives: Determinants and outcomes from serious infections may differ between urban residents as compared to those living in rural and remote areas. The purpose of this study was to compare the population incidence and outcomes of Staphylococcus aureus bloodstream infections (SaBSI) among those residing within a primary tertiary care center versus referral/secondary catchment areas. Methods: A population-based surveillance cohort design was used. All residents of the western interior of British Columbia who developed an incident community-onset SaBSI between April 1, 2010 and March 31, 2017 were included. The Kamloops local health area (population 2017, 115,482) was classified as the tertiary region and all other areas of the western interior as the non-tertiary region (population 2017: 67,359). Results: A total of 288 cases of SaBSI were identified for an overall incidence of 23.1 per 100,000/year; the tertiary and non-tertiary rates were 24.1, and 21.5 per 100,000/year, respectively (incidence rate ratio (IRR): 1.1, 95% confidence interval (CI):0.9-1.4, p-value: 0.2). There was an overall increasing incidence observed over the study period and this was similar for both cohorts. The proportion methicillin-resistant Staphylococcus aureus (MRSA) was higher among tertiary versus non-tertiary cases (22.9% versus 13%; p=0.04). Non-tertiary residents were similar to tertiary residents in age (median 64.6 versus 61.9 years; p=0.7), and median Charlson comorbidity scores (1.5 versus 1; p=0.4). The 30-day case-fatality rate was higher among non-tertiary (19%) as compared to tertiary area (12%) residents but this was not statistically significant (p=0.1). Conclusion: Residence within the tertiary catchment area was associated with similar overall incidence and fatality but a higher proportion of MRSA infection.

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**Objective:** Clinical syndromes associated with *Bartonella quintana* infection can be insidious and difficult to diagnose for multiple reasons. Clinically, *B. quintana* can manifest as asymptomatic bacteremia or with subtle subacute constitutional symptoms. The mainstay of literature surrounding *B. quintana* endocarditis is from Europe and developing nations. Herein we describe a case of native valve endocarditis secondary to *B. quintana* in a homeless male with pre-existing valvular disease and undertake a comprehensive literature review of documented *B. quintana* endocarditis in North America. **Methods:** A retrospective analysis via a comprehensive literature search was completed using MEDLINE publications from 1946-present and the PubMed database using the keywords “*Bartonella quintana*” and “endocarditis.” All published cases of *B. quintana* endocarditis from North America underwent content analysis and data reduction in an attempt to identify common characteristics. Such cases were analyzed while redundant cases were excluded. **Results:** Twelve patients (median age 52 (IQR 44-56, 83.3% male) each had an episode of *B. quintana* endocarditis. Of the 7 cases where outcome was known, one patient died and six were cured. All cases of *B. quintana* endocarditis had aortic valve involvement whereas only three cases had pre-existing valvulopathies. Of those with *B. quintana* endocarditis, 16.7% were HIV positive, 50.0% were homeless and 63.5% met criteria for alcohol abuse. In 8 patients who received antibiotics, median duration of therapy was 122 days (IQR 42-172) with 58.3% of cases going to surgery. **Conclusions:** This review represents the most up-to-date and comprehensive summary of *B. quintana* endocarditis cases within North America. It should be considered in homeless individuals even without pre-existing cardiac valvulopathy. Outbreaks of asymptomatic chronic *Bartonella* bacteremia within the homeless population coupled with challenges in finances and medication compliance makes infection prevention and control and public health measures important considerations. Surgery is almost always needed for cure.
Clinical spectrum of *Mycobacterium kansasii* infections in British Columbia, 2006-2018

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**Objective:** *Mycobacterium kansasii* is considered as more pathogenic amongst non-tuberculous *Mycobacteria* species (NTM). We aimed to characterize clinical and microbiological features of *M. kansasii* cases in B.C. **Methods:** Retrospective chart review was conducted on patients with positive *M. kansasii* cultures from 2006 to 2018. Student’s T-test and Fisher’s exact test were used for statistical analyses. **Results:** There were 48 cases of *M. kansasii* infection, of which 43 had clinical information available. Twelve patients (28%) underwent treatment; median duration was 12 months. Of the 8 patients with known follow-up, 6 reported clinical improvement, 1 did not improve, and 1 one was always asymptomatic. Between the treated and untreated cases, there were no statistically significant differences in respiratory and constitutional symptoms, radiographic findings or underlying lung disease (Table 1). The most common reasons for not treating *M. kansasii* infection were absent/improved symptoms (10 of 21), or severe comorbidities precluding therapy (7 of 23). The latter trended towards significance (p=0.07) as compared to treated group. All three isolates with susceptibility testing were sensitive to rifampin. Empiric anti-mycobacterial regimens were chosen for the remaining patients. **Conclusion:** *M. kansasii* infection in B.C. is uncommon and few diagnosed patients receive therapy. Isolates tested to date are susceptible to rifampin, but most clinicians choose treatment regimens empirically. **Table 1:** Characteristics of treated and untreated cases of *M. kansasii*. Subset of cases where information was available indicated in brackets.

