

JAMMI

Official Journal of the Association of Medical Microbiology and Infectious Disease Canada
Journal officiel de l'Association pour la microbiologie médicale et l'infectiologie Canada



AMMI Canada – CACMID Annual Conference

March 30–April 2, 2016 • Vancouver, British Columbia

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ORAL PRESENTATIONS

Thursday, March 31, 2016

11:15 – 12:15 Session A
Room: Port McNeill

A01

VALIDATION OF LOWER IDENTIFICATION CUT-OFF VALUES FOR IDENTIFICATION OF *CANDIDA* SP. BY BRUKER BIOTYPER™ MALDI-TOF USING EXTENDED DIRECT TRANSFER METHOD**P. Lagacé-Wiens^{1,2}, HJ Adam^{1,2}, P Pieroni¹, M Stein^{1,2}, C Turenne¹, A Rendina¹, J Carlson¹, J Terrick¹, C Espenell¹, J Karlowsky^{1,2}**¹Diagnostic Services Manitoba; ²University of Manitoba, Winnipeg, MB

OBJECTIVES: MALDI-TOF has been shown to be an accurate method for the identification of yeasts in the clinical microbiology laboratory. Using the Bruker MALDI Biotyper™ and applying the manufacturer's recommended cut-offs, identification is secure to species if the confidence score is 2.0 or above and identification is secure to the genus if the score is between 1.7 and 1.999. However, secure species-level identification of *Candida* species using these cut-off values typically requires a time-consuming and labour intensive tube extraction protocol as scores obtained by either the direct transfer method or extended direct transfer method fail to provide scores ≥ 2.0 . The purpose of this study was to determine the accuracy of a lower cut-off score for the identification of *Candida* spp. to reduce the need for additional biochemical testing or tube extraction.

METHODS: We performed parallel identification of 202 *Candida* spp. isolates from 12 different species using 1) The extended direct transfer method (a sample of a yeast colony is directly transferred to the steel target plate, mixed with 1 μ L of 70% formic acid, and overlaid with HCCA matrix) and 2) The tube extraction method (the yeast is subjected to extraction by serial washes and centrifugations in ethanol, formic acid, and acetonitrile). We compared the accuracy of results between the two methods and determined an optimal cut-off score for identification using the extended direct transfer method. Discordant results were resolved with biochemical testing using API AUX20 or Vitek™ YST cards.

RESULTS: 100% accuracy was achieved with a cut-off value as low as 1.4. However, minimal benefit in terms of reduced extra testing was observed with cut-off values lower than 1.7. A cut-off value of 1.7 maintained 100% accuracy while reducing the requirement for additional testing or tube extraction for species-level identification by 95%.

CONCLUSIONS: Using the extended direct transfer method, a cut-off score of 1.7 maintained 100% accuracy of identification while nearly eliminating the need of any additional testing.

A02

RETROSPECTIVE STUDY INVESTIGATING THE SEROPREVALENCE OF *ANAPLASMA PHAGOCYTOPHILUM* IN MANITOBA, 2011-2015**K Kadkhoda^{1,2}, A Gretchen¹**¹Cadham Provincial Laboratory; ²Department of Medical Microbiology; Department of Immunology; University of Manitoba, Winnipeg, MB

OBJECTIVE: *Anaplasma phagocytophilum* is an intracellular bacterium transmitted by black legged ticks. Despite prevalence studies in ticks and dogs, to date, there have been no studies done with an objective to investigate the sero-prevalence of *A. phagocytophilum* among humans in Canada. This study was designed and performed to fulfil the above-mentioned objective.

METHODS: A total of 446 residual serum samples submitted to Cadham Provincial public Health Laboratory from 2011 to 2014 for either organ donor screening or Lyme serology testing were de-identified and tested for *A. phagocytophilum* IgG and IgM using indirect immunofluorescence assay. Sera were screened at 1:64 dilution for specific IgG and the results were converted into titres defined as the reciprocal of the highest dilution giving at least 1+ fluorescence signal. For the IgM (where needed) the initial dilution was 1:20. There were several cohorts based on the previous C6 peptide ELISA and Lyme immunoblot blot results for the sera that were initially submitted for Lyme serology testing.

RESULTS: The positivity rates were: 3.89% for donors cohort, 15.93% for negative C6 cohort, 28.57% for low C6 (antibody index < 4) cohort, 30.76% for high C6 cohort, 34.78% Lyme immunoblot IgM+ cohort, and 28.37% for Lyme immunoblot IgG+ cohort. Geometric mean titre (GMT) was also calculated for each cohort. All cohorts (tick-exposed) vs. donors' and C6-positive vs. C6-negative cohorts showed statistically significant difference in positivity rates the latter two also showed significant difference in GMTs. The highest GMT (calculated among *Anaplasma* IgG-positive sera) was 378.06 in Lyme immunoblot IgM+ cohort (range: 64-2048); the latter also showed *Anaplasma*-specific IgM positivity rate of 82.25%.

CONCLUSION: This study demonstrates that sero-prevalence of *A. phagocytophilum* in at least one of the Lyme endemic regions in Canada is relatively high among tick-exposed individuals that merits further attention from both clinical and public health perspective.

A03

QUAKING INDUCED CONVERSION FOR CJD DIAGNOSIS**R Vendramelli¹, A Sloan¹, K Cheng^{1,2}, JD Knox^{1,2}**¹Public Health Agency of Canada; ²University of Manitoba, Winnipeg, MB

BACKGROUND: Creutzfeldt-Jakob Diseases (CJD) are rare, untreatable, uniformly fatal brain disorders. The highly heterogeneous nature of clinical presentation makes these conditions diagnostically challenging. Currently, the concentrations of certain proteins in cerebrospinal fluid (CSF) are used in the diagnostic investigation of CJD. Increased levels of these surrogate markers are consistent with a diagnosis of CJD, but they have variable sensitivity and specificity and consequently cannot be used to definitively diagnose CJD.

METHODS: At the molecular level the normally expressed cellular prion protein, PrP^c, interacts with the infectious form of the prion protein, PrP^d, which promotes its conversion to the infectious form. A new approach to the pre-mortem diagnoses of CJD exploits the ability of PrP^d to promote the conversion of PrP^c to PrP^d. In this method, known as quaking induced conversion (QuIC), a recombinant PrP (rPrP) made in the laboratory is used as the substrate and patient CSF samples, potentially containing PrP^d, are tested to see if they will 'seed' the conversion process. Cycles of shaking and incubation will cause infected CSF, containing PrP^d, to generate greatly increased amounts of rPrP^d facilitating subsequent detection by traditional methods.

RESULTS: In a retrospective study, CSF samples from 43 pathologically confirmed cases of CJD and 46 non-CJD CSF samples were subjected to QuIC analyses. Two variations of the QuIC method were used and both demonstrated an ability to detect the CJD positive samples in this cohort with specificities and sensitivities in excess of 90%. These results are compared and contrasted to the diagnostic sensitivity and specificity generated by an analysis of the surrogate markers on the same samples.

CONCLUSIONS: An ability to directly detect the etiologic agent represents a major advance in the diagnoses of CJD that will aid health care workers as well as patients and their families in dealing with suspected cases of CJD.

A04

EARLY IDENTIFICATION AND SUSCEPTIBILITY TESTING OF POSITIVE BLOOD CULTURES USING THE WASP™/ WASPLAB™ AUTOMATION SYSTEM AND MALDI-TOF VITEKMS™ AND VITEK2 SUSCEPTIBILITY INSTRUMENT

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OBJECTIVES: Rapid identification and susceptibility testing of positive blood cultures (BC) improves patient outcomes and is integral to antimicrobial stewardship. Optimization of workflow using the WASP™/ WASPLab™ (Copan) automation system to process, incubate, and read positive blood cultures was evaluated. The accuracy of identification of the MALDI-TOF VitekMS (MS) and susceptibility testing using the Vitek2 GN/GP card with early growth at 6 hours was assessed and compared to standard protocol.

METHODS: A total of 203 positive BC (BacTAlert™, BioMerieux) at the Hamilton Regional Laboratory Medicine Program microbiology laboratory were included. Blood samples were manually transferred to a Copan blood culture tube (BC+). The BC+ tubes were loaded on the WASP using a protocol which included gram smear, streaking of blood agar (BA), chocolate (CHOC) and MacConkey (MAC) plates and incubation in a CO₂ WASPLab™ smart incubator (WASPL) with automated digital imaging of the plates at 4, 6, 12 and 18 hours. Plates with any amount of growth at 6h were called out of the smart incubator and identification was performed using the MS. If adequate growth, sensitivities were performed using Vitek2 GP65 and N208. Plates were then loaded back into WASPL. Gram stain results, identification and sensitivity results were compared to the routine procedures.

RESULTS: Growth (haze to moderate) was detected in 43%, 93%, and 99% at 4, 6 and 12h respectively. Using 6h growth, 94% were identified accurately by MS and 5.6% were unidentified. In 9 polymicrobial cultures, 1 organism was identified. Susceptibility testing with 6 h growth, showed 100% essential and categorical agreement (EA, CA) for gram positive organisms except for clindamycin and coag negative staph (CA 57%). For gram negative bacilli, EA and CA were 99.1 and 99%. Two VME occurred with *E coli* to pip-tazobactam and co-trimoxazole. The BC+ tube was easy to use and the ease of scheduling the early read times using the WASPL optimized incubation and organization of work. Single sample processing with barcodes avoids errors in transcription and erroneous sampling.

CONCLUSIONS: Early identification and susceptibility testing at 6 hours using the WASP /WASPLab automation with VitekMS and Vitek2 is an accurate and efficient method to support antimicrobial stewardship and facilitate patient care.

as per CLSI M27-S4 broth microdilution method and interpretation guidelines for fluconazole (FLUC), and micafungin (MICA). Epidemiological cut-off values of ≤2 mg/L for amphotericin B (AMB) and 0.5 mg/L for voriconazole (VORI) against *C. glabrata* (CG) were used in the absence of M27 breakpoints.

RESULTS: Of 333 *Candida* spp. collected, *C. albicans* (CA) was predominant (46.8%), followed by *C. glabrata* (CG, 22.8%), *C. parapsilosis* (CP, 12.0%), and *C. tropicalis* (5.1%). The majority of cases were identified in ICU (35.8%), medicine (38.3%), and surgical wards (13.9%). Susceptibility (S) values are shown in the table below and limited acquired resistance was detected.

ID	No. Isolates	MIC90 (%R)				
		AMB	ITRA	FLUC	VORI	MICA
CA	156	0.5 (0)	0.03 (0)	0.5 (0)	0.03 (0)	<0.007 (0)
CG	76	0.5 (0)	0.5 (-)	8 (0*)	0.12 (3.2)	0.015 (0)
CP	40	1.0 (0)	0.12 (-)	2.0 (0)	0.06 (0)	1.0 (0)

ITRA, itraconazole; *, susceptible dose-dependent; -, no clinical breakpoint

CONCLUSION: CANWARD surveillance of invasive *Candida* isolates since 2011 indicates that the distribution of species and antifungal MICs in hospitalized patients remains stable, and that resistance is very uncommon. Consistent with practice guidelines, these data demonstrate that new cases of candidemia, which are presumed to reflect patients naive to recent antifungal exposure, are predictably caused by common species that are highly susceptible to antifungal agents.

B02

DIAGNOSIS OF CRYPTOCOCCUS GATTII INFECTION IN BC, 1999-2007

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OBJECTIVE: *Cryptococcus gattii* (Cg), an environmental fungus, has become endemic in BC with 267 culture-confirmed cases reported between 1999-2015. Our objective was to assess the methods used to diagnose this infection in BC.

METHODS: Medical records were reviewed for Cg patients diagnosed in BC in 1999-2007.

RESULTS: Among 152 patients, 105 (69.1%) had lung infection only (LIO) and 47 (30.9%) CNS infection. This included 41 probable cases (culture-negative, not immunocompromised) whose diagnosis was based upon histopathology, microscopy, or antigen detection. A total of 111 (73.0%) cases were culture-confirmed, 68 (61.3%) had LIO and 43 (38.7%) had CNS infection. Among culture-confirmed cases, respiratory tract cultures were positive from sputum in 48.8% (20/41), bronchoalveolar lavage (BAL) in 84.8% (50/59), percutaneous fine needle aspirate (FNA) in 87.5% (14/16), and lung biopsy in 84.6% (11/13). Spinal fluid (CSF) cultures were positive for 87.5% (35/40) of CNS cases who had a lumbar puncture. Cg was isolated from blood (5), and from 1 patient each in urine, bone, pleural fluid, and brain. Serum cryptococcal antigen (SCRAG) titre was determined in only 47.3% (72/152) of cases, whereas CSF CRAG was tested in 75% (30/40) of CNS cases with an LP. SCRAG titre was ≥1:8 in 71.4% (30/42) of cases with LIO (median titre 1:384), compared to 96.7% (29/30, p-value 0.0058) with CNS infection (median titre 1:1024). CSF CRAG titres were ≥1:1 in 100% (30/30) of cases with CNS infection (median titre 1:512). The median intervals from symptom onset to report of diagnostic tests for CNS infection and LIO were 43 and 55 days, respectively.

DISCUSSION: Invasive pulmonary diagnostics (BAL, FNA, or lung biopsy) had higher yield for culture of Cg compared to expectorated sputum. Increased utilization of SCRAG may facilitate earlier diagnosis of Cg infection in patients with a compatible clinical presentation.

11:15 – 12:15 Session B
Room: Port Alberni

B01

ANTIFUNGAL SUSCEPTIBILITY OF INVASIVE CANDIDA ISOLATES FROM CANADIAN HOSPITALS: RESULTS OF THE CANWARD 2015 STUDY

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OBJECTIVE: CANWARD is an ongoing national surveillance study that assesses pathogens causing infections in patients admitted to Canadian hospitals, as well as determines the prevalence of antimicrobial resistance (R) in these isolates. Here we present the antifungal susceptibility data for candidemia isolates collected in 2015.

METHODS: *Candida* species isolated from bloodstream infections were collected from 12 participating medical centres during the 2015 study period. Antifungal susceptibility testing and interpretation was performed

B03

EVALUATION OF THE IMMY CRYPTOCOCCAL LATERAL FLOW ASSAY COMPARED TO THE MERIDIAN CALAS™ LATEX AGGLUTINATION AND THE IMMY LATEX AGGLUTINATION IN IMMUNOCOMPROMISED PATIENTS AT HAMILTON HEALTH SCIENCES AND ST. JOSEPH HEALTHCARE HAMILTON

L Dalle Vedove¹, J Todd¹, R Marsh¹, D Yamamura^{1,2}

¹Hamilton Regional Laboratory Medicine Program; ²McMaster University, Hamilton, ON

OBJECTIVES: *Cryptococcus neoformans* is an important pathogen causing disease in immunocompromised patients and more recently, *C. gattii* has become an increasing important pathogen in immunocompetent patients. Detection of antigen using Latex agglutination (LA) is commonly used; however, the assay is labour and time consuming. The performance of the IMMY Cryptococcal antigen lateral flow assay (CrAg) was compared to the Meridian CALAS™ latex agglutination (CALAS) and IMMY latex agglutination (LA).

METHOD: Archived specimens previously tested with CALAS or LA were tested using CrAg. Serial positive samples were tested to compare titre results. For the CrAg, 1 drop of diluent was mixed with 40 µl of specimen; an immunochromatographic dipstick was inserted, incubated for 10 minutes and then read as positive or negative. A semi-quantitative titration procedure was performed with a modification to the manufacturer's instructions to change from a 1:5 initial titre to 1:4 titre. Manufacturer's instructions were followed for the CALAS and LA. Agreement between the methods was compared. Discordant results were evaluated by comparing to culture results and clinical features.

RESULTS: Sixty samples (47 serum, 13 SF) were tested:

		IMMY CrAg Lateral Flow	
		+	-
Meridian CALAS or	+	38	0
IMMY LA	-	4	18

Discordant results occurred in 4 specimens (2 patients) with negative CALAS. Repeat testing with CALAS was positive in ¾ specimens. Both patients were culture positive, had previous positive CALAS results and were on maintenance fluconazole. Titre results for CrAg vs CALAS were identical (n=4) or 1, 2 or >2 doubling dilutions higher for 4, 6, and 4 specimens respectively. Serial titres in two immunocompromised patients with invasive disease were persistently positive (8 months and 1 year).

CONCLUSION: IMMY CrAg lateral flow is a sensitive assay with increased detection of antigen at lower titres compared to the CALAS. Titres are ≥2 doubling dilution higher in 50% of samples. This simple method can be performed in a general microbiology laboratory with rapid availability of results.

B04

ANTIFUNGAL SUSCEPTIBILITY OF RESPIRATORY ASPERGILLUS ISOLATES FROM CANADIAN HOSPITALS: RESULTS OF THE CANWARD 2015 STUDY

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OBJECTIVES: CANWARD is an ongoing national surveillance study that assesses pathogens causing infections in patients attending Canadian hospitals, as well as determines the prevalence of antimicrobial resistance in these isolates. Here we present the distribution of species and *in vitro* antifungal susceptibility of *Aspergillus* isolates collected in 2015 from patients visiting Canadian hospitals.

METHODS: Clinical *Aspergillus* isolates recovered from respiratory specimens at 14 participating medical centres during the 2015 study period were tested against amphotericin B (AMB), itraconazole (ITRA), posaconazole

(POSA), voriconazole (VORI) and caspofungin (CASP) by broth micro-dilution using the CLSI M38-A2 method. Growth endpoints were measured as per CLSI M38-A2 and values above the published epidemiological cutoff values (mg/L) were scored as non-wildtype (non-WT). Clinical breakpoints are not available for *Aspergillus* susceptibility interpretation.

RESULTS: Of the 834 *Aspergillus* isolates recovered, *A. fumigatus*, *A. niger*, *A. flavus*, *A. nidulans*, and *A. terreus* represented 65.0%, 11.0%, 7.2%, 2.4%, and 1.7% of the population, respectively. *A. fumigatus* isolates were recovered primarily from sputa (60.0%) and bronchoscopy (31.2%) specimens of Clinic outpatients (55.7%), and inpatients admitted to Medicine (28.8%) and Critical care (10.1%) services. *A. fumigatus* exhibited WT MIC/MEC values against AMB, ITRA, POSA and CASP while five isolates (4.1%) had non-WT MICs of 2 mg/L against VORI. Non-WT azole MICs were also detected in *A. niger* (5.4%) and *A. flavus* (7.1%). There was very little evidence of microbiological resistance to echinocandins across the species. Eight *A. calidoustus* isolates from five centres were recovered, all exhibiting resistance to the azoles (MIC >16 mg/L) and CASP (MEC 2 to 4 mg/L).

CONCLUSION: This study marks the fourth consecutive year for CANWARD surveillance of *Aspergillus* respiratory tract isolates in Canadian hospitals. *A. fumigatus* was the most prevalent species across hospital sites and specimen sources and the *in vitro* activity of azole and echinocandin agents against *A. fumigatus* remains very high.

11:15 – 12:15 Session C
Room: Finback

C01

TRENDS IN ANTIBIOTIC UTILIZATION FOR URINARY TRACT INFECTIONS IN THE PROVINCE OF BRITISH COLUMBIA, CANADA

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INTRODUCTION: Guidelines for the treatment of urinary tract infections (UTIs) in the community and adaptation to observed resistance patterns can impact antibiotic prescribing practices. The goal of this study was to assess trends in antibiotic utilization for UTIs over an 18-year period in British Columbia, Canada.

METHODS: Anonymized, line-listed data on all BC outpatient oral antibiotic prescriptions entered in the BC PharmaNet database from 1996 to 2013 were obtained. Analysis of indication-specific utilization data for UTIs (including cystitis, pyelonephritis, prostatitis, symptoms involving urinary system, and other disorders of urethra and urinary tract) were conducted by linking PharmaNet records to diagnostic data from physician payment files. Drug utilization rates were derived using the BC population and expressed per 1000 persons per day (e.g. defined daily doses per 1000 inhabitants per day, DID)

RESULTS: Proportionate use of specific drugs to treat UTIs has changed substantially since 1996. Among UTIs overall, a 338% increase in nitrofurantoin use and a 67% decrease in sulfamethoxazole and trimethoprim use since 1996 have been observed. Ciprofloxacin use decreased 17% between its peak year in 2007 and 2013. Although representing little proportional use, cefixime use has risen substantially since 2010. Similar trends in nitrofurantoin, ciprofloxacin, and SMX-TMP use were noted for cystitis alone; however, ciprofloxacin use for pyelonephritis remains proportionally high. Overall utilization rates for UTIs have increased 25% between 1996 and 2013 and remain substantially higher among patients aged 60 years and older (2.3 DID in 2013) compared to all other age groups (< 1.2 DID in 2013).