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<th>Treated (n=12)</th>
<th>Untreated (n=31)</th>
<th>P-value</th>
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<tr>
<td>Mean Age</td>
<td>69</td>
<td>69</td>
<td>0.94</td>
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<tr>
<td>Male gender</td>
<td>67%</td>
<td>48%</td>
<td>0.33</td>
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<tr>
<td>Baseline respiratory symptoms</td>
<td>83%</td>
<td>87% (21 of 24)</td>
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<tr>
<td>Baseline constitutional symptoms</td>
<td>42%</td>
<td>27% (6 of 22)</td>
<td>0.46</td>
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<td>Radiographic findings of NTM disease</td>
<td>75%</td>
<td>44% (13 of 29)</td>
<td>0.10</td>
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<tr>
<td>Underlying lung disease</td>
<td>67% (6 of 9)</td>
<td>80% (20 of 25)</td>
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<td>Severe comorbidities</td>
<td>0%</td>
<td>30% (7 of 23)</td>
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<td>Smear positivity</td>
<td>42%</td>
<td>35%</td>
<td>0.74</td>
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A Case Report of Dengue Neonatal: the Concern About Vertical Transmission in Endemic Areas

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Background: Dengue is an arboviral infection of worldwide importance, mainly transmitted by the mosquito Aedes aegypti, found in tropical and subtropical regions of the world.

Objective: To report a case of neonatal dengue as a differential diagnosis with neonatal sepsis, which must be considered in endemic areas. Clinical case: This case report is a male newborn, 9 days old, full term, weighing 3400 grams at birth, admitted to the Emergency Room with fever, jaundice, and rash. Mother with suspected chikungunya. The neonate presented severe thrombocytopenia (64000 platelets / mm$^3$), increased C-reactive protein and positive anti-dengue immunoglobulin M (IgM). This last result was possible only after six days at the hospital. During this period, the neonate was treated with ampicillin and gentamicin according the Institution protocol of neonatal sepsis. After 8 days of hospital stay, the patient was discharged under medical guidelines. Conclusions: The reported cases in the literature show the importance of suspecting the disease in pregnant women, since even when the risk of vertical transmission is low, the prevalence of congenital infection could generate an important demand of health services in endemic areas of the disease. Given the epidemiological situation of dengue in the world and the possibility of complications of the disease, this report emphasizes the importance of the pediatrician to be aware of the possibility of vertical transmission of the virus. With a high index of suspicion, early diagnosis, close monitoring, timely intervention and critical consideration, a successful outcome is possible.
SP65

WITHDRAWN
Clinical Spectra of Non-O157 Shiga Toxin Producing *Escherichia coli* (STEC) Detected by the Hamilton Regional Lab Medicine Program Using a Molecular Assay

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**Objectives:** Compare the incidence of O157 STEC and non-O157 STEC detected using a multiplex enteric PCR versus culture methods and describe the clinical characteristics of patients diagnosed with non-O157 STEC. **Method:** Stool specimens submitted from June to November 2018 from the Hamilton-Niagara Region and North Toronto underwent multiplex bacterial PCR. The molecular targets used were STX1, STX2 and *E. coli* O157. A retrospective chart review of patients with O157 and non-O157 STEC was performed using a standardized data extraction form. **Results:** Out of a total of 2795 stool specimens tested, 26 (0.93%) were positive for STEC. Of the 26, 20 (76.9%) were non-O157 and 6 were O157. Serotyping was available for some isolates, and included O 113: H4, O26:H11 and O118:H2. In 2017, out of 2795 stool specimens tested by routine culture, four were positive for *E. coli* O157: H7. There were no non-O157 STECs detected since only sorbitol MacConkey agar plates were used for culture and many non-O157 STEC ferment sorbitol. Clinical information was available for 11 patients of which 9 were positive for non-O157 STEC. Patients ranged in age from one year three months to 86 years. Several of these patients were < 18 years. Clinical information included: bloody stools in 6 (54.5%), acute kidney injury in 2 (18%), fever in 2 (18%), Hemolytic Uremic Syndrome in 1 (9%). There was travel history in only one patient with non-O157 STEC. Four patients (36.3%) received antibiotics for treatment of diarrheal symptoms before receiving PCR results. **Conclusions:** In patients presenting with bloody diarrhea a diagnosis of STEC infection should be considered, especially among pediatric patients and antibiotics should be avoided until laboratory confirmation is obtained. Non-O157 STEC infections are more common than O157 and laboratories that do not routinely detect non-O157 STEC will miss the majority of STEC infections.
SP67

WITHDRAWN
There's more than meets the eye: the Hawthorne effect and hospital hand hygiene compliance

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Background: Direct, overt observations are the current gold standard for evaluating hand hygiene (HH) compliance rates. However, the Hawthorne Effect affects the accuracy of these values. The aim of this study was to quantify the contribution of the Hawthorne Effect on HH compliance rates at a tertiary care teaching hospital by comparing HH rates from covert and overt direct observations by indication for HH, and across healthcare profession groups, hospital areas, and clinical programs. Methods: Covert HH observations were made by two students over a two-month period at the Royal Alexandra Hospital in Edmonton, Alberta. Students received the same training as HH reviewers performing overt observations but were disguised as hospital staff to ensure they could move freely throughout the units without being questioned. Overt observations were simultaneously occurring on the same units. Compliance was defined as appropriate hand washing with either alcohol-based hand rub or soap and water during one of the four moments of HH as per the Alberta Health Services provincial guidelines (based on the Canadian Patient Safety Institute guidelines). Results were assessed using the two-tailed Fisher’s exact test, with a significance level of P<0.05. Results: There were a total of 3,078 covert observations on 27 inpatient units and the Emergency Department. Overall compliance was 57.9% (1,782/3,078). There were 26,253 overt observations over the previous 12-month period with a compliance rate of 86.4% (22,683/26,253; P<0.05). The covert HH compliance rates were significantly lower for each moment of HH, across healthcare profession groups and clinical programs, and in different hospital units. Conclusion: The Hawthorne Effect contributed to a 28.5% overestimation of HH compliance rates using overt observations. This must be considered both when interpreting HH data using the overt method, and when considering subsequent interventions to improve HH rates.
Two Cases of Alveolar Echinococcosis in Southwestern Canada

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Alveolar echinococcosis (AE) is a life-threatening disease caused by the zoonotic cestode Echinococcus multilocularis. In North America, Echinococcus multilocularis infection is rare, with only three reports of autochthonous cases of AE outside of Alaska and Northern Canada in the literature. We describe two cases of locally acquired AE in southwestern Canada, which, in combination with cases in dogs and high prevalence in Saskatchewan wildlife, suggest that a more pathogenic strain of the parasite may be expanding geographically.

Two patients presented within a month to the Infectious Disease service in our centre. The first case was a male with a history of chronic lymphocytic lymphoma identified with an enlarging liver mass. After biopsy revealed pathology consistent with AE, the mass was surgically resected, and the diagnosis confirmed by duplex PCR based on nad1 and rrnS loci. Peritoneal metastases were identified at surgery and the patient is currently on indefinite albendazole.

The second case was a female on long-term immunosuppression for a previous diagnosis of transverse myelitis. Further, she had a prior diagnosis of primary biliary cirrhosis based on liver biopsy. The liver mass was identified incidentally after she presented with pyelonephritis. A biopsy was done, and histopathology was identical to the first case. She was placed on albendazole and the lesion was treated with microwave ablation.

Neither patient had a history of travel to a region endemic to AE, and both patients reside in a similar area in southwestern Canada. The source of their infections has not yet been identified.

Although lack of AE reporting makes it challenging to assess incidence of this disease, its geographic distribution appears to be expanding and diagnosis can be elusive. AE should therefore be considered in immunosuppressed patients with liver masses in Canada, even when there is no travel history to endemic areas.
Patient Perspective on Hepatitis C Treatment Barriers and Delay

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Background: Hepatitis C (HCV) is a viral illness that infects about 1% of the Canadian population. Recently, there have been positive strides in improving treatment and at mitigating barriers to treatment such as opening treatment options to all individuals despite their level of liver fibrosis. Methods: This is a qualitative study using interview style surveys to understand the patient perspective of their HCV treatment delay before the change in policy. Convenience sampling was used to interview 15 patients about their risk factors, when they were diagnosed and whether or not they were treated for HCV. We compiled answers into various themes. Interviews were conducted from October 2017 until February 2018. Results: Of the 15 study participants, 13 were male and 2 were female. All patients were above the age of 40. Out of the sample, 9 were not undergoing treatment despite having HCV. Patients were allowed to give multiple reasons for their HCV treatment delay. The most common self-reported reasons were addiction to recreational substances, their disease not being progress enough, and too much paperwork. Conclusion: This study brings to light a different perspective when discussing HCV treatment barriers and delay. Our findings conclude that there is a need for greater education in those that engage in risky behaviours that increase risk to HCV infection. Similarly, education should be targeted at changing risky behaviours after diagnosis to avoid reinfection.
SP71

WITHDRAWN
Correlation between the MIC of Vancomycin and Those of Other Agents against Methicillin-susceptible Staphylococcus aureus Recovered from Bloodstream Infections