CONCLUSIONS: Although favourable shifts in treatment of UTIs have been observed, increased use in antibiotics overall, particularly among those 60+, may warrant targeted interventions.

C02

ANTIMICROBIAL STEWARDSHIP PROGRAMS REDUCE DAILY PRESCRIBING VARIABILITY IN ACADEMIC ICUS

L Dresser^{1,2}, **J Hughes**^{3,4}, **M McIntyre**¹, **S Nelson**³, **N Ferguson**^{1,3,5}, **S Lapinsky**^{3,5}, **N Lazar**^{1,5}, **S Mehta**^{3,5}, **L Burry**^{2,3}, **J Singh**^{1,5}, **C Bell**^{1,3,5}, **AM Morris**^{1,3,5}

¹University Health Network; ²Leslie Dan Faculty of Pharmacy, University of Toronto; ³Mount Sinai Hospital; ⁴York University; ⁵Faculty of Medicine, University of Toronto, Toronto, ON

OBJECTIVES: Antimicrobial stewardship programs (ASP) aim to optimize antimicrobial therapy through knowledge translation and changing prescribing behavior. ASPs have demonstrated an impact on consumption but the influence on prescribing patterns has not been measured.¹ Our objective was to examine the impact of an ASP on the variation in daily antimicrobial use before and after implementation of prospective audit and feedback (PAF) rounds in three academic medical-surgical intensive care units.

METHODS: ASP PAF rounds were introduced February 2009 in ICU 1, December 2009 in ICU 2 and October 2010 in ICU 3. In each ICU, the ASP PAF rounds initially occurred 5 times per week and decreased to 4 times and then 3 times per week after years 1 and 2 respectively. We analyzed daily aggregate consumption of antibiotics, measured in Defined Daily Doses (DDD) per patient day from January 2008 to December 2014. Interrupted time-series analysis was used to detect effects of ASP implementation on drug use. Autoregressive moving average (ARMA) models accounted for temporal autocorrelation and non-stationarity in drug consumption.

RESULTS: Prior to introduction of an ASP there was substantial variation in antibiotic use among days of the week at sites 1 and 3 ($p_1=0.008$, $p_2=0.694$, $p_3<0.001$). At sites 1 and 3 PAF rounds were associated with a significant decrease in daily variability ($p_1<0.001$, $p_3<0.001$). At sites 1 and 2, there was an overall decrease in antibiotic use ($p_1=0.001$, $p_2=0.044$). At site 3 variation in antibiotic use among weekdays decreased substantially ($p_3<0.001$). Changing the frequency of PAF rounds did not demonstrably alter variation among weekdays ($p_1=0.938$, $p_2=0.171$, $p_3=0.052$), or overall drug use ($p_1=0.364$, $p_2=0.499$, $p_3=0.738$) over the time period examined.

CONCLUSIONS: ASP PAF rounds in academic ICU's were associated with decreased variability in prescribing patterns. This impact was sustained over time and with a decrease in intervention frequency.

REFERENCE

Kaki R, Elligsen M, Walker S, Simor A, Palmay L, Daneman N. (2011) Impact of antimicrobial stewardship in critical care: a systematic review. *J Antimicrob Chemother* 66: 1223-1230.

C03

STRIBILD AND DARUNAVIR EVALUATION (STRIDE): A NEW STANDARD IN SALVAGE THERAPY

S Vafadari, **S Hakobyan**, **T Raycraft**, **G Kiani**, **S Sharma**, **B Conway**
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OBJECTIVE: Historically, patients who have received multiple antiretroviral regimens have been placed on more complex regimens termed "salvage therapy." These regimens are often multi-class, multi-tablet regimens with issues of drug interactions, side effects, and reduced adherence. The availability of potent single tablet formulations may provide us with the opportunity to simplify such salvage regimens, while maintaining long-term efficacy.

METHODS: We have evaluated 31 HIV-positive patients with complex prior treatment histories in whom we have simplified therapy to Stribild with or without Darunavir. These patients attended an inner-city tertiary clinic, had received 2 or more prior regimens, and did not demonstrate resistance to any prescribed agents (archived resistance to lamivudine and emtricitabine were allowed). Patients were followed quarterly.

RESULTS: Patients in this cohort had a mean of 7.4 prior regimens, with 4 (12.9%) being switched due to ongoing virologic failure, 10 (32.2%) requesting simplification, 4 (12.9%) with medication-associated toxicity, and 13 (41.9%) for other reasons. Within this cohort, 19 (61.3%) were started on Stribild, 12 (38.7%) received Stribild/Darunavir. The median follow-up period was 413 (range 157-804) days. After the switch, all 31 (100%) had suppressed VL below 400 copies/mL (range <40-154) and 26 (83.9%) had VL<40 copies/mL. There was a mean CD4 cell count increase

of 63 cells/ μ L. During treatment, 13 (41.9%) were actively using illicit drugs, all of whom had virologic suppression and 9/13 (69.2%) consistently below 40 copies/mL. Of 14 patients with archived M184V mutations conferring resistance to 3TC/FTC, all had maximal virologic suppression.

CONCLUSION: The STRIDE approach should be considered in all patients on complex salvage regimens as a tool for simplification and enhanced maintenance of long-term efficacy. A clinical trial to evaluate this approach more formally is planned.

C04

LESSONS LEARNED FROM A NATIONAL ANTIBIOTIC AWARENESS PILOT CAMPAIGN IN CANADA

C Soon, **I Smylie**, **J Arthur**

Public Health Agency of Canada, Ottawa, ON

OBJECTIVES: To improve knowledge and awareness of responsible human antibiotic use in Canada in order improve antibiotic seeking and prescribing behaviours.

METHODS: The Public Health Agency of Canada (PHAC) launched a pilot Antibiotic Awareness Campaign in November 2014 based on evidence of knowledge levels and prescribing behaviours. The campaign featured online and print-based communications and marketing activities designed to improve knowledge, awareness and behaviours relating to antimicrobial resistance (AMR) and antibiotic use among parents of young children and healthcare professionals. A post-campaign survey was conducted to measure knowledge, awareness and behaviours related to antibiotic use.

RESULTS: 765 members of the general public and 352 Canadian physicians completed the survey. The campaign had excellent reach; 50% of physicians surveyed received messages from the Government of Canada on AMR during the campaign period while 13% of the general public surveyed had recently seen ads or messages about the proper use of antibiotics and AMR. Self-reported awareness and knowledge of AMR was high among the general public. Among respondents, 58% could correctly define AMR. Healthcare professionals remain a key source of health information for Canadians. One in five respondents indicated that their doctor or pharmacist had talked to them about AMR when prescribing antibiotics. Among Canadian physicians, overall knowledge on AMR was high with an average of 94% answering AMR-related knowledge questions correctly. Approximately half of physicians indicated that they refer to PHAC to improve their professional knowledge or direct their patients to AMR-related resources.

CONCLUSIONS: Many Canadians remain unaware of the risks associated with misuse of antibiotics and would benefit from more resources on the appropriate use of antibiotics. This is an opportunity to build on the pilot campaign to continue educating Canadians on appropriate antibiotic use and infection prevention and control and to support good antimicrobial stewardship practices among healthcare professionals.

11:15 – 12:15 Session D
Room: Orca

D01

GENOMIC ANALYSIS OF WETLAND SEDIMENT AS A TOOL FOR AVIAN INFLUENZA VIRUS SURVEILLANCE IN WILD WATERFOWL

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OBJECTIVES: Avian Influenza (AI) is a viral disease of chickens and turkeys that has significant negative economic impacts on the poultry industry and can be zoonotic. The reservoir of AI is known to be wild waterfowl, which shed the virus in their feces and spread AI among different geographic locations during their annual migrations. Current surveillance techniques focused on testing individual wild birds for the presence of AI are known to be ineffective. Indeed, these techniques, which were in place prior to a

2014-2015 AI outbreak that affected multiple jurisdictions in Canada and the USA, failed to detect the presence of AI in waterfowl in advance of domestic poultry cases. The objective of this project was to develop a new AI surveillance approach based on genomic and metagenomics analysis of wetland sediments. Given that waterfowl congregate on wetlands, by testing wetland sediments we may be able to efficiently screen a large number of waterfowl encompassing a wide range of potential reservoir species.

METHODS: During the 2014 BC AI outbreak, sediment samples (n=341) were collected from large wetlands and smaller water bodies on infected farms. After RNA extraction, RT-qPCR for the AI Matrix gene was used to screen samples for the presence of AI. Positive samples are currently undergoing enrichment of AI specific sequences and Next Generation Sequencing to characterize the AI subtypes present.

RESULTS: Among the 300 wetland samples, 23 (7.7%) were positive and 49 (16.3%) were suspect-positive. Among the 41 on-farm samples, 15 (36.6%) were positive and 6 (14.6%) were suspect positive. On-farm sediment testing also revealed the presence of heavy waterfowl-related AI environmental contamination on farms believed to have been infected by wild waterfowl (termed 'independent incursions') but not farms that were infected through indirect contact with other infected farms.

CONCLUSIONS: Preliminary results suggest that this novel technique will be highly effective AI surveillance tool, particularly given that detection rates among individual waterfowl included in the current National Surveillance Program are ~1%. This tool may also help to elucidate how AI is transmitted from wild waterfowl to domestic poultry. Ultimately, our goal is to use sediment surveillance as the cornerstone for a provincial AI early warning system.

D02

MINING FOR AVIAN INFLUENZA VIRUS RNA IN WETLAND SOIL SEDIMENTS

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OBJECTIVES: The monitoring of avian influenza viruses (AIV) is important for poultry farming and human public health. The virus is spread through the secretions of reservoir hosts such as migratory waterfowl. The cost and difficulty of obtaining samples from waterfowl are presently the main impetuses for the search of a new AIV surveillance program such as detection of AIV in environmental samples. This research explores a strategy to detect the virus in soil sediment samples contaminated with wild bird feces. Due to the presence of large amounts of microorganisms and inhibitors in soil sediment samples, this study aims to optimize the extraction of RNA from soil sediment samples for the Matrix gene qPCR detection of AIV.

METHODS: Total RNA from soil sediment samples (n= 40) collected in different wetland sites in British Columbia was extracted using the original (ORK) and/or modified (MRK) protocol of a commercial RNA extraction kit (MO BIO RNA PowerSoil®). Extracted RNA samples were then analyzed by qPCR assay for AIV. In order to address the concern regarding PCR inhibitors (i.e soil inhibitors), a comparison of the ORK plus commercial clean-up kit, ORK plus ethanol precipitation and ORK plus chloroform extraction step (MRK) on soil samples spiked with *E. coli* (EC) DNA was conducted.

RESULTS: All soil sediment samples extracted using ORK were negative for AIV Matrix gene qPCR. The qPCR analyses of EC DNA-spiked samples indicated the presence of PCR inhibitors. The use of ORK plus the commercial clean-up kit led to an increase in the Ct value, whereas the use of ORK plus ethanol precipitation or additional chloroform steps in MRK led to improvements in the Ct value. The qPCR data indicate that additional clean-up steps during RNA extraction can aid in reducing soil inhibitors in extracted samples and may improve qPCR amplification. Consequently, several samples extracted using MRK were found to be AIV

matrix gene positive (n= 7) with Ct values ranging from 32.94-39.28.

CONCLUSIONS: The initial data indicate that the modified protocol of a commercial RNA extraction kit (MRK) can be used to successfully extract AIV RNA in wetland soil sediment samples that are amenable for molecular analyses. Our current work is focused on further optimization and automation of this RNA extraction method for soil samples.

D03

SEROLOGIC FOLLOW-UP OF HEALTHCARE WORKERS (HCWS) EXPOSED TO INFLUENZA A H5N1

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BACKGROUND: In January 2014, the first North American human case of laboratory confirmed Influenza A H5N1 was diagnosed in Alberta, Canada. Previous seroepidemiologic studies raised question about possible asymptomatic infections in HCWs who cared for patients with Influenza A H5N1.

OBJECTIVES: The objective of this study was to determine whether asymptomatic infection occurred among 36 exposed healthcare worker contacts of a patient with Influenza A H5N1.

METHODS: A historical cohort study was carried out, where the 36 HCWs who had cared for the index patient without consistently and/or properly using all recommended pieces of personal protective equipment (PPE) were considered an exposed group. An unexposed control group consisted of 31 HCWs who had cared for the patient using all recommended PPE and 115 HCWs from another facility who had not cared for the index patient. Participants were asked to submit a serum sample for Influenza A H5N1 and seasonal H1N1 (control) serology. Hemagglutination inhibition assays were analyzed according to World Health Organization criteria. Participants also completed a questionnaire to determine other risk factors for past Influenza A H5N1 exposure.

RESULTS: 25 of 36 eligible exposed HCWs and 27 of 31 PPE-wearing HCWs consented to participate and submitted samples. None of the exposed (n=25/36) or control [n=115 + (27/31)] participants tested had reactive Influenza A H5N1 serology.

CONCLUSIONS: Despite incomplete use of PPE in more than half of the HCWs who cared for a patient with Influenza A H5N1, no evidence of asymptomatic infection was detected by serologic follow-up. This finding is consistent with the relatively inefficient transmission described with previously isolated strains of this virus. This study also highlights the need for improved infection prevention practices; including routine HCW point of care risk assessments, and reliable use of appropriate risk-based PPE in the face of potentially novel, emerging or evolving pathogens.

D04

SEROPREVALENCE OF JAMESTOWN CANYON VIRUS IN NOVA SCOTIA

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BACKGROUND: Jamestown Canyon Virus (JCV) is a mosquito-borne arbovirus in the California serogroup (CSG) within the *Bunyaviridae* family. The primary reservoir host is believed to be the white-tailed deer. JCV is an emerging pathogen in North America, implicated in presentations ranging from subclinical illness to meningoencephalitis. Preliminary data demonstrated a high seroprevalence of JCV in white-tailed deer and humans in 2 district health authorities (DHAs) in Nova Scotia (NS).

OBJECTIVE: Determine the areas of highest seroprevalence of JCV among residents of NS.

METHODS: Anonymized residual sera from specimens submitted for diagnostic testing in each DHA in 2012 were randomly selected and screened for JCV antibodies, then subsequently confirmed using plaque reduction neutralization assay (PRNT). A PRNT titre $\geq 1:20$ was considered positive. Additional PRNT endpoint titrations were required in some cases to discriminate between JCV and other CSG viruses. Seroprevalence estimates and 95% confidence intervals (CIs) were calculated using the Clopper-Pearson Exact method. Design weights accounted for regional oversampling in the provincial estimate (SAS v9.4; SAS Institute, Inc., Cary, NC, USA). Population estimates for 2014 were based on Statistics Canada census data.

RESULTS: There were 251 samples across 9 NS DHAs tested. The overall seroprevalence of JCV was 21.2% (95% CI 16.1–27.0). Seroprevalence by DHA ranged from 12.9% to 48.2%, with low rates in DHAs containing NS's two largest urban centres, Halifax and Sydney. DHA 1, located in southern NS had a significantly higher seroprevalence than all other DHAs, at 48.2% (CI 35.1–61.3) vs. 20.5% (CI 14.8–26.2), respectively, with a p-value < 0.05 .

CONCLUSIONS: The seroprevalence of JCV in NS is high, with DHA variation. As there have been no known clinical cases of JCV infection in the province, this suggests the possibility of an under-recognized zoonotic disease in NS.

Friday, April 1, 2016

11:15 – 12:15 Session E
Room: Port McNeill

E01

VALIDATION OF THE FAST-TRACK DIAGNOSTICS BACTERIAL GASTROENTERITIS REAL-TIME PCR ASSAY

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INTRODUCTION: There is an increasing interest in the use of molecular diagnostics for the detection of enteric pathogens to improve turnaround time, streamline workflow, and allow the detection of pathogens missed by routine culture (e.g., non-O157 enterohemorrhagic *Escherichia coli* and *Yersinia enterocolitica*). We evaluated the performance of the Fast-Track Diagnostics multiplex real-time PCR assay for detection of *Salmonella*, *Shigella*, *Campylobacter coli*/*jejuni*/*lari*, enterohaemorrhagic *E. coli* (EHEC), and *Y. enterocolitica*.

METHODS: 131 clinical samples positive for *Salmonella*, *Shigella* spp., *Campylobacter* spp., or O157:H7 EHEC by routine culture, 64 negative stool samples inoculated with EHEC (various serotypes), *Salmonella enterica*, *Campylobacter* spp., *Shigella* spp. or *Y. enterocolitica*, and 8 culture-negative stools were tested using the assay. Limits of detection for each pathogen were determined in triplicate in a matrix of PCR-negative stool. The QIAamp viral RNA mini kit was used for DNA extraction. The PCR was performed according to the kit instructions. Discrepant results were analysed by culture, biotyping, or toxin assay, as required, to determine the source of the discrepancy.

RESULTS: Sensitivity and specificity were very high for all targets (see table).

Target organisms	LOD (CFU/mL)	Initial sensitivity	Initial specificity	Sensitivity post-hoc	Specificity post-hoc
<i>Campylobacter</i> sp.	10,000	94.3%	99.3%	98.1%	99.3%
EHEC	1,000	100%	96.8%	100%	100%
<i>Shigella</i> sp./EIEC	10,000	100%	99.4%	100%	99.4%
<i>Salmonella enterica</i>	1,000	100%	100%	100%	100%
<i>Y. enterocolitica</i>	10,000	55.6%	100%	100%	100%

CONCLUSIONS: The Fast-Track Diagnostics PCR assay for the detection of bacterial enteric pathogens is highly sensitive and specific. False-negative PCR results were largely explained by the recovery on culture of non-pathogenic strains of target organisms and false-positive PCR results by pathogens that were missed by routine culture or the presence of target genes in non-target organisms (e.g., *stx1* in *S. dysenteriae*).

E02

ZIKA VIRUS: A CANADIAN PERSPECTIVE

K Dimitrova, on behalf of the National Microbiology Laboratory's Zika virus team

Zoonotic Diseases and Special Pathogens, National Microbiology Laboratory, Public Health Agency of Canada

Zika virus is a mosquito-borne flavivirus related to Dengue virus which causes an illness in humans characterized by maculopapular rash, fever, myalgia and conjunctivitis. In 2014, Zika virus was first introduced into South America leading to a large outbreak which is currently affecting greater than 30 countries in this region. Of particular concern is the recent evidence of congenital malformations and neurological sequela associated with Zika virus infection. Additional, multiple cases of sexual transmission of Zika virus have been observed. Given that a large number of Canadians travel to the affected regions, it is not surprising that imported cases of Zika virus infections have been documented. This presentation outlines Canada's National Microbiology Laboratories response to Zika virus infection.

E03

PREVALENCE OF GENITAL *C. TRACHOMATIS*, *N. GONORRHOEAE* AND *T. VAGINALIS* AMONG YOUNG ADULTS IN QUÉBEC: RESULTS FROM THE 2013-2014 PIXEL STUDY

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BACKGROUND: Since 2000, the number of reported cases of *C. trachomatis* (CT) and *N. gonorrhoeae* (NG) has been constantly increasing in Québec. No data is available for *T. vaginalis* (TV).

OBJECTIVES: To estimate the prevalence of genital CT, NG and TV among young adults in Québec.

METHODS: PIXEL is a cross-sectional study on sexual health targeting young adults. The stratified multistage sample plan was based on geographical regions and school settings (e.g. adult and vocational schools, colleges, universities). Immediately after completing a self-administered questionnaire in class, women provided self-collected vaginal specimen; men provided first voided urine specimen. All tests were performed with BD Probe Tec. Detection of *T. vaginalis* was performed on a subsample of specimens. Vaginal specimens without human cells were excluded.

RESULTS: Among participants recruited between March 2013 and July 2014, 2461 were 17 to 29 years of age and sexually active (ever had oral, vaginal or anal sexual intercourse).