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Objective(s): The minimum inhibitory concentration (MIC) of vancomycin has been used as a marker for the response to anti-staphylococcal penicillins in methicillin-susceptible \textit{Staphylococcus aureus} (MSSA) bacteremia. This study evaluated whether an increase in vancomycin MIC in MSSA isolates would be associated with a concurrent rise in the MIC of the other antibiotics used to treat MSSA bacteremia, including telavancin, daptomycin, oxacillin and cefazolin. \textbf{Methods:} 305 MSSA strains recovered from hospitalized patients with bacteremia were tested for their susceptibility to vancomycin, telavancin, daptomycin, oxacillin and cefazolin by the Etest according to the manufacturer's instructions. MIC range, MIC mean, MIC\textsubscript{50}, MIC\textsubscript{90} and MIC\textsubscript{100} for all antibiotics tested were recorded, and data was categorized according to vancomycin MIC (0; 0.75; 1.0; 1.5; and 2.0) or oxacillin MICs (0.038, 0.094, 0.125, 0.19, 0.25, 0.38, 0.5, 0.75, 1.0, and 1.5) to evaluate the effect on MICs to other antibiotics tested. \textbf{Results:} When the MICs of the comparator antibiotic stratified by vancomycin MIC, a positive association in both means and ranges of telavancin and daptomycin were noted, but no associated was seen between vancomycin and oxacillin or cefazolin. However, when MSSA isolates were stratified by oxacillin MICs, the MICs for cefazolin followed the same trend, but not telavancin or daptomycin. \textbf{Conclusions:} This experiment proved a rise in vancomycin MIC of MSSA is associated with a parallel rise in the MIC of telavancin and daptomycin, and that an increase in MIC to oxacillin in associated with a parallel rise in MIC to cefazolin. Physicians should be aware of these associations when treating MSSA with increasing MICs to vancomycin or oxacillin. Clinical outcomes analyses are underway in cases fitting MSSA bacteremia with elevated MICs to vancomycin or oxacillin.
Mistaken Malignancy: A Case of *Streptococcus anginosus* Causing Osteomyelitis and an Extra-osseous Mass

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**Objectives:** *Streptococcus anginosus* is a common pathogen known to cause abscesses in various body systems. However, osteomyelitis is a rare manifestation and *S. anginosus* causing an extra-osseous mass has not been described. **Methods:** We present a case of a 62-year old immune-competent male with left thigh pain, fevers and constitutional symptoms. He had an elevated leukocyte count at 22x10^9/L and CRP of 200mg/L. A MRI found an 18cm mass along his left femur initially thought to be a malignant sarcoma or lymphoma. The diagnosis was questioned when initial biopsy was negative for malignancy cells and showed chronic inflammation. **Results:** Repeat biopsy of his extra-osseous femoral mass was culture positive for *Streptococcus anginosus*. Fungal and mycobacterial cultures, along with serology for HIV, Hepatitis, Syphilis were negative. He was initially treated with intravenous Ceftriaxone and received a percutaneous drain insertion. Ultimately, the patient underwent an en-block resection of his femur with sequestrectomy of the bone and antibiotic cement placement.
Conclusions: We present to our knowledge the first case of a solidified extra-osseous mass caused by *S. anginosus*. This was initially mistakenly diagnosed as a presumptive malignant tumour. Through this case, we review the common causative agents for osteomyelitis as well as the rare complications from streptococcal osteomyelitis.
Severity of Coronavirus Respiratory Infections in Adults Admitted to Acute Care

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**Background:** Recently, the WHO has highlighted the need for improved epidemiological surveillance and a better understanding of the health burden imposed by non-influenza RNA respiratory viruses. Human coronaviruses (CoVs) are a major cause of respiratory and gastrointestinal infections with associated morbidity and mortality. The objective of our study was to characterize the epidemiology of CoVs in our tertiary care health centre, and identify clinical correlates of disease severity. **Methods:** Nasopharyngeal and mid-turbinate swabs and bronchoalveolar lavages were tested for CoVs (OC43, 229E, NL63 and HKU1) by multiplex PCR (\textit{xTAG RVP}, \textit{xTAG RVP FAST v2} or RPP, Luminex). Demographic and clinical data was obtained from the charts of patients admitted between 2010 and 2016, and a univariate analysis was performed. A number of variables consistent with a severe disease burden were evaluated and included (but not limited to): patient outcome, ICU admission, number of symptoms and length of stay. **Results:** During our study period CoVs represented 11.2\% (542/4660) of all positive respiratory virus samples. OC43 was the most commonly identified CoV, followed by 229E, NL63 and HKU1. In contrast to what has been reported in US-based studies, no co-infections with multiple CoVs or other respiratory viruses were detected. The average length of stay for our cohort was 13.5 days, and it was noted that 17.5\% required admission to the ICU (mean ICU admission time = 13 days). Interestingly, increased number of symptoms was found to correlate with ICU admission (OR 1.293, 95\% CI 1.019-1.640). Overall mortality in our cohort was 7\%, although no statistically significant difference in mortality or ICU admission was associated with any specific CoV strain. **Conclusions:** This study highlights the underappreciated burden of CoVs in a hospital setting and suggests that more comprehensive study of CoV infections at the provincial and national level is necessary.
Development and validation of Loop-Mediated Isothermal Amplification (LAMP) assay for detection of Trichomonas vaginalis (TV) directly from vaginal swabs: A rapid, simple, sensitive and cost-effective alternative.