TABLE 1
Estimated STI prevalence [95% CI] among sexually active participants recruited in school settings, by sex and age group

Stratum	N	<i>C. trachomatis</i>	<i>N. gonorrhoeae</i>	N	<i>T. vaginalis</i>
Women 17-20 y	870	3.4% [2.3-4.7]	0.1% [0-0.3]	506	0.4% [0-1.0]
Women 21-29 y	512	2.0% [1.0-3.4]	0.0%	223	0.4% [0-1.4]
Men 17-20 y	546	1.8% [0.7-3.1]	0.0%	198	0.0%
Men 21-29 y	352	2.3% [0.8-3.9]	0.0%	118	0.0%

CONCLUSIONS: Among young adults attending various school settings (where vulnerable youths might be less represented), CT prevalence varies from 1.8% to 3.4%; only 1 woman was infected by NG, and 3 women were infected by TV. Although significant, these population-based prevalences are considered less critical than what was suggested by the increase in

Abstracts

reported cases; this could be explained by a definitive increase in number of screening tests performed in Quebec during the same period. Future observation cycles are needed to assess the trend.

E04

COMPARISON OF TWO DIGITAL PCR PLATFORMS AND DEVELOPMENT OF AN HIV-2 QUANTITATIVE ASSAY

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BACKGROUND: Digital PCR (dPCR) is an interesting alternative to traditional quantitative real-time PCR because quantitation does not require standard curves and several digital PCR platforms are now available. We present a comparison between the Bio-Rad QX200™ Droplet Digital™ PCR System and Life Technologies' QuantStudio™ 12K Flex Real-Time PCR System using international WHO-NIBSC HIV-1 and HIV-2 standards. Following the digital PCR evaluation, we developed an HIV-2 quantitative assay.

METHODS: To compare digital PCR systems, an EQAPOL HIV-1 RNA and the WHO-NIBSC HIV-1 controls were extracted, amplified into cDNA, quantified and compared on the two different dPCR platforms. The HIV-2 quantitative assay used primers and probes targeting the gag region of HIV-2. The WHO HIV-2 (1000IU/mL) International Standard was used as an external in-house control to validate the assay. A dilution series of 7 replicates using the WHO HIV-2 control was used to establish the lower limit of the assay.

RESULTS: The quantification of the EQAPOL reagent was comparable to within 0.20 log of the previously calculated value for the control (68,700cp/ml [4.84]). Interestingly, when using a one-step RT-PCR system specific for each digital PCR platform a significantly lower quantitation was observed for the EQAPOL reagent on the QuantStudio™ 12K Flex Real-Time PCR System (24,193cp/mL [4.38]) and the QX200™ Droplet Digital™ PCR System (12,953cp/mL [4.11]). The WHO HIV-2 standard curves demonstrated that the assay was sensitive and reproducible. All 7 replicates at 125IU/mL were quantifiable. 6/7 at 62.5IU/mL and 4/7 at 31.25IU/mL were quantifiable therefore the lower limit of detection was then set at 100 IU/mL.

CONCLUSION: All digital PCR systems evaluated gave comparable quantitation values for the HIV-1 controls. Finally, when quantifying RNA the choice of a 1-step or 2-step RT-PCR system may have significant impact on quantitation. Presently there is no quantitative HIV-2 assay commercially available and the lack of HIV-2 control reagents which makes development of in-house methods problematic. With the recent introduction of Bio-Rad's Automated Droplet Generator coupled with digital droplet PCR, we effectively identified HIV-2 in plasma as low as 100IU/mL. We have since been providing HIV-2 determinations to Canadian stakeholders.

11:15 – 12:15 Session F
Room: Port Alberni

F01

RETROSPECTIVE EVALUATION OF BIO-RAD'S β CARBA ASSAY FOR DETECTION OF A DIVERSE RANGE OF CARBAPENEMASE-PRODUCING ORGANISMS (CPO)

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OBJECTIVES: CPO PCR tests do not detect all CPO and are costly. Rapid phenotypic tests based on colour changes from pH changes due to imipenem hydrolysis are options but are unreliable for class D CPO. This study evaluated Bio-Rad's β CARBA assay, a rapid CPO assay based on colour changes reflecting hydrolysis of a chromogenic carbapenem.

METHODS: 259 species-diverse isolates, highly-characterized by PCR/sequencing, were included in this study comprising 221 CPO (108 class A: 99 KPC, 4 SME, 2 IMI-1, 2 GES, 1 NMC-A; 80 class B: 73 NDM, 6 VIM, 1 IMP7; 26 class D; OXA48; OXA181, OXA232, OXA244; 7 class B+D: NDM+OXA181, NDM+OXA232) and 38 non-CPO (derepressed/ plasmid-mediated *ampC*, ESBL, *ompC/ompF*-mutants, *ompK35/ompK36*-mutants, *cphA*, OXA252). On/after recovery from -80°C, ertapenem (ERT) discs were added to plates for selective pressure. All 259 isolates were tested by β CARBA from growth on Oxoid Columbia Sheep Blood agar (CSBA) and 76/259 [comprising 58 CPO (11 KPC, 3 SME, 2 GES, 1 IMI1, 1 NMC-A; 12 NDM, 6 VIM, 1 IMP7; 17 OXA48-like, 4 NDM+OXA48-like) and 18 non-CPO] were tested from growth on Mueller-Hinton agar (MHA). All 335 β CARBA tests were inoculated with 1 μ L-loopful of growth from around ERT and incubated at 37°C. Each tube was read at 30min independently by 5 blinded readers for colour-changes from yellow (negative) to orange, red or purple (positive). Consensus reads were analyzed.

RESULTS: Overall, β CARBA was 98.2% sensitive (95%CI: 95.8–99.3) and 100% specific (95%CI: 92.2–100) detecting 274/279 CPO in 335 tests. β CARBA performed equally well from CSBA and MHA detecting 218/221 (98.6%) and 56/58 (96.6%) of the CPO, respectively. Detection included 100% of OXA48-like CPO (CSBA: 33/33; MHA: 21/21). False-negatives from both agars included 1/1 NMC *Enterobacter cloacae* and 1/2 GES *Klebsiella oxytoca*. The only β CARBA false-positive was from an *Aeromonas hydrophila* (intrinsic carbapenem-resistance due to *cphA*). This species would be excluded from testing based on its identity, and thus was not included in specificity calculations.

CONCLUSIONS: β CARBA is a rapid low-complexity assay that detects CPO with high sensitivity and specificity from SBA and MHA with results in 30min using 1 μ L-loopful of organism.

F02

DETECTION OF CARBAPENEMASE-PRODUCING ENTEROBACTERIACEAE IN TIBDN LABORATORIES, 2014

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BACKGROUND: Carbapenemase-producing *Enterobacteriaceae* (CPE) were first identified in Toronto in 2007, and remain uncommon, although their incidence has been increasing: In 2014, 66 patients were identified as colonized or infected with CPE in TIBDN hospitals. We surveyed 19 TIBDN laboratories to identify adherence to the recommended guidelines of the Institute for Quality Management in Healthcare (IQMH) on identification of CPE from laboratory specimens, and the Provincial Infectious Disease Advisory Committee (PIDAC) recommendations regarding screening and control of antibiotic resistant organisms.

METHODS: A survey was sent to all 19 TIBDN laboratories (17 hospitals, 2 from the community).

RESULTS: All 19 laboratories responded. In 2014, 18 (95%) reported screening all clinically relevant isolates of *Enterobacteriaceae* for CPE; 1 laboratory reported screening cefpodoxime resistant isolates only. Eighteen (95%) followed IQMH guidelines for screening of isolates for CPE (screening isolates with ertapenem MIC of ≥ 1 mg/L or a meropenem disk diffusion (DD) of ≤ 25 mm); one laboratory reported using a meropenem disc diameter of ≤ 23 mm. For CPE confirmation, 10 (52.6%) laboratories used the ROSCO KPC + MBL Confirm kit; 7 (36.8%) referred all screen positive isolates to the Public Health Ontario Laboratory without any in-house phenotypic testing, 1 (5.3%) performed Modified Hodge tests, and 1 (5.3%) performed their own in-house PCR. Seventeen (89.5%) laboratories provided isolates to the voluntary Ontario provincial surveillance system. Twelve (63.2%) reported screening of rectal swabs to detect CPE; eleven of

these were able to provide the number of rectal swabs screened for CPE in 2014. The median number of specimens screened was 1124 (range 2-21573). **CONCLUSIONS:** The vast majority of laboratories reported adherence to IQMH recommendations for CPE detection; however more than half require PHOL for confirmation, which contributes to delays in CPE identification. Despite PIDAC recommendations, the voluntary provincial reporting system does not include all laboratories, and one-third of laboratories do not screen rectal swabs to detect colonization.

F03

A CROSS-SECTIONAL POINT PREVALENCE SURVEY (PPS) OF THE ANTISEPTIC RESISTANCE GENES QACA/B AND SMR IN CLINICAL ISOLATES OF STAPHYLOCOCCUS SPP. FROM ACROSS ALBERTA

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INTRODUCTION: Decreased susceptibility to quaternary ammonium compounds (QAC) and chlorhexidine (CHG) has been associated with the *qac* genes, which encode for proton-dependent proteins and multi-drug efflux pumps. We conducted a cross-sectional PPS of the presence of *qacA/B* and *smr* genes in a representative sample of clinical isolates of staphylococci from across Alberta.

METHODS: Blood culture isolates of *Staphylococcus* spp. from health zones across Alberta were collected in 2014-2015 focusing on isolates from ICUs, hemodialysis and medical wards. Following DNA isolation, isolates were screened for antiseptic resistance using a multiplex PCR assay incorporating 6 PCR targets, including *Staphylococcus* 16s rRNA and *nuc* (distinguishing *S. aureus* from coagulase negative staphylococci [CNS]), *qacA/B* and *smr*, *mupA*, and *mecA*. Results were analyzed based on methicillin resistance (MR) and also by hospital vs. community acquisition. Differences in discrete variables were analyzed by χ^2 with Yates correction or Fisher's exact as appropriate.

RESULTS: A total of 276 isolates (264 adult; 12 pediatric) were collected from across Alberta. Of the isolates 160 were MRSA, 51 were MSSA, 36 were MR coagulase negative staphylococci (CNS) and 29 were MSCNS. The overall prevalence of at least one of *qacA/B*, *smr*, and/or *mup* was 22.1% (6.6% *S. aureus* and 72.3% in CNS). There was a greater prevalence in MRSA vs MSSA isolates (12/160 [7.5%] vs 3.9% [2/51]; $p=NS$); in MRCNS vs. MSCNS (20/36 [93.1%] vs. 20/36 [55.6%]; $p<0.002$, Yates correction); and in HA-MRSA vs. CA-MRSA (14% [12/86] vs. 4.1% [3/74] $p<0.06$). Of the HA-MRCNS, 18/21 (85.7%) carried at least one resistance gene. The prevalence of positivity of the *mup* gene was 2.4% vs. 30.8% ($p<0.001$) in coagulase positive vs. negative staphylococci.

CONCLUSION: There is a relatively low prevalence of antiseptic-associated resistance genes within *S. aureus* isolates tested across the province but there was a higher prevalence in staphylococci spp. with MR and in HA strains. Serial point prevalence surveys and testing of CHG MICs in the future may be indicated, especially with increasing use of both CHG and QACs in both the hospital and the community.

F04

RETROSPECTIVE EVALUATION OF BIOMÉRIEUX'S CHROMID CARBA-SMART AGAR (C-S) BI-PLATE FOR DETECTION OF A DIVERSE RANGE OF CARBAPENEMASE-PRODUCING ORGANISMS (CPO)

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BACKGROUND: Optimum methods for detecting CPO from surveillance specimens are not clear. This study evaluated performance of bioMérieux's chromID C-S, a chromogenic CPO bi-plate (CARB agar selects for all CPO and OXA agar selects for OXA48-type CPO).

MATERIAL/METHODS: 259 highly characterized clinical isolates were included in this study including: 221 CPO (108 class A: 99 KPC, 4 SME, 3 NMC/IMI, 2 GES; 80 class B: 73 NDM, 6 VIM, 1 IMP7; 26 class D; OXA48; OXA181, OXA232, OXA244; 7 class B+D: NDM+OXA181, NDM+OXA232) and 38 non-CPO (derepressed-*ampC*, ESBL, *ompC/ompF* or *ompK35/ompK36* mutants, 1 *cphA*, 1 OXA252). Standard saline 0.5-MacFarland suspensions, prepared using colonies closest to eropenem discs on MacConkey agar for selective pressure, were transferred to emptied Copan eSwab tubes for automated inoculation (10 μ L/side) to C-S by the WASP system. After overnight incubation at 37°C, quantity, colour and size of colonies were documented independently by 5 blinded readers. Consensus data were analyzed for sensitivity (Sn) and specificity (Sp) for 1) all CPO on CARB-agar, 2) class D CPO on OXA-agar, and 3) all CPO of both agars combined.

RESULTS: Only 1 NDM+ *P. mirabilis* and 1 OXA48+ *E. coli* were not detected by either agar on C-S resulting in an overall Sn (95% CI) of 99.1% (96.6-99.97). The CARB-agar grew all but 6/221 CPO [1 NDM+ *Proteus mirabilis* and 5 OXA48-type *Escherichia coli* (2 OXA181, 3 OXA48)] resulting in a CPO detection Sn (95%CI) of 97.3% (94.1-98.9), and Sn by class: A (100%; 95.9-100), B (98.8%; 92->99.99), and D including B+D (84.9%; 68.6-93.8). The OXA-agar grew all but 1/33 class D (1 OXA48 *E. coli* that also failed on CARB) and also grew 1 class A (SME+ *Serratia marcescens*) and 2 class B (1 NDM+ *Acinetobacter baumannii*, 1 VIM+ *Pseudomonas putida*) CPO; corresponding Sn (95% CI) was 97% (83.4->99.99) for class D only. Of the 38 non-CPO, 12 grew on CARBA and 1 on OXA agars, resulting in Sp (95%CI) of 68.4% (52.5-81) and 98.2% (95.4-99.5), respectively.

CONCLUSIONS: This evaluation of the C-S chromogenic bi-plate found the OXA agar to complement the chromID CARB agar as 4/5 OXA48-type CPO not detected on CARB were detected on OXA, thus improving overall CPO detection (Sn) from 97.3% to 99.1%. Low specificity remains an issue. These data support prospective evaluation of C-S.

11:15 – 12:15 Session G Room: Finback

G01

A RANDOMIZED CONTROLLED TRIAL OF ORAL VANCOMYCIN FOLLOWED BY FECAL TRANSPLANTATION VERSUS TAPERING ORAL VANCOMYCIN TREATMENT FOR RECURRENT CLOSTRIDIUM DIFFICILE INFECTION

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OBJECTIVES: Recurrent *Clostridium difficile* infection (RCDI) is a debilitating problem affecting 20% to 47% of patients with *Clostridium difficile* infection (CDI). Fecal transplantation (FT) is a promising treatment for RCDI, but its true effectiveness remains unknown. We compared FT with standard of care oral vancomycin taper, in adult patients with RCDI.

METHODS: In a phase 2/3, single-centre, open-label trial, participants experiencing recurrence of CDI were randomly assigned in a 1:1 ratio to 14 days of oral vancomycin (125 mg orally four times per day) followed by a single FT of 500 mL volume by enema or a six week taper of oral vancomycin. The primary endpoint was recurrence of CDI within 16 weeks. Crossover to the alternate treatment was offered to those with recurrences during follow-up.

RESULTS: The study was terminated at the interim analysis, after randomization of 30 patients. Baseline characteristics were similar in both randomization groups. Nine of 16 (56.2%) patients who received FT and 5/12 (41.7%) in the vancomycin taper group experienced recurrence of CDI. The Bayesian 95% interval for the change in risk of CDI recurrence with FT ranged from a 2.8% reduction to a 47.3% increase. There was a posterior probability of 22.2% that the FT reduced recurrences at all and only a 2.8% probability that risk was reduced by 20% or more. A futility analysis did not support continuing the study. Adverse events were similar in both groups. Four serious adverse events were reported in three patients. None were deemed related to the study interventions.

Abstracts

CONCLUSIONS: A single FT by enema using fresh donor stools was not significantly different from oral vancomycin taper in reducing RCDI. Further research is needed to explore optimal donor selection, FT preparation and administration, including number of administrations.

G02

USE OF CEFTAROLINE IN PATIENTS WITH METHICILLIN RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) INFECTIVE ENDOCARDITIS DESPITE ADEQUATE SOURCE CONTROL

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OBJECTIVES: MRSA infective endocarditis presents many challenges. Increasingly, ceftaroline has been used in salvage therapy for persistent MRSA bacteremia. We describe two case reports utilizing ceftaroline combination therapy in persistently positive blood cultures despite heart valve replacement.

METHODS: Two patients who presented to Hamilton Health Sciences in 2015.

RESULTS: A 29-year-old female and 46-year-old male, presented with MRSA bacteremia and tricuspid valve infective endocarditis. Both patients were intravenous drug users (IVDU) and were persistently bacteremic despite monotherapy with vancomycin and daptomycin. Both required surgical valve replacement due to hemodynamic instability and failure to clear bacteremia. The first patient's valve tissue revealed MRSA with an MIC to Vancomycin of 2.0 mg/L, and daptomycin resistance and the second patient's tissue cultures revealed MRSA that was daptomycin susceptible (previously resistant), and Vancomycin MIC of 1.0 mg/L (previously 2.0 mg/L). Post-operatively, both patients remained bacteremic for 2 and 7 days, respectively, despite adequate source control. Given the lack of therapeutic options, both patients were started on a combination of daptomycin and ceftaroline, with clearance of bacteremia within 1 and 2 days, respectively.

CONCLUSION: MRSA bacteremia with daptomycin resistance and high Vancomycin MIC presents a therapeutic challenge with few bactericidal agents available. Ceftaroline may be an option in combination with other agents in this setting, particularly after source control has failed to sterilize the bacteremia.

G03

RISK FACTORS FOR MORTALITY IN PATIENTS WITH EXTENDED-SPECTRUM BETA-LACTAMASE-PRODUCING ENTEROBACTERIACEAE BLOODSTREAM INFECTIONS: A MULTI-CENTRE, COHORT STUDY

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OBJECTIVES: While controversy exists whether extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae increase mortality among hospitalized patients with bloodstream infections (BSIs), limited data exist regarding predictors of mortality. This study determined predictors of mortality and seven day and 30-day mortality rates among inpatients with ESBL-producing Enterobacteriaceae BSIs.

METHODS: This was a retrospective cohort study involving four tertiary care hospitals from November 2005 to November 2012. All adult inpatients with ESBL-producing Enterobacteriaceae BSIs during the study period were included (n=220). The primary outcome measures were seven and 30-day mortality rates. Cox regression analyses were conducted to determine associations between survival and potential risk factors.

RESULTS: Mortality rate at 30-days among inpatients with ESBL-producing Enterobacteriaceae BSIs was 50/209 (23.9%). Univariate analysis revealed that 30-day mortality rates for adequately and inadequately treated patients were 40/191 (20.9%) and 10/18 (55.6%), respectively; for patients with non-nosocomial and nosocomial-associated ESBL BSIs were 20/112 (17.9%) and 30/97 (30.9%), respectively; and for patients with Charlson co-morbidity indexes of 0-4 (reference), 5-6 and ≥ 7 were 33/162

(20.4%), 9/28 (32.1%), and 8/19 (42.1%), respectively. A Cox proportional hazards model revealed that inadequate therapy [hazard ratio (HR)=4.5; p<0.001], nosocomial-associated infections (HR=2.7; p=0.002) and a Charlson co-morbidity index ≥ 7 (HR=2.8; p=0.012) demonstrated a significant mortality risk at 30-days.

CONCLUSIONS: Among inpatients with ESBL-producing Enterobacteriaceae BSIs, inadequate therapy, nosocomial-associated infection and Charlson co-morbidity index ≥ 7 are associated with an increased risk of death. These clinical factors should be taken into consideration when assessing mortality risk amongst patients with ESBL-producing Enterobacteriaceae BSIs.