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Objectives: To develop and evaluate the performance of a LAMP assay for detecting Trichomonas vaginalis (TV) in vaginal swabs and compare to microscopy and PCR.

Method: We used 150 selected e-swab vaginal specimens sent for routine TV microscopy at the Hamilton Health Sciences and 7 External Quality Assurance specimens. For LAMP assay, 100µl e-swab fluid was mixed with 100µl lysis solution, then boiled for 10 mins and 5µl of the extract was used as template. A 182bp fragment of TV-specific repeated DNA sequence was amplified. LAMP was carried out at 65 °C for 30 mins using a standard reaction mixture. Amplification was detected using SYBR® Green in a Genie® II instrument. The Cut-off detection time was ≤25 min. Limit of detection (LOD) was determined, using known concentrations of serial dilutions of TV culture. For PCR, 200µl e-swab liquid was extracted and eluted in 55µl buffer using easyMag and 10µl was used for PCR. Two PCR methods were used for comparison. An LDT PCR amplified a 96bp 18S rDNA using QuantiTect® SYBR® Green-PCR Kit. The Altona RealStar® Trichomonas vaginalis PCR Kit 1.0 was used according to the Results: 45 clinical and 6 EQA specimens were positive for TV by LAMP and both PCRs. There was no discordance between LAMP and PCR. Only 15 of 45 LAMP/PCR positives (33.3%) were positive by microscopy. The LAMP LOD was 10³ organisms /ml. The turn-around-time for LAMP is under 1 hour as compared to 3 hours for PCR. Conclusion: Detection of TV by LAMP and PCR is more sensitive than microscopy. The performance of LAMP is comparable to PCR. However, LAMP is faster and more cost-effective than PCR. This assay provides promising results for accurate and faster detection of TV compared to PCR at a lower cost.
INCUBATOR POSTER VIEWING AND PRESENTATIONS  
Thursday, April 4 and Friday, April 5, 2019  
Room: Confederation Ballroom  
IP01 – IP09  
Viewing Dates & Times: Thursday, April 4, 2019 12:30 – 14:30; 17:00 – 19:00, Friday, April 5, 2019 11:00 – 14:00 *all posters will be up for both days  
Presenting Dates & Times: Thursday, April 4, 2019 12:30 – 14:30

IP01  

**Appropriate Antibiotic Prescribing Module - How to Choose Which Drug to Use**

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**Objective:** Antibiotics are a class of medication which can be challenging for medical students to learn, as microbiology and pharmacology must be learned in addition to the diagnostic component of infectious disease content. A learning need was identified by pre-clerkship medical students for supplemental learning material on antibiotics to complement didactic lectures in the pre-clerkship curriculum. **Methods:** A module covering common antibiotic classes was created to assist pre-clerkship medical student learning. Objectives were developed to guide student learning. They include recalling spectrum of activity, mechanism of action, and adverse reactions of antibiotic classes covered, as well as selecting treatment on a case-by-case basis, based on patient-specific factors. The module was designed to optimize recall of information through the use of mnemonics, questions, cases and a historical description of antibiotic design as it pertains to spectrum of activity for β-lactam antibiotics. A post-module evaluation was conducted to determine the opinion of twenty-five pre-clerkship medical students. Eight questions used a 1-5 Likert scale and two questions assessed student opinion on module strengths and areas for improvement. **Results:** Responses to quantitative questions ranged from 4.3 to 4.6, with “amount of detail” scoring lowest and “recommending module to others” scoring highest. Areas for improvement included adding more cases to provide a broader range of difficulty and including more information on certain classes. Strengths included mnemonics, simplified spectrum of activity, and review questions and cases. **Conclusion:** The module received positive feedback and evaluation results were used to make changes to improve the module for future students. Additions include more clinical cases, more information on certain antibiotics, and appendices to summarize module topics. The module is available to undergraduate medical students online to be used as a supplemental learning tool.
A Point-of-Care Diagnostic Tool to Replace Chest X-Ray for the Diagnosis of Childhood Pneumonia

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Background: Pneumonia is the leading cause of mortality in children under 5 years globally and a major cause of hospitalization of Canadian children. Accurate diagnosis is critical for the appropriate and judicious use of antibiotics, and is challenging in contexts without easy access to a chest x-ray (CXR). In low-income settings, identifying children with pneumonia at high risk of mortality is important when allocating scarce resources. Novel solutions for pneumonia diagnosis are required in these settings. Objectives: Our team identified novel biomarkers for childhood pneumonia, including chitinase-3-like-1 (CHI3L1), lipocalin-2 (LCN2), tissue inhibitor of metalloproteinase 1 (TIMP1) and surfactant protein-D (SP-D) in several African cohorts. These are newly described putative biomarkers for diagnosis and prognosis for pneumonia and could be incorporated into a point-of-care diagnostic test.

Methods: 114 children with WHO-defined pneumonia presenting to two hospitals in Jinja and Kambuga, Uganda were enrolled. Plasma samples were obtained and analyzed via ELISA to measure serum host-response biomarkers: CHI3L1, LCN2, TIMP-1, SP-D and C-reactive protein (CRP). Results: We identified a novel marker, CHI3L1, with strong predictive value (93% sensitive and 81% specific) for the detection of primary endpoint pneumonia. In combination, these biomarkers are strongly predictive for chest x-ray consolidation, with 80% probability with all five biomarkers above threshold, and less than 10% probability with no biomarkers above threshold. In a separate cohort of children from Uganda with hypoxic pneumonia, we found that CHI3L1 and LCN2 distinguish between children with lobar consolidation vs no consolidation. Conclusions: These newly identified biomarkers are strongly predictive of chest x-ray consolidation in children. Applied to a point-of-care diagnostic mechanism, these biomarkers could transform pneumonia diagnosis in low-resource settings across the globe.
Figure 1. Used in combination, five novel biomarkers discriminate between radiographic pneumonia and normal chest x-ray in Ugandan children with clinical signs of lower respiratory tract infection. When all five biomarkers are elevated, the probability of lobar consolidation is \( \sim 80\% \); when none are elevated, the probability is less than 10\%, demonstrating the clinical utility of these biomarkers.
Rapid and Sustained Adoption of a Novel Antimicrobial Stewardship Mobile App throughout Saskatchewan

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Background: Smartphones are ubiquitous amongst clinicians and smartphone apps are increasingly being used to support clinical decision making. Spectrum is a novel, mobile antimicrobial stewardship app that can be customized to deliver local guidelines, pathogen information, antimicrobial information and local antibiogram data. Spectrum was launched in the Saskatoon Area of the Saskatchewan Health Authority on April 12, 2018. Objectives: To study the user engagement and most commonly accessed content of Spectrum over a seven-month period in the Saskatoon Area of the Saskatchewan Health Authority. Methods: The number of active users and sessions, use by healthcare profession and location, daily user engagement time, and accessed content sections categorized by guidelines, pathogens and antimicrobials was analyzed. Results: Seven months following the launch of Spectrum, there were 744 active users (Figure 1) with an average daily user engagement time of two minutes and forty-two seconds. Active users were composed of the following healthcare professions: physician (28.1%), pharmacist (23.8%), resident/fellow (20.0%), nurse practitioner/registered nurse (11.8%), medical student (9.8%) and other (6.5%). In November 2018, there was a total of 2418 Spectrum sessions and an average daily Spectrum usage rate of 1.4 sessions per user (Figure 1). The most commonly accessed guidelines were urinary tract infection (20.1%), community-acquired pneumonia (14.7%) and non-purulent cellulitis (8.3%). The most commonly accessed pathogens were Enterococcus faecalis (10.0%), Escherichia coli (8.1%) and Klebsiella pneumoniae (5.1%). The most commonly accessed antimicrobials were ceftriaxone (9.2%), ciprofloxacin (7.7%) and piperacillin-tazobactam (7.2%). Conclusions: Spectrum has been widely used amongst healthcare professionals throughout Saskatchewan and its sustained usage supports this innovative app being an effective, localized antimicrobial stewardship tool in providing clinical decision support.
Figure 1. Number of active users (solid line) and number of sessions per user (dotted line) of Spectrum over a seven-month period.
Leveraging an Electronic Medical Record System to Reduce High Blood Culture Contamination Rates in the Emergency Department of a Large Community Hospital

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Objective: International standards recommend blood culture contamination (BCC) rates be continuously monitored and not exceed 2-3%. False-positive results lead to unnecessary Emergency Department (ED) call-backs, hospital admissions, increased length-of-stay, inappropriate antimicrobials use and increased costs Blood cultures (BC) are frequently drawn in our ED by nursing staff, where there is no dedicated phlebotomist; the ED contamination rate was calculated to be 4.6%. To address the high rate of BCC, a quality improvement (QI) project was initiated to implement strategies to reduce BCC to the acceptable benchmark. Methods: A multidisciplinary QI team was assembled. A retrospective chart review established the baseline BCC rate from April 1- June 31, 2018, using the standard definition provided by Institute for Quality Management in Healthcare. The hospital implemented a new electronic medical record system (EPIC), which provided the specific individual who drew every BC. Those individuals with BCC rates >3% were directly observed and provided education. Education focused on collection technique, identifying opportunities for contamination when deviating from best practice, and discussing negative resulting outcomes. For the next 3-months (July 1 to September 31, 2018) individuals received feedback when their rate was > 3% and the BCC rates was shared corporately. Results: The frequency of BCC in the ED in the 3 months prior to the QI initiative was 4.6% (range 3.6–5.3). Following individual feedback and education, the rate was reduced to 3.1% (range 2.8-3.5) over the subsequent 3-months representing a statistically significant decrease of 31% (p < 0.05, Chi-square analysis). Direct observation identified a large variation in practice. By calculating individual rates, we identified one clinician whose collection technique was responsible for 40% of BCCs. Conclusion: BCC rates were successfully reduced by leveraging an EMR system to track individual contamination rates. This allowed direct observation and education in the prevention of BCC.
Creation of an evidence-based background for developing a comprehensive scoring system for targeted admission screening for colonization with carbapenemase-producing organisms (CPO)