G04

C-EDGE CO-STAR: EFFICACY OF ELBASVIR AND GRAZOPREVRIN IN PERSONS WHO INJECT DRUGS (PWID) RECEIVING OPIOID AGONIST THERAPY (OAT)

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OBJECTIVES: The fixed-dose combination of elbasvir 50mg (HCV NS5A inhibitor) + grazoprevir 100mg (HCV NS3/4A protease inhibitor) (EBR/GZR), an all-oral, once-daily regimen, is effective and well tolerated for the treatment of HCV infection. C-EDGE COSTAR, a phase 3 trial, evaluated efficacy and safety of EBR/GZR among treatment-naive HCV GT1/4/6-infected patients receiving methadone or buprenorphine, a population with a high prevalence of HCV infection not previously evaluated in large clinical trials.

METHODS: This double-blind, placebo-controlled study randomly assigned patients 2:1 to an immediate treatment group (ITG, EBR/GZR for 12 weeks) or a deferred treatment group (DTG, placebo for 12 weeks, then open label EBR/GZR for 12 weeks). Non-prescribed drug use was monitored by urine drug screening, but was not exclusionary to study participation. Primary endpoints were sustained virologic response (SVR, HCV RNA <15 IU/mL) at follow-up week 12 in the ITG.

RESULTS: A total of 301 patients were randomized (mean age 47 years; 76% male; 12% black; 76% GT1a; 21% cirrhotic, 7% HIV+, 79%/21% receiving methadone/buprenorphine). In the ITG, 99% (199/201) completed 12 weeks of treatment, despite 79% with ongoing drug use (amphetamines 16%, benzodiazepines 39%, cocaine 19%, and opioids 41%) during treatment. In the ITG, SVR12 was 91.5% (184/201). Seventeen patients did not achieve SVR12 (relapse [7], early reinfection [5], LTFU/non-virologic failure [5]). AEs and SAEs were identical in the ITG and DTG groups (83%/83%; 4%/4%). The most common AEs included fatigue (20%), headache (15%), nausea (12%) and diarrhea (12%). There were no ALT/AST elevations >5 \times ULN after on-treatment normalization.

CONCLUSION: EBR/GZR is safe and highly effective in patients with chronic HCV GT1, 4, or 6 receiving methadone or buprenorphine. These data support enhanced efforts to offer HCV treatment to this patient group while enhancing measures to prevent reinfection.

11:15 – 12:15 Session H
Room: Orca

H01

CUMULATIVE ANTIBIOGRAM FOR THE EMPIRICAL TREATMENT OF UNCOMPLICATED URINARY TRACT INFECTIONS IN WOMEN: SHOULD WE REALLY CARE ABOUT WHICH ISOLATES TO INCLUDE?

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BACKGROUND: Empirical treatment guidelines of urinary tract infections (UTIs) in women should be based on local susceptibility data. A cut-off of 80% susceptibility for *E. coli* is generally considered adequate for this purpose. Few studies have investigated the impact of different selection criteria on the proportion of susceptible isolates. The objective of this study was to determine whether basic patient characteristics have a clinically significant impact on susceptibility results.

METHODS: All significant urine samples from females obtained in the outpatient setting, positive for *E. coli* between April 1, 2010 and March 31, 2015 from 4 hospitals (Centre hospitalier universitaire de Québec [CHUQ], CSSS de Rimouski-Neigette [CHRR], l'Enfant-Jésus de Québec [CHA] and McGill University Health Center [MUHC]) were included. The cumulative antibiograms for ciprofloxacin, nitrofurantoin, and trimethoprim-sulfamethoxazole (tmp-smx) were calculated according to CLSI guidelines. A clinically significant difference in susceptibility profile was defined as factor(s) that lowered susceptibility proportion below 80%. Ethics approval was obtained.

RESULTS: A total of 69 684 isolates of *E. coli* were included in the analysis (7 140 from children <18 years old and 25 026 from seniors >65 years of age). The overall susceptibility proportion for ciprofloxacin, nitrofurantoin and tmp-smx were 87.4%, 95.5% and 82.6%, respectively. The following factors significantly lowered the susceptibility profile for ciprofloxacin: seniors from MUHC (71.3%) and seniors with recent hospitalization from all hospitals (76.3%). For TMP-SMX, the following were significant: isolates from MUHC (75.0%), isolates from children (77.2%) and isolates from patients recently hospitalized (79.7%). No factors significantly lowered the susceptibility for nitrofurantoin.

CONCLUSIONS: This study confirms that basic patient characteristics influence susceptibility profiles of *E. coli* and should be used to stratify published cumulative antibiogram.

H02

A LABORATORY WORKFLOW ALGORITHM USING URINARY NITRITE AND LEUKOCYTE DIPSTICK RESULTS IN CONJUNCTION WITH A URINARY TRACT INFECTION MANAGEMENT BUNDLE

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OBJECTIVES: The Moncton Hospital has implemented a urinary tract infection management bundle as an antimicrobial stewardship initiative. One component of the bundle is suppression of identification (ID) and susceptibility results from positive urines on selected inpatient units. We determined the impact a screening dipstick for nitrites and leukocytes could have in determining the need to perform ID and sensitivities of these urines.

METHODS: The specimen processing area of the microbiology laboratory performed dipsticks on inpatient urines from study floors. Specimens with no growth, no clinically significant growth or mixed growth were reported

as such. All remaining positive cultures were worked up (ID and susceptibility) however the results were suppressed and a comment was reported indicating that the majority of inpatient urines represent asymptomatic bacteriuria. The physician was directed to call the lab if they required ID and susceptibility results.

RESULTS: A total of 150 urine samples from inpatients on selected units were collected, and a dipstick urinalysis was performed along with routine workup. 108/150 samples were reported as no growth (n=47), no clinically significant growth (n=31), or mixed growth suggesting contamination (n=30). 42/150 urines were positive and reported with the asymptomatic bacteriuria comment. Of the urine samples with negative leukocytes and negative nitrites on dipstick, only 2/65 (3%) had positive culture results, whereas 88% and 9% were no growth/no clinically significant growth or mixed cultures, respectively. None of the urine samples positive for both leukocytes and nitrites showed no growth or no clinically significant growth; 68% of these were positive for a potential pathogen. There was only 1 request for ID and susceptibility from all urine samples that were negative by urinalysis (n=65), whereas there were 12 requests for results of urine samples that were positive for nitrites and/or leukocytes (n=85).

CONCLUSION: A dipstick screen for nitrites and leukocytes can be used as the initial step in an algorithm for urine culture workup. Those that are positive for nitrites and leukocytes would be worked up and the results suppressed. Those negative for both would not be worked up unless requested by a physician. This would support antimicrobial stewardship efforts and reduce unnecessary laboratory work without impacting turnaround times in cases where ID and susceptibility results are desired.

H03

ANTIMICROBIAL RESISTANCE FOR FIRST LINE AGENTS ON URINE ISOLATE *STAPHYLOCOCCUS SAPROPHYTICUS*

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INTRODUCTION: Local, national and international surveillance programmes are important in monitoring the level of antimicrobial resistance, as it is a growing problem. We decided to examine the susceptibility profile of urine isolate, *S. saprophyticus*, as currently no susceptibility testing is routinely done on this organism as per CLSI document M100-S25. The last susceptibility profile was done in 2001 and very little resistance was recorded. **METHODS:** For each year of the study (2012–2015), we performed susceptibility testing on the first 100 *S. saprophyticus* (outpatient) isolates that were worked-up as per Urine bench protocol, repeat patient specimen were excluded. Susceptibility testing was performed against recommended antimicrobials: Nitrofurantoin, trimethoprim-sulfamethoxazole, and alternate option, Ciprofloxacin, as per IDSA guidelines. Susceptibility testing and interpretation to these three antibiotics was performed using disk diffusion, as per CLSI document M100- S25. Antibiotic disks were purchased from Oxoid.

RESULTS: During this study period, we isolated 441 *S. saprophyticus*, submitted from individual outpatients from 63 communities in southwestern Manitoba. No resistance was noted for Nitrofurantoin and Ciprofloxacin and only 1.6% resistance to Trimethoprim-sulfamethoxazole was recorded.

CONCLUSIONS: Little to no resistance was noted to Trimethoprim-sulfamethoxazole, Nitrofurantoin, and Ciprofloxacin for *S. saprophyticus* isolates in southwestern Manitoba. As in 2001, *S. saprophyticus* resistance development is rare.

H04

URINARY *E. COLI* ANTIMICROBIAL SUSCEPTIBILITY PROFILE ISOLATED FROM ADULT WOMEN IN THE PROVINCE OF QUÉBEC, 2010-2015

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BACKGROUND: Empirical treatment of uncomplicated urinary tract infections (UTI) in women should be based on local susceptibility data, which is often unavailable for clinicians. The objective of this study was to determine if data from different laboratory information system (LIS) could be combined to generate a regional and provincial cumulative antibiogram.

METHODS: All urine samples obtained in outpatient settings from women 18-65 years of age, not hospitalized in the past month, positive for *E. coli* > 10⁷ CFU/L between April 1, 2010 and March 31, 2015 from 4 hospitals (Centre hospitalier universitaire de Québec [CHUQ], CSSS de Rimouski-Neigette [CHRR], l'Enfant-Jésus de Québec [CHA] and McGill University Health Center [MUHC]) were included. Data were extracted and pooled using Nosokos (Nosotech, Rimouski, Canada). The cumulative antibiogram for ciprofloxacin, nitrofurantoin, and trimethoprim-sulfamethoxazole (tmp-smx) was calculated according to CLSI guidelines. Ethics approval was obtained in each hospital.

RESULTS: A total of 36,293 urines positive for *E. coli* were analyzed. The overall proportion of susceptibility for ciprofloxacin, nitrofurantoin and tmp-smx were 91.1%, 96.2% and 82.3%, respectively. There was variability in the susceptibility profile for each antibiotic by laboratory, but the only susceptibility proportion that was below 80% was for tmp-smx from the MUHC, during the five years of the study. When the 2014-2015 proportions were compared with 2010-2011, there was a statistically significant decrease in susceptibility for ciprofloxacin (92.1% to 90.3%; p<0.001) and nitrofurantoin (97.1% to 95.4%; p<0.001), but not for tmp-smx.

CONCLUSIONS: Overall, all three antibiotics remain acceptable choices for empirical treatment of uncomplicated UTIs in women in Quebec. Tmp-smx resistance proportions are higher in the Montreal region. The clinical significance of this result is unknown. The regional variability in susceptibility data from the same province emphasizes the clinical importance of local susceptibility data to inform the development of empirical treatment guidelines for UTIs.

16:00–17:00 Session I
Room: Orca

I01

GENOME SEQUENCING OF *SALMONELLA* JAVIANA IN BRITISH COLUMBIA: GAINING PERSPECTIVE ON RARE SEROTYPES IN A CLINICAL GENOMICS WORKFLOW

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OBJECTIVE: Salmonellosis is one of the most costly foodborne illnesses in North America, and outbreaks occur regularly in British Columbia (BC). *Salmonella enterica* serovar Javiana is a relatively rare serotype in BC, ranging from 5-14 cases per year. Nevertheless, outbreaks do occur, and pulsed-field gel electrophoresis (PFGE) is used as the method of subtyping for lab confirmation. Genome sequencing has been successfully used in

several countries as a subtyping method in outbreak investigations of common *Salmonella* serotypes (e.g., *S. Enteritidis*, *S. Typhimurium*). It is also important to assess its applicability to rare serotypes, as suitable datasets (e.g., outbreak isolates) become available. The BCCDC and BCCDC Public Health Laboratory (BCCDC PHL) investigated whether genome sequencing could replace the current clinical workflow for *Salmonella* identification and subtyping.

METHODS: A total of 23 (13 epidemiologically linked) recent human isolates of *S. Javiana* from BC were sequenced at the National Microbiology Laboratory (NML-Winnipeg), on an Illumina MiSeq and analyzed bioinformatically to identify the organism, determine serotype, and assess the use of single nucleotide variant based methods for phylogenetic and outbreak inference.

RESULTS: For all 23 isolates, identification was successful to the species level and serotype prediction was as accurate as traditional Kauffman-White serotyping. Cluster analysis was concordant with epidemiologic results and was superior to PFGE results.

CONCLUSIONS: The genome analysis workflow used at BCCDC PHL was able to predict identity (species), serotype, and clustering for outbreak and non-outbreak isolates of *S. Javiana*. These results provide further evidence of the applicability of genome sequencing to both common and rare serotypes of *Salmonella*, and help support the replacement of the current clinical workflow for *Salmonella* serotyping and cluster analysis.

I02

REBUILDING OF A LABORATORY SURVEILLANCE SYSTEM

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BACKGROUND: A paradigm shift in our approach to infectious disease diagnostics and public health is on the horizon. Introduction of a single assay to replace multiple conventional diagnostic and public health tests will inevitably change the way clinicians, public health practitioners, and laboratories work together to deliver health care. Technical revolutions in DNA sequencing have already triggered the upheaval of well-established laboratory surveillance programs.

OBJECTIVE: To validate the genetic markers and analytical approach to genomic subtyping for PulseNet Canada surveillance and outbreak response to bacterial enteric pathogens.

METHODS: Genomics analyses on 3000+ human clinical isolates of *E. coli* O157, *Listeria monocytogenes*, and common *Salmonella* Serovars was performed. Isolates associated with outbreaks and PFGE clusters were compared against concurrent background strains using two different genomics analysis approaches: 'whole genome' multilocus sequence typing (wgMLST) using BionumericsV7 and 'core genome' single nucleotide variant (cgSNV) analysis using SNNVphyV1.

RESULTS: Topologies of cgSNV and wgMLST trees correlated for all pathogens tested although proportional branch lengths differed significantly. For epidemiologically-characterized outbreaks represented by multiple similar PFGE patterns, both approaches converged outbreak-isolates into a single genetic clade – supporting a hypothesis of better epidemiological concordance of genomics compared to PFGE. Among concurrent isolates bearing common PFGE patterns, both approaches uncovered underlying diversity, indicating that most common PFGE patterns do not represent clonal strains but rather sporadic disease. However, among the genetic diversity uncovered lay 'genomic clusters' of cases that likely represent small, undetected outbreaks.

CONCLUSIONS: Interpretive guidelines for public health genomic analyses must include both genetic distance and phylogenetic relationship. This study also provides the validation of wgMLST and cgSNV to replace PFGE, the foundation of modern PulseNetCanada databases, and a dataset from which to build clinical diagnostic tools to simultaneously detect genetic markers for bacterial identification, virulence and antimicrobial resistance.

I03

A GENOMIC PICTURE OF NDM-PRODUCING ORGANISMS ISOLATED IN BRITISH COLUMBIA

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OBJECTIVE: New Delhi metallo- β -lactamase (NDM)-producing organisms were present in British Columbia as early as 2008, and was the predominant mechanism associated with plasmid-mediated carbapenemase activity in British Columbia (BC). All NDM-producing organisms in BC identified between 2008 and 2014 were sequenced to better understand their molecular epidemiology and genetic diversity.

METHODS: One hundred and eighty-one *bla*_{NDM}-positive carbapenemase-producing organisms (CPO) isolated in BC were sequenced by the National Microbiology Laboratory. These sequences were used to investigate the inter- and intra-species diversity within healthcare facilities and patients, as well as extrapolate antimicrobial resistance and plasmid profiles.

RESULTS: *Klebsiella pneumoniae*, *Escherichia coli*, *E. cloacae*, and *Citrobacter freundii* were the most common *bla*_{NDM}-positive CPO identified. Most *bla*_{NDM}-positive Enterobacteriaceae were genetically diverse except for non-travel related *E. cloacae*, which were clonal. Plasmid diversity and distribution was assessed by incompatibility group profiling. Complete plasmid sequences were used to show the predominance of IncA/C (n=42) and IncL/M (n=80) plasmids in this diverse set of organisms. Plasmids within these two incompatibility groups shared a high degree of similarity in their genetic content and organization, but evidence of gene gain, loss and rearrangements suggest on-going recombination. IncF and IncX plasmids were also found to carry the *bla*_{NDM}; however, their distribution within this CPO population was limited.

CONCLUSIONS: CPO are undeniably complex; multiple organisms share resistance plasmids, with the potential of further dissemination of a small transposable element. Due to the mobility of the plasmids, transmission by clonal species may not be the appropriate thinking for CPO outbreaks or clusters, and genome data can help unravel some of the complexity.

I04

GENOME SEQUENCING TO TRACK SPREAD OF NDM-PRODUCING *KLEBSIELLA PNEUMONIAE*

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BACKGROUND: The number of NDM-producing organisms has been rising in our province, partly due to enhanced surveillance efforts. Infections with and colonization by these organisms pose increasing therapeutic and infection control challenges.

OBJECTIVES: To track the transmission of a cluster of NDM-producing *Klebsiella pneumoniae* (NDM-Kpn) using genome data.

METHODS: Sequence data was used to determine MLST and core single nucleotide variants (SNV). A subset of strains was typed using pulsed-field gel electrophoresis (PFGE) and had the restriction fragment length polymorphisms (RFLP) of their NDM-containing plasmids analyzed. We attempted to reconstruct the transmission network of isolates involved in a putative cluster by aligning the timeline of NDM-Kpn strains detection with their genomic variability.

RESULTS: We identified a cluster of 32 genetically-related strains isolated from 27 patients from a single health authority belonging to sequence type (ST)340 isolated between 2011 and 2014. The strains exhibited a high degree of overall similarity, except for one strain that was more divergent from the rest (~10-fold more SNVs than the rest). This strain was isolated from a patient who was previously colonized with a ST15 NDM-Kpn. Four patients had more than 1 ST340 NDM-Kpn isolated in 2011-2014, with some of the isolates being 7 to 12 months apart, yet closely genetically related to each other. NDM-Kpn isolated from one patient in 2011 and 2012 were designated as putative "founder strains", to which the rest of the isolates were compared. NDM-Kpn strains genetically close to the "founder strains" were isolated up to 2 years later. PFGE-analyzed strains belonged to 14 different PFGE profiles. RFLP analysis of NDM-containing plasmids demonstrated 3 dominant and related plasmid profiles in most isolates, while the more divergent NDM-Kpn strain harboured a plasmid with an unrelated profile.

CONCLUSIONS: Genome sequencing provides insights into relatedness of NDM-Kpn strains not always demonstrable by other typing methods, and could, in correlation with epidemiological data, be used to track their transmission.

16:00–17:15 Session J
Room: Port Alberni

J01

DECREASED RATES OF HOSPITAL-ASSOCIATED MRSA AND VRE WITH DAILY CHLORHEXIDINE GLUCONATE BATHING FOR MEDICAL INPATIENTS

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OBJECTIVES: To evaluate the effectiveness of utilizing chlorhexidine gluconate (CHG) for daily bathing of patients admitted to General Medicine to reduce hospital-associated MRSA and VRE.

METHODS: A prospective crossover study in an urban academic hospital was conducted on 4 medical inpatient wards (25 beds each) from May 1, 2014 until September 10, 2015. In Phase 1, 2 wards used CHG cloths for daily bathing over 7 months (1 month wash-in and 6 month trial) compared to 2 control wards (soap and water). In Phase 2, practices were crossed over so that intervention wards became control wards and vice versa. Hospital-associated MRSA and VRE (patients with colonization or infection identified >72 hours after admission, or <72 hours after admission with an admission in the previous 4 weeks) were tracked during the study (cases/10,000 inpatient days), as were hospital-associated cases of *Clostridium difficile*. Comparisons were described using chi-squared or Fisher's exact with cells of 5 or less, with two-tailed p-value and p<0.05. Compliance with CHG was monitored weekly.

RESULTS: Compliance with CHG in Phase 1 was 61%, while in Phase 2, it was 54%, p<0.001. Overall, a reduction in the rate of hospital-associated MRSA (5.1 vs 11.4; p=0.039) and VRE (23.2 vs 36.0; p=0.028) was observed in the intervention wards. In Phase 1, a statistically significant reduction in MRSA (4.4 vs 15.9, p=0.027) and VRE (16.6 vs 34.1, p=0.02) was seen with CHG. However, this was not evident in Phase 2 for MRSA (5.8 vs 6.9; p=0.999) or VRE (30.2 vs 37.8; p=0.39), though rates were lower on CHG wards. No significant differences between intervention and control wards were identified for blood cultures positive >72 hours after admission (both Phase 1 and 2). Hospital-associated rates of *C. difficile* were not significantly different throughout the study (10.2 vs 6.8; p=0.285), which was expected since CHG does not have sporicidal activity.