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Introduction: Identification of CPO carriers at admission is critical for hospital transmission risk mitigation; however, no standardized cohesive approach exists for admission screening practices. Objectives: Our objectives were to (1) review available literature; (2) collect and appraise criteria recommended by various studies/organizations to identify the greatest at-risk population; (3) create an evidence-based background for developing a comprehensive scoring system for targeted admission screening. Methods: PubMed, EMBASE, Web of Science, and Cochrane Library (January 2000 to August 2018) were searched. Retrospective and prospective cohort and case-control, cross-sectional studies, reviews, local, regional and international guidelines were included. The criteria identified were categorized into three main clusters: healthcare interaction (international, domestic hospitalizations, procedures, transfers, etc.), epidemiological (high-risk unit admission, contact with CPO, etc.) and individual (history of CPO, general health status, immunosuppression, etc.) factors. Frequencies of various criteria appearing in the literature were calculated. Results: Twenty studies from 10 different countries with various CPO endemicity levels were analyzed. Three studies (15%) utilized criteria from all three clusters. Healthcare interaction factors only were used by 5 studies (25%), epidemiological factors only by 3 (15%), and individual factors only by 4 (20%). Two studies (10%) concluded that CPO admission screening is not needed at all. The most common criteria used were international hospitalization within the last 12 months (n=9, 45%), previously receiving care in/transferred from CPO-prevalent areas/facilities (n=6, 30%), and current admission to a high-risk unit (n=5, 25%). A risk scoring system was proposed based on these factors. Conclusions: Criteria for CPO admission screening vary considerably across jurisdictions with different CPO endemicity levels. Assigning criteria with different weights and ranks, correlation with local epidemiological patterns and individual test results, and further development and subsequent validation of a comprehensive scoring system will help to most accurately identify the greatest at-risk population for targeted CPO admission screening.
The Real-World: Opportunities and Challenges of Pragmatic Implementation Studies for Tackling Infectious Diseases for Vulnerable Populations

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**Background:** Novel approaches will be required to tackle infectious diseases for vulnerable populations and best practices remain unclear. Pragmatic embedded study design, in real-world settings, will likely be imperative to understanding these complex health system changes. Most academic organizations have rigorous processes for evaluating clinical trials, however there remains a knowledge gap with pragmatic study designs that may substantially impair the ability to conduct research in a timely and meaningful manner. Our objective is to describe the challenges and solutions of pragmatic study design approval in the context of an HCV elimination strategy. **Methods:** A prospective evaluation and health outcomes research plan has been integrated into Nova Scotia’s HCV elimination strategy. Two previously described tools will be implemented and evaluated in Phase 1 of the strategy: training providers in motivational interviewing and point of care testing. During the 24 month development of Phase 1, barriers and solutions to ethics approval, as well as the estimated temporal impact on research progression, were determined. **Results:** Three main challenges were identified during the ethics submission for the implementation and design of the pragmatic embedded study: 1) Potential for informed consent in vulnerable individuals; 2) Scientific validity of synonymous interventions; and 3) Lack of pragmatic embedded study design knowledge. Ethics board education on pragmatic trials and extensive re-consultation before resubmission were key to addressing concerns. This iterative process of ethics submission took approximately 18 months compared with an average time of less than 2 months for non-pragmatic trials within our group. **Conclusions:** To successfully tackle infectious diseases for vulnerable populations evaluation of methods in complex, real-world settings involving pragmatic study designs are required. It is important to include pragmatic study training resources to investigators and institutional ethics boards when developing coordinated elimination strategies to reduce delays associated with adoption of newer research tools for elimination.
Using toys’ humanoid robots to get better hand hygiene compliance

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**Background:** Even nowadays compliance with hand hygiene practices is still unacceptably low. In this study we want to answer three questions: a) How to adapt a toy robot as an instrument of continuous education of healthcare workers? b) What is the effectiveness of the use of a humanoid robot to improve hand hygiene performance? **Methods:** MeccaNoid G15KS, a humanoid robot 122 cm tall, it was released as a toy in the beginning of 2015. It can be purchased for less than US$ 200. It is a programmable robot mainly designed to interact with children. It became “he” when MeccaNoid was baptized Ozi res, in honor of the Brazilian engineer Ozires Silva, from Embraer. The robot was adapted with mini projector, an automatic alcohol hand sanitizer dispenser, and an audio amplifier. The mini projector allows video lessons even in small rooms. Ozires, accompanied by infection control practitioners, performs short video-lecture presentations and own reports of the institution’s data regarding infections and the hand hygiene rate, working from 10 to 15 minutes in each target sector. Ozires was engaged as a hand hygiene improvement strategy in two hospitals from Belo Horizonte, Brazil: Hospital-A: Hospital-A (Jan-Nov/2016) and Hospital-B (Jul/2017-Dec/2018). **Results:** After the insertion of Ozi res in three ICUs of Hospital-A, hand hygiene rate increased from about 36%, between January-July, to 65% in August-November/2016. In all months of 2017, consumption of alcohol preparation remained above 20 ml/patient-day, the minimum expected consumption recommended by the World Health Organization. Hospital-B: Ozires started his lectures in May/2018. Hand hygiene adherence increased from about 23%, between July and December/2017, to 60% in June-December/2018. **Conclusion:** We succeeded in adapting a toy robot as instrument of continuous education of healthcare workers, creating a new education tool, a robot tutor. Hand hygiene compliance raised significantly after the intervention in both hospitals.
Diagnostics for the Discrimination of Viral and Bacterial Infections in a Cohort of Children Hospitalized for Respiratory Infection