CONCLUSION: Despite suboptimal compliance, daily bathing with CHG on Medicine as an intervention to reduce rates of hospital-associated MRSA and VRE was effective. Further study is required before routine implementation as effectiveness of CHG is dependent on compliance and appropriateness of use, which can be more variable on non-ICU wards.

J02

VRE POSITIVE BLOOD CULTURE RATES BEFORE AND AFTER DISCONTINUATION OF VRE SCREENING: A QUASI-EXPERIMENTAL STUDY OF VRE RATES IN ONTARIO CANADA FROM JANUARY 2009 TO JUNE 2015

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OBJECTIVES: Since July 2012, some Ontario hospitals have stopped screening patients for vancomycin resistant enterococci (VRE). The objective of this study was to examine the impact of VRE screening discontinuation by comparing the rates of VRE-positive (+) blood cultures before and after this practice change.

METHODS: All Ontario hospitals are mandated to report VRE+ blood cultures to the Provincial Patient Safety Public Reporting database. All confirmed VRE+ blood cultures between January 2009 and June 2015 were included. Using a quasi-experimental study design, hospital sites were stratified into two cohorts; a non-screening hospital cohort (hospitals without a VRE screening program as of June 2015) and a screening hospital cohort (hospitals with a VRE screening program). Poisson regression over time was used to assess changes in incidence of VRE+ blood culture rates before and after discontinuation of VRE screening (non-screening cohort) and before and after July 2012 (screening cohort). Rates were adjusted for hospital type (acute teaching/community) and clustering within hospital site using generalized estimating equations.

RESULTS: There were 395 confirmed VRE+ blood cultures reported from 63 Ontario hospital sites during the study period. Non-screening hospitals (n=13) reported an increase in VRE+ blood cultures after discontinuation of screening when compared to before (1.16 to 2.81 per 100,000 patient-days, p=0.0006); before discontinuation of VRE screening, there was a 10% annual relative decrease in VRE+ blood cultures, however once screening was discontinued there was a 12% annual relative increase in rate (adjusted p=0.04). Screening hospitals (n=50) also reported an increase in the VRE+ blood culture rate before versus after July 2012 (0.49 to 0.89 per 100,000 patient-days, p=0.001); however, the annual rate of rise was not significantly different before July 2012 when compared with after (31% versus 6% annual relative increase in rate, adjusted p=0.24).

CONCLUSION: Rates of VRE+ blood cultures are increasing in non-screening and screening hospitals sites in Ontario. A significant increase in the rate of rise of VRE+ blood cultures was seen in hospitals where VRE screening was discontinued, but not in hospitals that continued to screen for VRE.

J03

PREVENTION OF POST-OPERATIVE CATHETER-ASSOCIATED URINARY TRACT INFECTION ON SURGICAL WARDS FOLLOWING IMPLEMENTATION OF A MULTI-FACETED INTERVENTION

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OBJECTIVE: Presence of indwelling urinary catheter is the main risk factor for development of post-operative urinary tract infection. We performed a multifaceted, multidisciplinary improvement study to decrease the incidence of post-operative catheter-associated urinary tract infections (CAUTI) across five surgical wards.

METHODS: Following a 5-month baseline period, a three-pronged intervention was implemented over 2 months including: 1) re-training of operating room staff to insert urinary catheters using sterile technique, 2) restrictive urinary catheter insertion in the operating room, and 3) implementation of a post-operative medical directive allowing nurses to remove all urinary catheters on post-operative day 2 for patients lacking the following exclusion criteria: pre-admission urinary catheter, urology involved, continuous bladder irrigation, stage 3 or 4 sacral ulcer in incontinent

female patient, comfort care at end of life as per patient wishes, admitted with spinal cord injury, or following radical pelvic surgery involving bladder, uterus, cervix, or vulva. Catheter-days per patient-days and CAUTI per patient-days (by random chart audits) were compared before and 4-months following the intervention period.

RESULTS: At baseline, urinary catheter-days per patient-days were 4235/24,777 (17.1% [95% CI 16.6% to 17.6%]) associated with CAUTI rate of 15/456 (3.3% [95% CI 2.0% to 5.4%]). Following implementation of intervention, urinary catheter use decreased significantly to 4889/35,058 (14.0% [95%CI 13.6% to 14.2%]; p<0.0001) associated with CAUTI rate of 4/456 (1.1% [95% CI, 0.5-2.6%; p=0.02). During weekly random audits during the intervention period, 426/485 (87.8%) of urinary catheters on surgical wards met the exclusion criteria for nurse-initiated urinary catheter removal.

CONCLUSIONS: A three-pronged intervention was associated with decreased urinary catheter use and CAUTI rates among surgical patients. A longer period of observation is needed to confirm the sustainability of this intervention.

J04

ASSESSMENT OF THE DEVELOPMENT OF CHLORHEXIDINE GLUCONATE RESISTANCE IN STAPHYLOCOCCUS AUREUS ON MEDICAL INPATIENT UNITS

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OBJECTIVES: To assess for chlorhexidine gluconate (CHG) resistance in hospital-associated *Staphylococcus aureus* identified on medical inpatient wards in which daily CHG bathing was introduced.

METHODS: A prospective crossover study of CHG on 4 medical wards was conducted from May 1, 2014 until September 10, 2015, at an urban, academic hospital in Vancouver, Canada. Intervention with daily CHG bathing was introduced to 2 medical wards over 7 months, and then transitioned to the other 2 wards for 7 months. Overall compliance was estimated at 58%. All nosocomial isolates of methicillin-resistant *Staphylococcus aureus* (MRSA) from any clinical site [>3 days after admission or ≤3 days with a previous admission in the past 4 weeks], as well as all blood cultures positive for methicillin-susceptible *Staphylococcus aureus* (MSSA) identified >3 days after admission were included. For patients with multiple isolates, only the first isolate was tested. An in-house developed real-time PCR for the *qacA/B* and *smr* genes was utilized. CHG MIC was assessed by agar dilution based on CLSI standards. Isolates were considered susceptible to CHG if the MIC was ≤4µg/mL, based on previously published reports. Significance was assessed with Fisher's exact test with two-tailed p-value and p<0.05.

RESULTS: Thirty *S. aureus* (2 MSSA and 28 MRSA) were included in the study, 11 from the CHG cohort and 19 from the control cohort (soap and water). One MRSA isolate (sputum) was positive for *qacA/B* (MIC 2) and 1 MSSA isolate (blood) was positive for *smr* (MIC 2) on the CHG intervention wards. No *qacA/B* or *smr* positive isolates were identified on the control wards (2/11 vs 0/19; p=0.25). All isolates tested by agar dilution had an MIC ≤4µg/mL, except for 1 nares screening swab from a patient on the CHG intervention unit with an MIC 8 (*qac* and *smr* PCR negative).

CONCLUSION: No significant difference in the detection of *qacA/B* and *smr* genes or CHG non-susceptibility by agar dilution was identified in *S. aureus* recovered from the intervention wards utilizing CHG, estimated at 58%. However, ongoing study is needed if CHG is adopted into routine practices on non-ICU wards due to the potential for inducing resistance as a result of low compliance.

J05

PROVINCIAL SURVEILLANCE FOR CARBAPENEMASE-PRODUCING ORGANISMS IN BRITISH COLUMBIA: 2014-15

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OBJECTIVES: The emergence of carbapenemase-producing organisms (CPO) in BC was initially identified and monitored through the provincial microbiology laboratories network. In July 2014, the BC Ministry of Health mandated that the Provincial Infection Control Network (PICNet) of BC lead and coordinate a systematic screening and surveillance program that links epidemiological and laboratory information. We present a summary of the first year surveillance information.

METHODS: Patients presenting to healthcare facilities were screened for defined risk factors during admission and specimens were collected if warranted. Frontline microbiology laboratories in BC implemented phenotypic screening for carbapenem resistance in gram negative organisms. Any phenotypically positive isolates were forwarded to the BC Centre for Disease Control Public Health Laboratory (BCCDC PHL) for *bla*_{ndm}, *bla*_{kpc}, *bla*_{oxa-48}, *bla*_{vim}, and *bla*_{imp} PCR. Additionally *bla*_{smc} (*Serratia marcescens*) and *bla*_{oxa-family} were screened by NML. All CPO positive cases, excluding *Pseudomonas aeruginosa*, are followed up with a patient questionnaire according to the PICNet surveillance protocol (<https://www.picnet.ca/wp-content/uploads/Surveillance-Protocol-for-CPO-2014-08-11.pdf>).

RESULTS: Between July 2014 and March 2015, 410 isolates were submitted to the BCCDC PHL for PCR testing. The majority of the isolate sources were urine (34%) and screening rectal swabs (35%). Twenty-two percent (91 isolates) were positive for CPO gene. Of these, 49 were identified as new CPO cases, 28 were known positives, 9 cases originated from the community setting, and 5 cases were from residential care setting or other healthcare providers. Of the new cases, 61% were NDM, 14% OXA-48 and 8% KPC, and other CPO's accounted for the rest. Nearly half of the new cases (23/49) had healthcare exposure outside Canada, while nine cases had known CPO contacts.

CONCLUSIONS: CPOs are ongoing emerging threats to healthcare facilities. The PICNet CPO Surveillance Program allows for consistent and coordinated screening and testing practices province-wide to rapidly identify high risk CPO colonizers and closely monitor transmission of these organisms in BC healthcare settings.

16:00–17:15 Session K
Room: Finback

K01

PASSIVE SURVEILLANCE OF BORRELIA BURGdorFERI IN BRITISH COLUMBIA (2002 TO 2013)

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OBJECTIVES: Lyme disease cases are increasing in many parts of Canada but cases remain low in British Columbia (BC). Passive tick/*Borrelia burgdorferi* surveillance has been ongoing in BC since 1992 which allowed the monitoring of Lyme disease risk in the vector population. We summarized 12 years' worth of data to help us perform a risk analysis of Lyme disease in BC.

METHODS: Ticks removed by veterinarians, doctors and the general public were submitted to the BCCDC Public Health Laboratory for

identification. The meta-data was analyzed using Microsoft Excel Statistic Package. Lyme disease carrying tick vectors then were subjected to a dual polymerase chain reaction test, which targeted the 23S rRNA gene of *Borrelia* spp. and *ospA* gene of *B. burgdorferi*.

RESULTS: A total of 10,117 ticks at different developmental stages (mostly adult) were collected and speciated. The majority of these ticks were from humans (53.49%) and dogs (37.60%). The ticks identified were mainly *Ixodes pacificus* (60.02%), followed by *Dermacentor andersoni* (25.12%), *Ixodes angustus* (6.67%), *Rhipicephalus sanguineus* (3.12%), and *Dermacentor albipictus* (1.59%). The PCR positive rates of *Ixodes* ticks for each year ranged from 0.15% to 0.61%.

CONCLUSIONS: The positivity rate of *B. burgdorferi* in the BC *Ixodes* tick population remains low (average 0.32%) which is very close to our previous finding (0.4%, from 1993 to 1996). This result also echoed the results gathered from the active BC rodent surveillance in 2013 and 2014 (average 0.6%) where we focused on previously positive geographical locations. The low incidence in the vector population found from both surveillance methods explained the continual, low incidence of Lyme disease in BC.

K02

ANTIMICROBIAL SUSCEPTIBILITY PROFILE OF HELICOBACTER PYLORI ISOLATES FROM 2009-2015, AT ST-PAUL'S HOSPITAL, VANCOUVER, BC

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BACKGROUND: Infection with *Helicobacter pylori* is common cause of gastric/duodenal ulcers, as well as gastric cancer. Patients first diagnosed with *H. pylori* infection often received empiric treatment with triple therapy. Patients failing therapy are referred to gastroenterologists at St-Paul's Hospital for gastric biopsy, which is sent for culture and susceptibility testing. We reviewed our laboratory data for the past 6 years to determine culture success rates and susceptibility profiles.

METHODS: All cultures submitted from 2009-2015 were reviewed. Information was collected on specimen transport time, gram smear, direct urease test, culture positivity, and susceptibility interpretations. Susceptibility testing was performed for amoxicillin, clarithromycin, metronidazole and tetracycline using E-test methodology. Interpretations were based on EUCAST Clinical Breakpoints.

RESULTS: During the study period, 84/150 (56%) of biopsy specimens were culture positive for *H. pylori*. There were 113 specimens with a Gram smear result for white blood cells (Inflammation). Of those positive for inflammation 49/86 (57%) were culture positive. If the Gram smear was negative for inflammation, 12/27 (44%) were culture positive. There were 148 specimens with a result recorded for presence of curved Gram negative rods (CGNR). If specimens were positive for CGNR, 42/46 (91%) were culture positive. If specimens were negative for CGNR, 42/102 (41%) had a positive culture. When the direct urea slant was positive, 46/61 (75%) of cultures were positive. If the urea test was negative, 28/76 (37%) were culture positive. The *H. pylori* isolates were susceptible to: 81/82 (99%) amoxicillin, 12/82 (15%) clarithromycin, 19/82 (23%) metronidazole, and 83/83 (100%) tetracycline. The recovery rate for specimens with transport times less than two hours versus two hours or greater was 65% and 52%, respectively.

CONCLUSIONS: Culturing of *H. pylori* requires expertise, however recovery rates are improved with transport times <2 hours. Resistance rates to clarithromycin and metronidazole were high, although the activity of amoxicillin and tetracycline was well preserved.

K03

SELF-STOOL BANKING AS A SOURCE FOR FECAL TRANSPLANTATION: A PILOT STUDY

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BACKGROUND: Fecal transplantation is a promising therapeutic alternative for refractory *C. difficile* infection. Self-stool donation can overcome

the complexities of donor identification and screening, and eliminate the risk for blood borne pathogen exposure. We assessed the feasibility of a fecal banking protocol.

METHODS: All admitted adult medicine patients over 15 months were screened. Patients with gastrointestinal co-morbidities or factors impacting intestinal microbiota were excluded. Participants were administered a survey and given the option to bank a sample. Samples were processed during defined laboratory hours. Feasibility was assessed on process indicators, resource issues, and sample management. Success was pre-defined as a 50% consent rate to banking. A secondary objective was to describe perceptions and satisfaction around fecal banking.

RESULTS: A total of 4675 patients were screened for eligibility. The majority (60%) of patients were excluded, primarily due to antibiotic exposure (1343, 48%). A total of 537 consented to the study, with 392 (73%) consenting to fecal banking as well. The primary reason for not consenting to bank a sample was that it was 'too gross' (34%). Of the fecal samples provided (n=72), 27 samples were successfully banked. The primary reason for not providing a sample was lack of a bowel movement (54%), and the top reason for rejecting a collected sample was inadequate sample quantity (63%). Average processing time for a fecal sample was 58 min (22 min to 640 mins). The majority of participants reported a preference for using their own stool than samples from a healthy screened donor (81.5%) for transplantation purposes, with 89% (n=72) willing to donate again.

CONCLUSIONS: Our pilot study demonstrated the feasibility of implementing a self-donor fecal banking protocol. Scalability of this process is easily addressed through dedicated resources for collection and processing of fecal samples from larger cohorts. Formal evaluation of the efficacy of self-donated fecal samples for auto-fecal transplants is required.

K04

USE OF WHOLE GENOME SEQUENCING TO ASCERTAIN THAT *BREVIBACTERIUM MASSILIENSE* (ROUX, RAOULT 2009) IS A LATER HETEROTYPIC SYNONYM OF *BREVIBACTERIUM RAVENSPURGENSE* (MAGES 2008)

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BACKGROUND AND METHODS: Urine isolate (NML 140868) was found by 16S rRNA gene sequencing (16S) to have 99.6% identity to sequence from the type strains of both *Brevibacterium ravenburgense* and *B. massiliense*. Those species were validly described within ~8 months of each other in 2009, raising the possibility that these may be taxonomic synonyms coincidentally described at nearly the same time. The clinical isolate and CCUG type strains (*B. ravenburgense* CCUG 56047^T, *B. massiliense* CCUG 53855^T) were analysed biochemically, for CFAs, by 16S, MALDI-TOF (Bruker) and by AST using standard methods. Whole genome sequencing (WGS) was applied to the three strains with results being compared with the annotated WGS for *B. massiliense* CIP109422^T (GB no.NZ_CAJDO1000000).

RESULTS AND DISCUSSION: *B. ravenburgense*, *B. massiliense* and 140868 could not be differentiated by 16S, CFAs, MALDI-TOF and biochemically; all 3 were non-reactive to nearly all conventional biochemical tests/or substrates in API Coryne, API-CH50 or BIOLOG panels. Resistance was variably observed for GEN, ERY, CIP, TET, CLIN and T/S. A WGS comparison between the three strains and the published *B. massiliense* WGS found that the pairwise average nucleotide identity (ANIb) values were all greater than 95%, supporting our hypothesis that they all belonged to the same species. The three draft genomes ranged from 2.29 Mb to 2.42 Mb in length and had an average G+C content of 62.37%, which was consistent with the 2.35Mb length and G+C content value of 62.3% as described for CIP109422^T after WGS. We therefore propose that *B. massiliense* is a later heterotypic synonym of *B. ravenburgense* and these observations will be formally described in IJSEM.

16:00–17:15 Session L
Room: Port McNeill

L01

FACTORS ASSOCIATED WITH 30-DAY SURVIVAL IN INFECTIONS CAUSED BY *STREPTOCOCCUS PNEUMONIAE*

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BACKGROUND: *Streptococcus pneumoniae* is the leading bacterial cause of community-acquired pneumonia (CAP) among adults. North American guidelines recommend prompt administration of broad-spectrum empiric therapy for patients hospitalized with CAP. We evaluated the relationship between the timing of correct antibiotic therapy and survival in adults with *S. pneumoniae* CAP or bloodstream infection (BSI).

METHODS: The Toronto Invasive Bacterial Disease Network (TIBDN) prospectively collects clinical and microbiological information on all invasive *S. pneumoniae* cases in the Toronto and Peel regions (Ontario, Canada, population 4 million) since 1995. Antibiotic susceptibility testing was based on the Clinical and Laboratory Standards Institute (CLSI) guidelines. Patients treated prior to presentation, or who did not receive antibiotics on the first day of admission were excluded. Survival analysis was performed using Cox proportionate hazards (SAS version 9.4) adjusting for confounding, interactions, and any time-dependent variables.

RESULTS: A total of 4096 patients were included in the study, with an overall 30-day in-hospital mortality rate of 22.0%. There were numerous independent predictors of death, including increased age, cirrhosis, non-hematologic malignancy, bacteremia without focus, and ICU admission on date of presentation. 3838 (93.7%) patients received correct antibiotic therapy within 24 hours and 258 (6.30%) patients did not. After adjusting for confounders, the hazard ratio for in-patient death within 30 days was 1.05 (0.78–1.41) in those receiving incorrect empiric antibiotic therapy in the first 24 hours.

CONCLUSION: We were unable to demonstrate a significant difference in 30-day mortality in patients with proven pneumococcal CAP or BSI who did or did not receive correct empiric therapy within 24 hours of presentation. Additional studies are required to determine if this association is found with other aetiologies of CAP.

L02

SYSTEMATIC REVIEW OF FACTORS ASSOCIATED WITH ANTIBIOTIC PRESCRIBING FOR RESPIRATORY TRACT INFECTIONS

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OBJECTIVE: Antibiotic use is an important and modifiable driver of antibiotic resistance. In most circumstances, antibiotic use for respiratory tract infections (RTIs) is overly broad or unnecessary and does not ameliorate the course of this predominantly viral syndrome. In order to effectively design interventions to foster appropriate prescribing habits, a better knowledge of the factors that promote inappropriate prescribing is needed. Therefore, we systematically assessed factors associated with increased antibiotic prescribing for RTIs.

METHODS: We conducted a systematic review of the literature on factors associated with antibiotic prescribing for RTIs. Studies were included if they used actual prescribing data, assessed factors associated with antibiotic prescribing for RTIs, and performed multivariable analysis of associations. We searched Medline, Embase, and International Pharmaceutical abstracts using keyword and MeSH search terms. Two authors reviewed each abstract and independently appraised all included texts. Data on factors affecting antibiotic prescribing were extracted.

RESULTS: Our searches retrieved a total of 2848 abstracts, with 97 included in full-text review and 30 meeting full inclusion criteria. Comparatively, the

diagnosis of acute bronchitis was associated with increased antibiotic prescribing (adjusted odds ratio [aOR] 1.56–15.9). Features on physical exam such as fever, purulent sputum, abnormal respiratory exam, tonsillar exudate and lymphadenopathy were also associated with higher odds of antibiotic dispensing. Patient desire for an antibiotic was not associated or modestly associated with prescription (aOR 0.61–9.87), in contrast to physician perception of patient desire for antibiotics, which was more strongly associated with antibiotic prescribing (aOR 2.11–23.3).

CONCLUSION: Our review highlights several factors associated with antibiotic prescribing for RTIs. Physician's perception of patient desire for antibiotics was strongly associated with antibiotic prescribing. Antimicrobial stewardship programs should continue to expand in the outpatient setting, and should emphasize clear and direct communication between patients and physicians regarding the need or lack of need of antibiotics for acute respiratory tract infections.

L03

OF MICE AND MEN IN UNIFORM – A CLUSTER OF HANTAVIRUS PULMONARY SYNDROME AMONGST CANADIAN MILITARY PERSONNEL

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BACKGROUND: As of December 2014, 109 Canadian cases of Hantavirus pulmonary syndrome (HPS) have been laboratory confirmed, mainly in the western provinces. The Sin Nombre strain is most commonly associated with HPS in Canada, reflecting the distribution of its reservoir, *Peromyscus maniculatus*. Until recently, only a single laboratory-confirmed case of HPS has been reported in Quebec.

CASE: In June 2015, a previously healthy 22-year-old male presented with fever and gastrointestinal symptoms. He had returned from military training in Alberta from April until May 2015. Bloodwork revealed hemocytopenia, thrombocytopenia, granulocytosis and immunoblasts on smear. Chest radiograph showed bilateral pulmonary infiltrates with effusions. Rapid and refractory hypoxia resulted in intubation, mechanical ventilation and extracorporeal membrane oxygenation. Based on his epidemiological risk factors, Hantavirus serology was sent and was positive for Sin Nombre IgG and IgM, and was confirmed by PCR performed on a nasopharyngeal sample. This prompted public health notification, which helped identify two subsequent cases, both young men from the Canadian Armed Forces who presented similarly but followed a milder clinical course. The three patients had returned from a common large-scale military training exercise in Alberta. They reported mouse sightings and rodent excreta in the campsite and were exposed to aerosolized soil through military vehicle driving, trench excavation, live fire field exercises, and detonation of ammunition shells. The last case of Hantavirus from this region was reported in 1999.

CONCLUSION: We report a rare occurrence of HPS in a cluster of three patients in Quebec, who shared a common epidemiological exposure. HPS remains an important consideration in the differential diagnosis of severe respiratory illness, particularly in context of outdoor military activity in areas of high Hantavirus prevalence. Furthermore, we emphasize the importance of public health notification, and their role in identifying and tracking new cases in order to mitigate further infection risk.

L04

CHARACTERISTICS OF ANTIMICROBIAL STEWARDSHIP PROGRAMS AT PAEDIATRIC CENTRES ACROSS CANADA

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OBJECTIVE: Since Antimicrobial Stewardship Programs (ASPs) became a Required Organizational Practice instituted by Accreditation Canada in 2013, paediatric hospitals have been in various stages of ASP development. The objective of this study is to assess the implementation of ASPs by determining the prevalence and characteristics of ASPs at Canadian academic paediatric centres.

METHODS: Physician and pharmacy ASP practitioners from 16 academic children's hospitals across Canada were contacted. An electronic survey (using the REDCap™ database system) was used to gather information including details of the institution's ASP, metrics collected and measured, and process measures of the ASP. Institutional demographic information was also collected from websites and survey respondents.

RESULTS: We received 24 completed surveys representing 15 of the paediatric institutions (institution response rate 94%). Respondents included Infectious Diseases physicians (n=12 [50%]), pharmacists (n=10 [41.7%]) and Infectious Diseases trainees (n=2 [8.3%]). Of the 15 institutions, 11 reported having established ASPs (73.3%). The most common ASP strategies used hospital wide were clinical guidelines (n=12) and order sets (n=12). All sites had critical care units (both neonatal and paediatric intensive care units), and 10 sites had specific ASP strategies in both areas. Ten sites monitored antimicrobial usage using a combination of Days Of Therapy (n=9 [60%]), cost (n=9 [60%]) and resistance patterns (n=12 [80%]). Twelve sites had data management systems, with 9 sites (60%) documenting ASP recommendations and/or adherence to ASP recommendations.

CONCLUSIONS: The results of our survey suggest that most academic paediatric hospitals in Canada have established ASPs that are using a variety of ASP strategies. While all established ASPs monitor antimicrobial usage, there is significant variability in data collected and metrics reported. There is a necessity for both a description of the best metrics to measure the impact ASPs are having; and publications of these findings for benchmarking and quality improvement initiatives.

L05

TRANSMISSION RATE OF HIV FROM INFECTED HEALTHCARE WORKERS TO PATIENTS, A META-ANALYSIS

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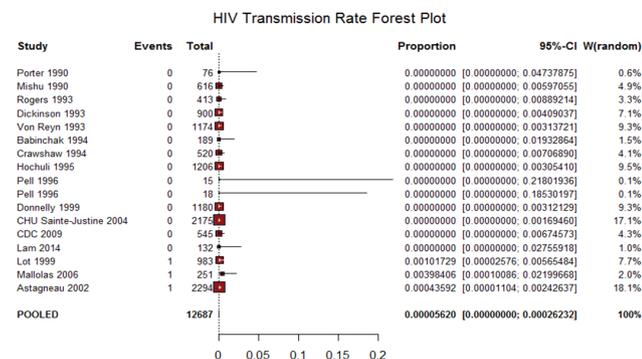
²Centre for Communicable Diseases and Infection Control, Public Health Agency of Canada, Ottawa, ON

OBJECTIVES: (1) To identify the risk of transmission of HIV from infected healthcare workers (HCWs) to patients during exposure-prone procedures from reported incidents; and (2) to incorporate an understanding of this risk into the recommendations for the prevention of transmission of bloodborne pathogens from infected HCWs to patients.

BACKGROUND: Although rare, transmission of HIV from infected HCWs to patients has been documented. As a result, guidelines for managing HCWs infected with bloodborne viruses are necessary for healthcare organizations and health professional regulatory authorities developing policies for patient safety. The Public Health Agency of Canada is conducting systematic reviews to inform the development of an evidence-based guideline on this topic. Quantifying the HIV transmission rate from published look-back investigations was identified as a sub-objective.

METHODS: A systematic review was conducted to identify investigations describing exposure of patients to an HIV-infected HCW. All studies in the systematic review were assessed for eligibility into a meta-analysis. A DerSimonian-Laird random effects model with inverse-variance weighting was used to pool the individual transmission rates of each study. Heterogeneity was assessed using the Cochran Q and Higgins I² statistics.

RESULTS: Seventeen exposure incidents were eligible for the meta-analysis. The pooled transmission rate for HIV was 0.0000562 (95% CI 0.0000–0.0002623). As the Q statistic and I² values were 9.16 (p=0.9069) and 0% (95% CI 0%–14%) respectively, the source(s) of heterogeneity was not explored.



CONCLUSION: In accordance with previous investigations and modeling studies, the risk of transmission of HIV from infected HCWs to patients is minimal and the management of these HCWs should reflect that level of risk.

Saturday, April 2, 2016

11:15–12:15 Session M
Room: Port McNeill

M01

DETERMINATION OF THE ABILITY OF THE CARBAPENEMASE INHIBITION METHOD (CIM) TO ACCURATELY IDENTIFY CARBAPENEMASE-PRODUCING ORGANISMS (CPO) AND THE IMPACT OF DECREASING CARBAPENEM INACTIVATION TIMES (CIT)

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BACKGROUND/OBJECTIVES: The CIM is recommended as an accurate low-cost method to detect CPO within 24h that utilizes supplies available in most laboratories. This study assessed CIM performance and impact of decreasing CIT to streamline workflow.

METHODS: The CIM by Tijet JAC 2015 was followed. 10µg meropenem (MER) discs were added to >2 MacFarland suspensions (MFS) prepared in 400µL sdH₂O then tubes were placed at 35°C. After 2h-CIT, MER discs were placed on Mueller-Hinton agar pre-seeded with 0.5 MFS *Escherichia coli* ATCC 29566 for 37°C incubation overnight. Zones <21mm around discs were considered positive (carbapenemase inactivation of MER), while zones >20mm were negative. This study compared varied CIT using blinded pre-characterized clinical isolates: 2h-CIT: n=258 [221 CPO of classes: A (108: 99 KPC, 4 SME, 2 GES, 2 IMI, 1 NMC), B (80: 73 NDM, 6 VIM, 1 IMP7), D (26: 15 OXA48, 6 OXA181, 4 OXA232, 1 OXA244), B+D (7: 4 NDM+OXA181, 3 NDM+ OXA232); non-CPO (37)]; 1h-CIT: n=211 [174 CPO: A (69: 62 KPC, 2 SME, 2 GES, 2 IMI, 1 NMC), B (72: 65 NDM, 6 VIM, 1 IMP7), D (26), B+D (7); non-CPO (37)]; and 30min-CIT: n=219 [182 CPO: A (69), B (80: 73 NDM, 6 VIM, 1 IMP7), D (26), B+D (7); non-CPO (37)]. Zones were read independently by 5 readers. Sensitivities/specificities (Sn/Sp) were determined from consensus reads.

RESULTS: CPO detected/CPO tested (% Sn) by CIM overall [and by class] using the above criteria were as follows: **2h-CIT – 204/221 (92.3%)** [A: 107/108 (99.1%); B: 77/80 (96.3%); D: 13/26 (50%); B+D: 7/7 (100%)]; **1h-CIT – 149/174 (85.6%)** [A: 67/69 (97.1%); B: 67/72 (95.8%); D: 7/26 (26.9%), B+D: 6/7 (85.7%)]; and **30min-CIT – 155/182 (85.2%)** [A: 65/69 (94.2%); B: 77/80 (96.3%); D: 7/26 (26.9%), B+D: 6/7 (85.7%)]. If pinpoint colonies inside zones >20mm were considered positive, Sn increased to 95.5% for 2h-CIT, 89.1% for 1h-CIT and 83.1% for 30min-CIT. Sp for all CIT was 97.3% due to a single CIM-positive MER-resistant *Aeromonas hydrophila* (chromosomal *cphA*) considered falsely positive.

CONCLUSIONS: While CIM with 2h-CIT is a relatively accurate way to separate CPO/non-CPO in 24h, it missed 7.7% CPO (mostly OXA48-type). If pinpoint colonies inside zones are considered positive, the proportion of CPO missed could be reduced to 4.5%. Using CIM with 1h or 30 min CIT is associated with excessive missed CPO.

M02**CARBAPENEMASE-PRODUCING ORGANISMS (CPO) ISOLATED FROM ENVIRONMENTAL WATER SAMPLES (EWS) COLLECTED IN THE GREATER TORONTO AREA (GTA), ONTARIO, CANADA**AJ McGeer^{1,2}, BM Willey^{2,3}, DA Boyd⁴, L Mataseje⁴, V Porter⁵, K Fakharuddin⁴, MR Mulvey⁴, T Edge⁶¹Mount Sinai Hospital; ²University of Toronto; ³University Health Network, Toronto, ON; ⁴National Microbiology Laboratory, Winnipeg, MB; ⁵Sunnybrook Health Sciences Centre, Toronto; ⁶Environment & Climate Change Canada Water Science & Technology Directorate Aquatic Contaminants Research Division, Burlington, ON**OBJECTIVES:** There has been a gradual yearly increase in CPO in the GTA (42 incidence cases in 2012; 64 in 2014) accompanied by a diversification of genotypes. This study, conducted between Jun-Nov 2012, investigated whether CPO were detectable in sewage treatment plant (STP) influents (IN), and if so, did CPO resist treatment in final effluents (FE) released by STP, and if so, was it possible to detect CPO in the urban watershed.**METHODS:** On 16 days, IN and FE from 5 STP, and on 14 days, surface water (SW) from 7 monitoring locations (5 Etobicoke Creek points, 2 proximate Lake Ontario beach points) were collected across the GTA for a total 250 samples. After sample filtration the 0.45µm filters were placed on Oxoid's MacConkey CV w/2mg/L cefpodixime or w/0.125mg/L meropenem plus 12mg/L cefsulodin. Oxidase-negative isolates from filters were tested phenotypically for CPO (ROSCO meropenem ± inhibitors). Filter-sweeps (FS) and suspect CPO were tested by PCR for GES, IMP, KPC, NDM, OXA-48-like, and VIM genes. When possible, amplicons were sequenced to distinguish CPO from ESBL-encoding genotypes.**RESULTS:** Overall, 33/180 (18%) STP samples grew 51 distinct CPO (1/ species/date): 27 from IN and 6 from FE, including 5 GES (2 *K. oxytoca*, 1 *K. oxanae*, 2 *R. planticola*), 43 KPC (5 *C. freundii*, 5 *E. cloacae*, 1 *E. coli*, 8 *K. oxytoca*, 3 *K. pneumoniae*, 21 *R. planticola*) and 3 OXA48 (2 *E. coli*, 1 *R. planticola*). Some FS were PCR+ but a correlating CPE could not be identified due to overgrowth. 60/180 (33.3%) STP-FS from 50 IN and 10 FE were PCR+, often for multiple genotypes: 47 bla_{KPC} (30 culture+), 3 bla_{OXA-48} (all culture+), and 1 bla_{OXA-181}, 2 bla_{GES-5}, 1 bla_{GES-15} (all culture-neg); 7 GES and OXA48-type PCR+'s have yet to be sequenced. The remaining 120 STP-FS (65 IN, 55 FE) were PCR-neg/culture-neg, as were 67/70 SW. The isolate was not isolated in 1 Etobicoke creek WS PCR+ for bla_{GES-5} but *A. baumannii* with bla_{OXA-24} was isolated from 1 Etobicoke creek and 1 beach sample.**CONCLUSIONS:** In 2012, diverse carbapenemase genes were identified by PCR and recovered in culture in multiple *Enterobacteriaceae* from untreated IN sewage collected from all 5 GTA STP studied. CPE were also isolated from treated FE released from 2 STP. Studies are currently underway to further elucidate the epidemiology of environmental CPE and their healthcare links, as clinical relevance of these findings has yet to be determined.**M03****RAPID ENZYMATIC DETECTION OF CLINICALLY-RELEVANT CLASS D-TYPE CARBAPENEMASES IN CARBAPENEMASE-PRODUCING ORGANISMS (CPO) USING CORIS BIOCONCEPT'S OXA48 K-SET ASSAY**BM Willey^{1,2}, R Iaboni¹, X Trimmi¹, DN Grohn⁴, G Ricci⁵, DA Boyd⁶, D Terenzi¹, A Mazzulli¹, P Lo^{1,2}, Tony Mazzulli^{1,2,3}, SM Poutanen^{1,2,3}¹Mount Sinai Hospital; ²University Health Network; ³University of Toronto; ⁴Michener Institute, Toronto; ⁵William Osler Health Sciences Centre, Brampton, ON; ⁶National Microbiology Laboratory, Winnipeg, MB**OBJECTIVES:** Distinguishing highly-significant CPO from less-significant carbapenem-resistant (CR) non-CPO is challenging. Rapid phenotypic tests are needed to improve recognition the inhibitor-negative class D OXA48-related CPO. This study evaluated Coris BioConcept's OXA48 K-Set lateral-flow line assay, a rapid low-complexity test that claims enzymatic confirmation of OXA48 and variant genotypes from isolates in 15 minutes.**METHODS:** The 259 highly-characterized blinded study Gram-negatives included 33 class D [26 class D (15 OXA48, 6 OXA181, 4 OXA232, 1 OXA244), 7 class B+D (4 NDM+OXA181, 3 NDM+OXA232)] CPO and 226 non-class D [108 class A CPO (99 KPC, 4 SME, 2 IM11, 2 GES, 1 NMCA), 80 class B CPO (73 NDM, 6 VIM, 1 IMP7) and 38 non-CPO]. Most non-class D isolates had multiple mixed resistance mechanisms, some including class D-related genes relevant to this study: 14 had confirmed OXA1 and 1 ea. had intrinsic OXA51 and OXA252. As directed, K-SeT inoculation used 1 colony (from around ertapenem discs) from MacConkey, Blood or Mueller-Hinton agars (Oxoid). At 15min, 5 independent readers documented results as negative (1 control band) or positive (2 bands - test/control). Sensitivity (Sn)/specificity (Sp) for OXA48-type CPO detection were from consensus reads, and 95% confidence intervals (CI) were calculated in www.graphpad.com.**RESULTS:** The OXA48 K-Set detected two clear brick-red bands in 26/26 strains carrying single class D carbapenemase genes (OXA48, OXA181, OXA232, 1 OXA244) as well in 7/7 strains carrying a class D carbapenemase gene accompanied by NDM (OXA181 and OXA232). The resulting sensitivity was 100% (95% CI 87.6–100). Conversely, the OXA48 K-set detected only the single control band in 226/226 non-class D isolates including in the *Shewanella putrefaciens* with its intrinsic OXA252 progenitor gene and in all isolates with known OXA1 that is commonly associated with the pandemic CTXM-15 ESBL. The resulting specificity was 100% (95% CI 98–100).**CONCLUSIONS:** This study found the low-complexity Coris Bioconcept OXA48 K-Set assay to be extremely easy to use, to produce rapid results and to be very simple to interpret. It proved highly accurate (100% sensitive and 100% specific) when used directly from colonies grown on all commonly used agars, providing results within 15 minutes of set-up.**M04****MOLECULAR AND EPIDEMIOLOGICAL FEATURES OF CARBAPENEMASE PRODUCING ENTEROBACTERIACEAE AND ACINETOBACTER IN ALBERTA 2013-2015**A Rusk^{1,2}, K Bush¹, J Fuller³, K Simmonds^{2,4}, G Taylor^{1,5}, K Fakharuddin⁶, MR Mulvey⁶, EA Henderson^{1,2}¹Alberta Health Services Infection Prevention and Control Surveillance Program; ²Community Health Sciences, University of Calgary, Calgary; ³Provincial Laboratory for Public Health; ⁴Alberta Health; ⁵Division of Infectious Diseases, University of Alberta, Edmonton, AB; ⁶National Microbiology Laboratory, Winnipeg, MB**OBJECTIVES:** Since the emergence of carbapenemase producing organisms (CPO), most epidemiologic studies have reflected single institutions or convenience samples. We have created comprehensive population-based surveillance for CPO in Alberta, Canada and report molecular and epidemiologic findings.**METHODS:** In response to the provincial Notifiable Diseases mandate, microbiology laboratories submitted all *Enterobacteriaceae* and *Acinetobacter* species isolated from patient clinical specimens that tested non-susceptible to at least one carbapenem. Isolates were investigated for the presence of carbapenemase genes at the National Microbiology Laboratory. Patient data were extracted and compiled from three provincial surveillance databases (Alberta Health Services Infection Prevention and Control acute care; Alberta Health public health; and the referent Provincial Laboratory for Public Health) from January 1, 2013 to April 31, 2015.**RESULTS:** Forty-nine incident CPO species were identified in forty-three patients, with a match rate of 85.7% and incidence rate of 5.2 per million population. NDM-1 cases (n=26) included isolates of *Klebsiella pneumoniae* (n=12) and *Escherichia coli* (n=9). KPC (n=2) was detected in *K. pneumoniae* and OXA subtypes (n=7) were detected in *Acinetobacter*, *E. coli*, and *K. pneumoniae*. Eighty-two per cent (40/49) were identified in Edmonton or Calgary facilities with >250 beds: 62.5% (25/40) had NDM-1; 5.0% KPC (2/40), and 15.0% OXA (6/40). Travel with healthcare outside of Canada (21/49, 42.9%) was the most commonly identified risk factor; this included NDM-1 (fifteen cases), KPC (one case), and OXA subtypes (seven cases). Another seven NDM-1 cases had a history of recent travel outside of Alberta without healthcare. Thirty-five cases with NDM, KPC or OXA were detected through urine or rectal specimens.