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Background: Lower respiratory tract infections (LRTI) prompting hospitalization are common in Paediatrics. Children with a bacterial cause for their illness should be given antibiotics, however establishing microbiological diagnoses is challenging. Molecular testing can reliably identify viral pathogens in nasopharyngeal swabs (NPS) but viral-bacterial coinfections are common and no criteria reliably identify bacterial pneumonia. Consequently, diagnostic tools that distinguish between bacterial and viral infections would be useful. Our aim was to investigate salivary C-reactive protein (CRP) and quantitative pneumococcal NPS carriage.

Methods: In this prospective study, we enrolled a convenience sample of previously healthy children hospitalized with LRTI between October 2015 and December 2018. Only those with respiratory signs/symptoms and fever (unless diagnosed with bronchiolitis) were eligible. Participants were categorized as: bronchiolitis, asthma exacerbation, uncomplicated pneumonia, pneumonia complicated by effusion, or indeterminate. S. pneumoniae NPS density was quantified via PCR. CRP levels were assayed in serum and salivary swabs.

Results: There were 118 eligible participants. The median age was 1.8 years (25-75%ile 0.6-4.4 y). Forty-nine (42%) participants had bronchiolitis or asthma, 47 (40%) had pneumonia or an ‘indeterminate’ diagnosis, and 22 (19%) had complicated pneumonia. Overall, 24% of participants had no respiratory virus detected, including 8% of the bronchiolitis/asthma group, 26% of the pneumonia/indeterminate group, and 55% of the complicated pneumonia group. There was no difference in pneumococcal NPS density seen between groups, though 26% of participants received antibiotics for >24h before collection. Serum CRP correlated with salivary CRP and varied significantly between groups, with highest values in complicated pneumonia and lowest in bronchiolitis/asthma. Conclusions: In children with LRTI, pneumococcal carriage was not associated with bacterial pneumonia. Serum and salivary CRP were correlated and were lowest in children with viral disease. Salivary CRP merits further study as a non-invasive test to identify those at low risk for serious bacterial infection.
Results of Introducing a Lab Developed Molecular Assay for Bacterial Enteric Pathogens that Includes Detection of STEC and *Escherichia coli* O157 on the BD MAX

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**Objective:** To replace enteric culture with a Lab Developed Test (LDT) for *Salmonella, Shigella, Campylobacter, Yersinia enterocolitica, Escherichia coli* O157 and the stx1 and stx2 genes of STEC (shiga toxin producing *E.coli*).

**Methods:** Validation compared culture to the LDT and used the BD Max IVD Enteric Panel for discordant resolution. Starting June 4th 2018, we tested exclusively with the molecular assay. The LDT is a Taqman multiplex in a two tube format. The base is Luna Universal Probe qPCR Kit (New England Biolabs). TNA2 strips are loaded on the BD Max with both master mixes and neutralization buffer. Sample buffer tubes are inoculated with 5ul stool in Cary Blair transport medium (Para-Pak™ Enteric Plus, Meridian Bioscience). BD Max extracts the nucleic acid, sets up the PCR and analyzes the results. **Results:** There was an increase in detection by PCR for *Salmonella, Shigella, Campylobacter* and *Yersinia* vs culture. The ratio of non-O157 STEC to O157 STEC was 23:6 from 3491 specimens (as of January 7, 2019). A method of isolating these strains was introduced. Culture of STEC was performed on Colorex STEC (CHROMagar, Paris France produced by Dalynn Biologicals, Canada). If the Colorex was no growth, the specimen was cultured to Urine Orientation agar (BBL). *E.coli* colonies were isolated to blood agar for identification and stx typing by singleplex PCR. A serogrouping PCR based on O antigens was done from the isolation. Various serogroups were detected including O26, O103, O118 and O113. **Conclusion:** Molecular methods are more sensitive than culture for enteric pathogens. Molecular methods that detect STEC allow a greater appreciation of disease burden caused by these organisms vs O157:H7. The use of Chromogenic media to isolate STEC is recommended. The development of a typing PCR may permit rapid detection of local outbreaks.