CONCLUSIONS: Designating CPOs as Notifiable and creating an aligned provincial definition has facilitated and standardized laboratory coordination for case identification, optimizing the surveillance data for both community and acute care needs. Through review of the three different databases we have been able to establish a comprehensive baseline population CPO rate in Alberta over a 28-month period. Having identified travel with healthcare outside of Alberta as a local risk factor, we can focus screening on this population when they come in contact with healthcare facilities.

11:15–12:15 Session N Room: Port Alberni

N01

CEREBRAL PHAEOHYPHOMYCOSIS CAUSED BY *FONSECAEA*

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BACKGROUND: Cerebral phaeohyphomycosis (CP) is a rare cause of fungal central nervous system infection. Among the many fungal species associated with CP, *Fonsecaea* species are quite rare. As such, CP due to *Fonsecaea* is poorly understood with few cases reported in the literature.

CASE: The authors report a case of a progressive brain abscess caused by *Fonsecaea* species in a 63-year-old male with poorly controlled type 2 diabetes, liver cirrhosis due to hepatitis B and recent travel to South Sudan.

PRESENTATION: The patient presented to a Calgary emergency room with headache and a four month history of progressive malaise, weight loss and diarrhea two days after returning from South Sudan. Initial CT head was negative. Repeat CT head approximately one week later revealed a left frontal lobe abscess.

DIAGNOSIS: Diagnosis was made from microscopy and culture identification of a dematiaceous mould in a biopsy of a single left frontal abscess. *Fonsecaea* genus was confirmed using 28S ribosomal RNA gene sequencing of the isolated fungus.

TREATMENT: Despite treatment with liposomal amphotericin B and voriconazole the patient clinically deteriorated and passed away.

CONCLUSIONS: Dematiaceous fungal brain abscesses are rare causes of central nervous system infections. Early diagnosis with tissue biopsy is essential for timely access to appropriate antifungal therapy. Complete surgical resection is associated with improved outcomes.

N02

REPORT OF 2 CASES OF PROSTHETIC JOINT INFECTIONS DUE TO *NEISSERIA SKKUENSIS*, A NOVEL *NEISSERIA* SPECIES

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BACKGROUND: We describe the first 2 reported cases of prosthetic joint infection due to *Neisseria skkuensis*. The organisms were isolated from knee synovial fluid samples. *Neisseria skkuensis* has only been previously described in 2 case reports. The first case being a bacteremia in a diabetic patient with a foot ulcer, and the other a case of prosthetic valve endocarditis.

METHODS: Standard biochemical, automated identification panels and MALDI-TOF MS were performed. The isolates underwent molecular identification with 16S rRNA gene sequence analysis, first with a 500 bp amplicon, and then with a 1500 bp amplicon. To characterize the novel species further, both isolates were subject to whole genome shotgun sequencing, with a phylogenetic tree generated based on 40 marker genes.

RESULTS: Both organisms failed to be identified by conventional biochemical tests, automated identification systems and MALDI-TOF MS. The 500 bp 16S rRNA gene segment was unable to identify *N. skkuensis* to a species level. The identification of both isolates was confirmed with further testing of the 16S rRNA gene, with amplification and sequencing of

the full ~1500 bp segment at the National Microbiology Laboratory (Winnipeg, Canada), having a 100% match to the novel species, *Neisseria skkuensis*. The phylogenetic tree, generated from whole genome sequencing, confirmed the separation of *N. skkuensis* from other species suggesting that it indeed is a novel species

CONCLUSIONS: Given the difficulty in identifying these isolates to a species level using conventional biochemical tests, automated identification systems and MALDI-TOF MS, any suspected isolate should be referred onto a reference laboratory for molecular identification. Amplification of a larger segment of the 16S gene (1500 bp) and whole genome sequencing results do allow unambiguous identification of this novel species and should be used if *N. skkuensis* is suspected.

N03

MORBILLIFORM RASH ASSOCIATED WITH CORONAVIRUS DETECTION DURING AN OUTBREAK OF MEASLES IN MANITOBA

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³Department of Pediatrics & Child Health, University of Manitoba;

⁴Public Health Agency of Canada/National Microbiology Laboratory, Winnipeg, MB

BACKGROUND: Measles is a highly infectious, vaccine-preventable virus that has had an increased incidence due to under-vaccinated populations. During the increased incidence of confirmed and suspected measles cases in 2014/2015 in Manitoba, clinicians observed many morbilliform rashes. Clinical suspicion was supplemented by molecular diagnostics for measles virus, however, many cases were negative for measles virus. Further viral investigation was proposed to understand the various causes of presumed viral morbilliform rash seen in this timeframe.

METHODS: All samples in the province for measles polymerase chain reaction (PCR) are sent to CPL. From January 1, 2014 to June 30, 2015, 23 samples representing 15 individuals were positive for measles. Fifteen samples (from 15 individuals) were negative. These 15 samples were tested on the Seeplex® RV15 respiratory virus multiplex PCR assay.

RESULTS: In 7 (46.6%) samples, no respiratory virus was detected. RSV was found in 2 (13.3%) and influenza A and B (1 [6.7%] each). Interestingly, coronavirus was detected in 5 (33.3%) samples. Coronavirus OC43 was detected in 4 (26.7%) cases (1 co-infection with RSV and 1 with influenza A). A single (6.7%) coronavirus 229E/NL63 was also detected.

CONCLUSIONS: Morbilliform rashes are associated with a variety of infectious and non-infectious processes, including many viral agents, making clinical diagnosis to determine etiology challenging. This represents the first time, to our knowledge, coronavirus has been found in association with morbilliform rash. These data are important to help guide clinicians in their differential diagnoses and consider epidemiology in determining the etiology of suspect measles cases.

N04

TICK-TOCK, THE CURIOUS CASE OF AN ID TIME BOMB – PULMONARY MELIOIDOSIS IN QUÉBEC, CANADA

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³McGill University, Montréal, QC

BACKGROUND: Melioidosis is caused by a saprophytic gram negative rod, *Burkholderia pseudomallei*, which is readily recovered from water and wet soils, particularly from rice paddy fields. It is endemic to South and South East Asia, China as well as Northern Australia. The last documented case of imported melioidosis in the province of Québec was in 1989.

CASE: In September 2014, a previously healthy 24-year-old Canadian female presented with pleuritic right-sided chest pain, in the context of insidious respiratory and constitutional symptoms including progressive dyspnea on exertion, a productive cough, fever, chills and night sweats. The patient had lived in Singapore for 10 years during her childhood. She was currently attending medical school in France. She recently travelled to Cambodia and Singapore from June until August 2014. She stayed mainly

in Phnom Phnh, where she was working in a medical clinic. She travelled to rural locations, and had hiked through rice paddy fields. On presentation, laboratory investigations revealed leukocytosis and hyponatremia. A chest radiograph and computed tomography scan revealed a right apical cavitary lung lesion. Bronchoalveolar lavage was performed and tested negative for mycobacterium on microscopy, PCR and culture. Fungal culture, respiratory virus PCR, *Pneumocystis* and *Legionella* were also negative. At 24 hours, growth was noted on both non-selective and *Burkholderia cepacia* selective media, leading to the presumptive diagnosis of melioidosis. The specimen was sent to the provincial laboratory for identification by 16S sequencing, confirming *Burkholderia pseudomallei* infection. She was treated with a 21-day course of imipenem and doxycycline. Following completion of acute phase therapy, she began a three month course of eradication therapy with trimethoprim-sulfamethoxazole.

CONCLUSION: We present a rare Québec case of imported pulmonary melioidosis, in a patient who failed to demonstrate any of the risk factors traditionally associated with progression to clinical disease. Although a rare imported disease in Canada, a surge of cases in the Caribbean and sporadic autochthonous cases in the United States increase the likelihood that we will encounter more patients with melioidosis in Canada.

11:15–12:15 Session O Room: Finback

O01

HEPATITIS C VIRUS (HCV) MORTALITY PATTERNS IN THE BRITISH COLUMBIA HEPATITIS TESTERS COHORT (BC-HTC)

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OBJECTIVE: To describe the population-level impacts of HCV acquisition risks versus chronic infection on mortality for HCV negative and positive testers.

METHODS: The BC-HTC includes 1,135,947 individuals tested for HCV (1992-2013) or reported as a HCV case (1990-2013), linked to their corresponding healthcare administrative data. We computed age-adjusted annual all-cause, liver- and drug-related mortality rates/100,000 population and age-, sex- and year-adjusted standardized mortality ratios (SMRs) for: 1) seroconverters (known HCV acquisition timeframes and risks); 2) anti-HCV positive on initial testing (the majority are chronically infected and no longer engage in acquisition risk activities); and 3) HCV negatives.

RESULTS: Of 1,035,155 HCV tests/cases included in this analysis, 64,295 (6.2%) were HCV positive. Overall, 16.2% (10,430/64,295) of HCV positive vs. 6.4% (61,759/970,860) of HCV negative individuals died. For HCV positives, age-adjusted all-cause mortality increased from 1993-2005 and remained stable thereafter. Liver-related mortality increased continuously from 1993-2013. Drug-related mortality increased from 1993 to a peak in 2005, then declined until 2013. Mortality rates were consistently higher for males versus females. All-cause mortality for seroconverters was significantly higher than those with chronic HCV and HCV negatives (SMRs: 6.3, 3.1 and 1.2). Liver-related mortality was significantly lower for seroconverters than for chronic HCV and was lowest for HCV negatives (SMRs: 12.4, 17.3 and 2.3). Liver cancer mortality was significantly lower for seroconverters than for chronic HCV and was lowest for HCV negatives (SMRs: 3.8, 17.9 and 1.8). Drug-related mortality was highest for seroconverters compared to chronic HCV and HCV negatives (SMRs: 21.9, 11.6 and 1.3).

CONCLUSIONS: The BC-HTC enables comprehensive assessment of the mortality impacts of HCV infection and is able to differentiate acquisition risk mortality from the impacts of chronic infection. The excess mortality related to HCV acquisition risks is distinct from viral sequelae for a significant proportion of the HCV infected population. Therefore, antiviral treatment on its own will not optimize mortality reductions in the affected populations.

O02

MAPPING THE GAPS AND OPPORTUNITIES FOR IMPROVED KNOWLEDGE TRANSLATION AND EXCHANGE CONCERNING TUBERCULOSIS AMONG PRIORITY POPULATIONS IN CANADA

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BACKGROUND: In Canada, the burden of Tuberculosis (TB) is concentrated among Indigenous and foreign-born populations. This disproportionate burden underlies the need to foster greater exchange between affected communities, researchers, policy makers and practitioners to improve the effectiveness and implementation of existing national strategies for TB control. In response, we have undertaken an initiative to identify and map opportunities for improved knowledge translation and exchange (KTE) concerning TB among priority populations in Canada.

OBJECTIVE: To develop a framework that can guide the development of future KTE resources and activities targeted at public health practitioners, researchers and policy makers. To inform this framework, a summary of gaps between current TB guidelines, evidence and practice, as well as opportunities for improved TB strategies has been developed. This work is focused on Indigenous and foreign-born populations.

METHODS: We have reviewed TB guidelines and national strategies, and have conducted interviews with key informants to evaluate alignment between existing evidence, practice and strategies in terms of active and latent TB prevention, diagnosis and management.

RESULTS: Identified gaps include issues surrounding jurisdictional divides, surveillance systems, performance indicators, social determinants (e.g. housing conditions), early diagnosis and treatment adherence. Our framework will allow us to develop a range of KTE products and activities including webinars, comprehensive reviews, plain language materials, interactive systems/issues maps, platforms for knowledge exchange and training for researchers, policy makers, practitioners and community members.

CONCLUSION: A number of KTE gaps and opportunities exist in TB prevention. This work will facilitate the bridging of research and practice to inform decision makers and improve access to knowledge among those working with populations with the greatest burden of disease. It will help connect knowledge users and key experts in Canada and create a space for reflection on Canadian TB issues.

O03

ANALYZING YOUR SEQUENCE DATA

MA Croxen¹, **KA Macdonald**^{1,3}, **L Hoang**^{1,2}

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OBJECTIVE: There is a plethora of bioinformatics software available that is generally freely available, open-source with permissive licenses. Sorting out useful and relevant tools to align with workflow can be a challenging task. We here describe available bioinformatics tools to address common (meta)genomics questions.

METHODS: PubMed, bioarxiv, and social media were used to keep up to date on the latest bioinformatics tools. Popular choices and considerations will be discussed here in context of their usefulness in analysing genome data for clinical and public health infectious disease purposes. Specific examples will be provided based on pipelines that are used by the BCCDC Public Health Laboratory, as well as those described in literature.

RESULTS: There are many bioinformatics tools available to analyse genome data. These tools can be used for quality assurance, antimicrobial resistance and virulence profiling, species identification, rare pathogen detection, strain typing, serotyping, and phylogenetic inference for surveillance and outbreak investigations. Very few tools offer an all-in-one solution, so understanding the utility of each tool is needed for appropriate data analysis. One example of this is finding (and removing) sequence contamination in your sample. Pan-genome analysis is useful for

Abstracts

identifying relevant markers for the design of diagnostic assays, while surveillance and outbreak investigations benefit from the high resolution provided by the genome sequences. Finally, the use of metagenomics has been used in the identification of rare pathogens, when all other diagnostic tests were indeterminate.

CONCLUSIONS: The explosion of high-throughput sequencing capabilities sets it as a disruptive technology in clinical microbiology and public health reference microbiology. Analysis of genomic data is computationally expensive and requires understanding of both programming languages and biology. The described software will help in setting up pipelines that may suit your diagnostic needs. User-friendly solutions exist that should make routinely running these analytical pipelines less cumbersome.

O04

HOSPITAL PANDEMIC PREPAREDNESS: ARE WE READY? A SIMULATION-BASED ASSESSMENT

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INTRODUCTION: Outbreaks of severe infectious diseases (ID) are dangerous, costly, and may disrupt fundamental health services. Hospital preparedness requires planning, development, education, practice and evaluation with periodic revision. Simulation-based education is a valuable teaching tool, as well as a hazard free opportunity to assess protocols and health-care workers (HCW) proficiency in hospital management of emerging IDs.

OBJECTIVES: Our main goal was to use simulation to assess our institution's pandemic preparedness plan (PPP) in action.

METHOD: A longitudinal and interprofessional simulation was planned by ID and simulation experts. In-situ hybrid simulation model was chosen: standardized patient for screening at triage and high fidelity patient simulator for clinical management. Scenario design allowed for involvement of HCW most exposed from an infectious disease standpoint. Participation was determined at random as simulation was unannounced. Four observers used checklists to rate several critical events including case identification, isolation and use of personal protection equipment. Management of acute pulmonary distress and cardio-pulmonary resuscitation (CPR) were also observed from an infection control perspective. A 30 min debrief geared towards global HCW safety was held with participants immediately after the exercise.

RESULTS: The case was identified and isolated quickly. However, several non-conformities were observed, such as improper N-95 and PPE use resulting in potential HCW exposure, and technical challenges with facilities. We observed a need for increased personnel and better coordination in the ICU in case of CPR. Recommendations were made based on observations and feedback.

CONCLUSION: Simulations appear to be interesting tools to achieve the goals of hospital PPP and to justify ongoing resource allocation. Lessons learned in this experiment have guided changes in protocols and have helped identify areas where additional educational tools are needed. In order to maintain motivation and interest, our periodical simulations program is ongoing to further improve our institution's PPP and HCW safety.

11:15–12:15 Session P
Room: Orca

P01

A LEARNER-CENTERED ANTIMICROBIAL STEWARDSHIP EDUCATIONAL CURRICULUM: RESULTS OF THE NEEDS ASSESSMENT PILOT STUDY

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BACKGROUND: Antimicrobial stewardship (AS) is an effective strategy for limiting inappropriate antimicrobial use, preventing the emergence of pathogen resistance, while improving clinical outcomes. There is a gap

in key stakeholder input from physicians and pharmacists regarding AS education. A formal needs assessment for an AS educational curriculum for clinical teams (pediatrics residents, intensivists and hospital pediatricians) has yet to be conducted.

OBJECTIVES: 1.To determine AS concerns in clinical practice on the clinical teaching unit (CTU) and the Pediatric Intensive Care Unit (PICU) so as to inform a competency based AS curriculum for clinical teams 2. To ensure feasibility and applicability of this curriculum by understanding the targeted learning environment pertaining to the interaction between pharmacists and physicians on CTU and PICU teams.

METHODS: Phase 1 will determine what AS concerns clinical teams face by having pharmacists on team rounds submit feedback cards as they identify these concerns, for three months. Phase 2 will conduct six clinical team group interviews exploring AS learning preferences. The educational strategies developed and implemented will be based on both phases of this mixed methods study.

RESULTS: The 15 pharmacy cards collected during the first half of the needs assessment pilot study reveal CTU AS concerns: using antibiotics in bronchiolitis cases and failing to narrow therapy once a source pathogen is identified. In PICU, the concerns were narrowing therapy and empiric usage of antibiotics.

CONCLUSIONS: This project addresses an identified educational need in everyday practice. It provides an understanding of local antimicrobial utilization patterns and AS educational opportunities during clinical rounds. It applies a learner-centered approach, identifying AS needs at the point of care to inform a curriculum tailored to the clinical team. If successful it could have widespread impact on AS education and could be applied to other programs.

P02

AN APPARENT INCREASE IN DEFINED DAILY DOSES PER PRESCRIPTION CAN BE EXPLAINED BY A CHANGE IN THE AGE DISTRIBUTION OF ANTIBIOTIC USE

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INTRODUCTION: The defined daily dose (DDD) is a standard measure used for comparison of drug utilization trends across jurisdictions. However, rates are typically reported without adjusting for the underlying age structure of the population. The goal of this study was to compare age-adjusted antibiotic utilization and prescription rates to crude estimates over time in BC.

METHODS: Anonymized, line-listed data of all BC outpatient oral antibiotic prescriptions from 1996 to 2013 were obtained from the BC PharmaNet database. Analyses were conducted in SAS and Excel using Anatomical Therapeutic Classification (ATC) standard codes and defined daily dose (DDD) values. Rates of prescriptions (Rx) and utilization were normalized to the BC population and expressed in either Rx or DDD per 1000 persons per day (DID). Indirect age-adjustment was performed using 2006 BC population estimates.

RESULTS: Overall, decreases of 13% and 16% in crude and age-adjusted utilization rates were observed between 1996 and 2013, respectively. All age-specific utilization rates decreased since 1996 with the exception of those aged 60 or older. Age-adjusted overall utilization and prescription rates followed crude rates closely. However, average DDD per prescription trends, used as a proxy for duration of treatment, differed, with crude rates increasing over time (9.22 in 1996 to 10.50 in 2013) and adjusted rates remaining relatively stable (9.78 in 1996 to 9.97 in 2013). A similar trend was observed among records restricted to BC physicians and surgeons and BC dental surgeons.

CONCLUSIONS: The apparent increase in DDD per prescription can be explained by a change in the age distribution of prescriptions, rather than an increasing duration of therapy for a given indication. However, there remains room to shorten duration of therapy for many indications.

P03

A POINT-PREVALENCE SURVEY OF ANTIMICROBIAL UTILIZATION WITHIN NEW BRUNSWICK HOSPITALS TO FOCUS ANTIMICROBIAL STEWARDSHIP EFFORTS

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OBJECTIVES: To assess current patterns of antimicrobial utilization in the province of New Brunswick and identify targets for Antimicrobial Stewardship interventions.

METHODS: A point prevalence survey was completed in 21 hospitals in New Brunswick, Canada. All admitted inpatients receiving at least one systemic antimicrobial at the time of the survey were included. Main outcome measures included: patterns of utilization, based on indication and specific antimicrobial prescribed; appropriateness of utilization, based on simple predetermined criteria developed by the research team; and duration of surgical prophylaxis. Descriptive statistics and chi-squared test of independence were used to analyse the data.

RESULTS: The survey was completed between June and August 2012. Of 2244 eligible patients, 529 (23.6%) were on systemic antimicrobials. A total of 691 courses of antimicrobials were prescribed, 587 (85%) for treatment, 104 (15%) for prophylaxis. Within the treatment group (n=587), the most frequently prescribed classes were: fluoroquinolones (25.6%), extended-spectrum penicillins (10.2%) and metronidazole (8.5%). The most common treatment indications were pneumonia (30%), gastrointestinal infections (16%), and skin and soft tissue infections (14%). Based on predefined criteria 23% (n=134) of the treatment orders were inappropriate and 20% (n=120) of the antimicrobial prescriptions had absolutely no documented indication. Areas of inappropriateness included: lack of appropriate IV-to-PO step-down (n=34 [6%]), inappropriate dose (n=30 [5%]), treatment of asymptomatic bacteriuria (n=24 [4%]) and inappropriate duplication of antimicrobial coverage (n=22 [4%]). 33% (n=27) of surgical prophylaxis orders exceeded 24 hours.

CONCLUSIONS: The findings support the need for Antimicrobial Stewardship efforts focused on established interventions: improved documentation, optimised fluoroquinolone use, and minimized length of surgical prophylaxis. The data also provide a baseline from which to measure the effectiveness of future stewardship initiatives.

P04

THE IMPACT OF REPORTED BETA-LACTAM ALLERGY ON INPATIENT OUTCOMES: A PROSPECTIVE MULTICENTER OBSERVATIONAL STUDY

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OBJECTIVE: Beta-lactam antibiotics are the preferred class of antimicrobial for many infectious syndromes, yet reported beta-lactam allergy often prevents their use. We sought to evaluate the impact of receipt of non-preferred therapy due to reported beta-lactam allergy on clinical outcomes.

METHODS: We conducted a prospective trainee-led cohort study on the prevalence and clinical impact of reported 'beta-lactam' allergy at three academic hospitals in Toronto, Canada. The primary outcome was a composite measure of readmissions, acute kidney injury, *C. difficile* infection, and drug-related adverse reactions. The predictor of interest was beta-lactam allergy history and receipt of preferred beta-lactam therapy.

RESULTS: A total of 507 patients were included in the analysis. Of 95 patients (23%) with reported beta-lactam allergy, preferred therapy was a beta-lactam in 72 (76%) of cases and non-beta-lactam in 23 (24%) cases. When beta-lactam was preferred therapy, 47 (65%) received beta lactam therapy, but 25 (35%) received non-beta-lactam therapy due to reported beta-lactam allergy. Less than half (48%) of patients who did not receive preferred beta-lactam therapy had a severe reaction on history. Adverse outcomes were greatest in the group of patients with a history of beta-lactam allergy that did not receive preferred beta-lactam therapy (40%) with

an unadjusted odds ratio of 3.43 (95%CI 1.48-7.96) and adjusted odds ratio of 3.18 (95%CI 1.28-7.89) compared to no history of beta-lactam allergy. **CONCLUSIONS:** Patients with reported beta-lactam allergy who receive non-preferred beta-lactam therapy are at increased risk for adverse events. Less than half of these patients have a history in keeping with a prior severe reaction. Development of inpatient antimicrobial stewardship programs aimed at preserving the use of beta-lactam therapy among these patients are needed.

STUDENT POSTER PRESENTATIONS

Thursday, March 31, 2016
Room: Grand Ballroom

SP01

INFECTIOUS DISEASES CONSULTATION AT ACADEMIC TERTIARY CENTRES IN TORONTO, ONTARIO

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OBJECTIVE: Little data have been collected on the nature and variety of consultations seen by Infectious Diseases (ID) trainees and consultants. We aimed to systematically collect these data in order to understand the nature of ID practice, its value, and determine whether trainees are meeting specialty training requirements as outlined by the Royal College of Physicians and Surgeons of Canada.

METHODS: Data regarding consultations seen by the ID services at three academic tertiary care centres (St Michael's Hospital [SMH], Sunnybrook Health Sciences Centre [SHSC] and Toronto General/Mount Sinai Hospital [TGH/MSH] Toronto, Canada) were documented by a resident physician over a combined 22-week period. The reason for consultation, referring service, and date and time of consultation was documented.

RESULTS: A total of 560 consultations were seen (SMH – 251, SHSC – 240, TGH/MSH – 69 at TGH/MSH) over 75, 50, and 14 days, respectively. An average of 3.8, 6.1, and 4.0 consults were seen during working weekday hours at the respective sites. Weekday consultations comprised 85% of all consultations at all sites. Overall, the most common reason for consultation was bacteremia, followed by sepsis of unclear origin, osteomyelitis, and *C. difficile* infection, with inter-site variation. Mandatory *Staphylococcus aureus* bacteremia consultations comprised 5.2%, 5.0%, and 7.2% of ID consultations at SMH, SHSC, and TGH/MSH, respectively. Overall, the most common referring services at all sites were General Internal Medicine, Critical Care, and Orthopedic Surgery. The ten most common reasons for consultation differed significantly between sites and only accounted for half of all consults.

CONCLUSION: A diversity of consultations is seen by Infectious Diseases specialists and trainees in tertiary centres in Toronto, both between and within sites. Comparison with additional centres is needed to further understand the role of ID consultation and resident training experiences.

SP02

ENTEROVIRUS AS AN EMERGING RESPIRATORY PATHOGEN: THE NL PAEDIATRIC EXPERIENCE

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BACKGROUND: Non-polio enteroviruses are a common cause of childhood illness, typically seen in late summer/early fall. In 2014, cases of Enterovirus-D68 were reported in children presenting with severe respiratory symptoms across the US and Canada. Cases of viral acute flaccid myelitis have been associated with non-polio like enteroviruses and were reported during this time.

OBJECTIVE: To understand the impact of enteroviruses on paediatric patients (≤ 18 years of age) admitted to the Janeway Children's Hospital who presented with respiratory illness from September 2014 to August 2015.

METHODS: Retrospective observational study of all laboratory-confirmed cases of enterovirus in NL from September 2014 to August 2015 was conducted. Paediatric cases were examined to determine outcome and severity of disease as measured by patient length of stay, PICU admission, oxygen requirements and intubation, pulmonary comorbidities (ie. history of asthma, RAD, or other chronic lung disease), and occurrence of adverse neurologic events.

RESULTS: A total of 162 laboratory-confirmed cases of respiratory enterovirus were received from the NL Public Health Laboratory, of which 68 paediatric cases were included in the analysis. 48 cases (70.6%) required hospital admission and 13 (27.1%) of these required time in the PICU. The average length of stay was 4.37 days. 27 (39.7%) of patients had a history of asthma or lung disease. The mean length of stay for patients with asthma/lung disease was 1.36 days shorter than for patients with no previous diagnosis. Two-thirds of admitted patients required some form of supplemental oxygen; 2 children required intubation.

CONCLUSION: There was a significant burden of respiratory illness due to enterovirus in children of NL during 2014-2015. Pre-existing history of asthma/lung disease did not influence length of stay. No death or adverse neurologic events occurred as a result of enterovirus infection.

SP03 ABSTRACT WITHDRAWN

SP04

DETECTION OF GROUP B STREPTOCOCCI (GBS) BY ISOTHERMAL AMPLIFICATION: AN AFFORDABLE, AND RAPID POINT-OF-CARE ALTERNATIVE TO EXPENSIVE COMMERCIAL MOLECULAR DIAGNOSTIC TESTS

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INTRODUCTION: GBS is the most common cause of life-threatening septicemia and meningitis in neonates and infants <3 months. The rate of vertical transmission among neonates born to women colonized with GBS at the time of delivery is about 50%. Maternal intrapartum antibiotic prophylaxis can prevent neonatal GBS infection. Lower vaginal and rectal swab screening cultures performed at 35 to 37 weeks of gestation for all pregnant women.

OBJECTIVES: To evaluate the performance of a LAMP assay to detect GBS colonization in the anogenital tract of pregnant women as compared to the current method of broth enrichment followed by culture.

METHODS: Randomly selected E-Swab specimens from 617 women sent for routine screening at Hamilton Health Sciences were used for testing after routine culture was complete. Each specimen was tested twice with and without enrichment broth. *Streptococcus agalactiae* ATCC 12386, and *S. pyogenes* ATCC 19615 were used as the positive and negative controls, respectively.

RESULTS: One hundred-thirty specimens were positive for GBS by LIM/LAMP and original culture. Only 116 were positive for GBS by direct e-swab LAMP and original culture. There were 15 discordant results of which 12 were culture negative and LIM/LAMP positive and 1 was LIM/LAMP negative and culture positive. Discordance analysis was done by repeated culture and LAMP followed by PCR. All 12 culture-negative LAMP-positive specimens and one LAMP-negative culture-positive were PCR positive.

The performance characteristics of e-Swab/LAMP as compared to culture were as follows: 89.2% sensitivity, 97.7% specificity, 91.3% positive predictive value and 97.1% negative predictive value. The respective performance values for LIM/LAMP as compared to culture were 99.2%, 97.5%, 91.5%, and 99.8%, respectively.

CONCLUSION: Detection of GBS by LIM/LAMP has a better and faster performance than culture. Direct e-swab /LAMP is about 10% less sensitive than LIM/LAMP even though it has a TAT of about 90 min. Since the accuracy of detection of GBS in screening is more important than rapid results LIM/LAMP is recommended as the new test. The TAT for the LIM/LAMP test is about 20 – 24 hrs compared to 48 to 72 hrs for culture.

SP05

VERIFICATION OF THE ALERE™ I INFLUENZA A & B TEST FOR THE RAPID DETECTION OF INFLUENZA A/B FROM NASOPHARYNGEAL SWABS AND ASPIRATES

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OBJECTIVE: Accurate point-of-care testing for the diagnosis of influenza is desirable for the prompt initiation of antivirals, avoidance of unnecessary antibiotics, and quick implementation of infection control measures. This study verified the Alere™ i Influenza A & B Test for the rapid detection of influenza A/B from nasopharyngeal swabs and aspirates.

METHODS: The study included NP swabs (NPS) and aspirates (NPA) collected and tested during the 2014-2015 influenza season by the reference standard: a CDC-developed real-time PCR assay for influenza A/B and by the Luminex xTag® Respiratory Viral Panel Classic assay for other respiratory viruses. Positive specimens for circulating influenza A (pdm09), influenza A (H3N2) and influenza B, and negative specimens including those negative for these targets but positive for other respiratory viruses, were randomized from a database of all available specimens from the respiratory season. Limit of detection (LOD) panels for influenza A (pdm09), influenza A (H3N2), influenza B (Massachusetts/02/12-like), and influenza B (Brisbane/60/2008-like) were generated. The accuracy, sensitivity, specificity, and inter- and intra-run reproducibility were assessed. Basic time course analysis was undertaken.

RESULTS: Twenty (10 pdm09 and 10 H3N2) influenza A positive and 20 influenza B specimens were assessed. Specimen types were as follows; influenza A pdm09 (10 NPS), influenza A H3N2 (6NPS, 4 NPA), influenza B (14 NPS, 6 NPA), other respiratory viruses (8 NP, 2 NPA), and negative for all respiratory viruses (4 NPS, 6 NPA). Sensitivity of the system was 65% for influenza A (combined pdm09 and H3N2) and 90% for influenza B compared to the CDC-developed assay. Specificity for influenza A and B was 100%. The 50% LOD for the Alere assay was generally 1-2 log less sensitive than the CDC assay for all targets. Reproducibility was good for all targets. The assay could be completed in <20 minutes.

CONCLUSION: The Alere™ i Influenza A & B Test provides a rapid, simple method for the detection of influenza A/B from NPS and NPA during peak periods of a respiratory season. However, specimens that generate a negative result should be forwarded to a laboratory that can undertake a more sensitive assay for influenza A/B.

SP06

12 WEEKS OF SOFOSBUVIR-LEDAPASVIR VERSUS SOFOSBUVIR-LEDAPASVIR-RIBAVIRIN IN CHRONIC HEPATITIS C, GENOTYPE 1: A SYSTEMATIC REVIEW AND META-ANALYSIS

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BACKGROUND: 12 weeks of Sofosbuvir (SOF) and ledipasvir (LDV) is one of several first line therapies recommended in patients with chronic Hepatitis C (CHC), genotype 1. The addition of ribavirin (RBV) is recommended for a subpopulation of those with CHC (with cirrhosis and who have failed prior therapy), though the efficacy of 12 weeks of SOF/LDV compared to SOF/LDV/RBV has not yet been established.

OBJECTIVES: to compare the failure of achieving sustained virologic response at 12 weeks (SVR12) and adverse events with the use of 12 weeks of SOF/LDV versus SOF/LDV/RBV in patients with CHC, genotype 1 who have cirrhosis and have previously failed therapy.

METHODS: We conducted a systematic review and meta-analysis. Two investigators independently searched electronic databases and relevant conference proceedings for randomized controlled trials that compared SVR12 rates when using 12 weeks SOF/LDV versus 12 weeks SOF/LDV/RBV in patients with CHC, genotype 1. Relative risks of failing to achieve SVR12 for SOF/LDV/RBV compared with SOF/LDV were pooled across studies using random effects models.

RESULTS: Our search strategy yielded 596 articles, 120 abstracts, and 89 conference proceedings. Five full-text articles were included in the systematic review and meta-analysis. Though studies had adequate allocation concealment and randomization, all studies had issues with lack of blinding and heavy pharmaceutical involvement. Among previous null responders with cirrhosis, the pooled RR of not achieving SVR12 with SOF/LDV versus SOF/LDV/RBV was 1.21 (95% CI 0.42–3.48). Adverse events were lower in the SOF/LDV compared to the SOF/LDV/RBV arms (pooled RR 0.87, 95% CI 0.79–0.96). There was a suggestion of publication bias with funnel plot asymmetry.

CONCLUSIONS: There is a non-statistically significant trend that 12 weeks of SOF/LDV increases the risk of failing to achieve SVR12 compared with 12 weeks of SOF/LDV/RBV in patients with CHC genotype 1, with cirrhosis and who are null responders. Due to the wide confidence intervals and evidence of publication bias, we are unable to conclude neither superiority nor non-inferiority of either regimen. Further research is needed to determine if 12 weeks LDV/SOF can be used over LDV/SOF/RBV in this subpopulation.

SP07

A CASE OF SUBACUTE NATIVE-VALVE INFECTIVE ENDOCARDITIS CAUSED BY *CARDIOBACTERIUM HOMINIS*

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BACKGROUND: HACEK organisms are a group of Gram-negative organisms that are well-established, albeit infrequently occurring causes of infective endocarditis (IE). This case is an example of IE caused by a HACEK organism, *Cardiobacterium hominis*, presenting as a subacute illness in a patient with an absence of prosthetic valves and no history of intravenous drug use (IVDU).

CASE: A 42-year old man with a history of mitral valve prolapse (MVP) presented to hospital following an in-office transthoracic echocardiogram (TTE) concerning for IE. His only symptoms were a few-month history of generalized fatigue and malaise, but no fevers or other infectious symptoms. Four months prior to the onset of his symptoms, he had a complication-free dental cleaning. He had no history of immunosuppression, IVDU or chronic lines or catheters. On examination, he had a grade III/VI holosystolic murmur best heard at the apex, radiating to the axilla, with no stigmata of IE. Blood work showed a mild leukocytosis and an elevated CRP. Serial ECGs showed only mild sinus tachycardia. A transesophageal echocardiogram showed severe thickening and myxomatous degeneration of the mitral valve and could not rule out vegetation. Given the patient's hemodynamic stability and unclear valvular pathology, empiric antibiotics were not continued. Blood cultures drawn on admission both grew Gram-negative bacilli after 43.2 hours, however both the longer incubation time for the bacteria and the staining itself was inconsistent with most Gram-negative bacteria. The following day, *Cardiobacterium hominis* was isolated. The patient remained clinically stable and was discharged with a PICC line and a 4-week course of ceftriaxone.

DISCUSSION: This case brings up several learning points about the presentation of subacute IE, the risk of dental procedures in patients with structural cardiac abnormalities and a classical presentation of *C. hominis*, an uncommon but well-described cause of endocarditis.

SP08

CHARACTERISTICS OF PNEUMONIA ADMISSIONS IN HIV-POSITIVE INDIVIDUALS: A SINGLE-CENTRE, 10-YEAR CROSS-SECTIONAL RETROSPECTIVE ANALYSIS

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OBJECTIVE: A recent study from our centre identified pneumonia as the most common reason for admission in HIV positive individuals. The objective of the present study is to further characterize these admissions, including index of disease severity, causative organisms, method of diagnosis and choice of initial empiric therapy.

METHODS: Our centre's medical database was used to identify all HIV-positive patients admitted to medical wards with a diagnosis of pneumonia from January 2005 to January 2015 in one tertiary care hospital, yielding a total of 389 admissions. Patient demographics, length of stay, and survival data were obtained through the medical database and supplemented with hospital chart reviews. At the time of abstract submission, a total of 79 admissions had been reviewed.

RESULTS: The median CD4 count for 62/79 (78%) admissions was 119 (Q1 to Q3 = 38 to 283). For all admissions, an organism was isolated in only 37% (25/68). Regarding method of diagnosis during admission, only eight bronchoalveolar lavages (BAL) were performed. For admissions with an organism isolated, the most common organism was *Pneumocystis jirovecii* with a frequency of 16.2% of all admissions. Using the CURB-65 score as an index of disease severity, 85% of presentations were mild, 15% were moderate, and were severe by the CURB-65 criteria. We determined the initial choice of antibiotic therapy for each admission and further categorized it as following IDSA guidelines or not. For the 69 admissions where this data was available, 56% of physicians followed the IDSA guidelines.

CONCLUSIONS: For all hospital admissions, there was a low percentage of an isolated organism at only 37%, possibly related to underutilization of BAL. Despite advanced HIV disease as determined by low CD4 count, less than 12% of admissions had a BAL performed. Only 56% of physicians followed IDSA guidelines for empiric antibiotic therapy for inpatient pneumonia. The IDSA guidelines do not address HIV positive individuals, suggesting a more important role for diagnostic methods in this population. The infrequent use of diagnostic BAL may contribute to low rate of etiologic diagnosis and suboptimal antimicrobial therapy.

SP09

FIRST REPORTED HUMAN CASE OF *CRYPTOCOCCUS GATTII* MENINGOENCEPHALITIS WITH LOCAL ACQUISITION IN EASTERN CANADA

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BACKGROUND: *Cryptococcus gattii* is an encapsulated fungus known to cause meningoencephalitis in non-immunocompromised hosts. Its ecological niche has expanded from eucalypts in tropical areas to coniferous trees on the North American West Coast, where there have been ongoing outbreaks of *C. gattii*, mainly in British Columbia.

CASE: A case of *C. gattii* meningoencephalitis was diagnosed in a previously healthy 20-year-old female from the greater Montreal area. CSF cultures were positive for *C. gattii* and sequencing confirmed VGIIa molecular subtype. She responded well to treatment with liposomal amphotericin B, 5-flucytosine and external ventricular derivation. No immune deficits were identified. The patient had no prior travel history outside the province, but had worked in a pet shop until her illness. Because animals can be carriers, an investigation of the workplace was carried out including cultures of cages and environment, but no *C. gattii* was isolated. The patient also had dogs and cats at home which were not tested for *C. gattii* although cases of asymptomatic carriage, for up to 8 years, have been reported in domestic animals.

CONCLUSION: Although two human cases of local acquisition of *C. gattii* in New England have been reported, this is the first reported case depicting local human acquisition in Eastern Canada. While epidemiological investigation could not confirm zoonotic transmission, *C. gattii* acquisition through close contact with animals cannot be excluded with certainty. This case supports the possibility that *C. gattii* might be dispersing to East Coast North America, thus representing an emerging infectious disease.

SP10

FREQUENCY AND TYPES OF POSITIVE BLOOD CULTURE GRAM STAIN INTERPRETATION ERRORS – ASSOCIATION WITH TECHNOLOGISTS' EXPERIENCE

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OBJECTIVES: We determined the frequency and types of errors made in the interpretation of positive blood culture Gram stains and the clinical impact of such errors over a 12-month period. This was compared to a similar audit in 2007/08 to determine if there had been any changes in frequency and types of errors.

METHODS: Blood cultures were processed using the BactT/Alert system (SA, SN & PF bottles). All positive blood culture results from 1/13 – 12/13 were reviewed. Sources of information included a blood culture bench log book, LIS worksheets and a LIS line listing of corrected blood culture reports. Final culture results were used as the reference for comparison. All discrepancies between initial Gram stain and culture results were reviewed. The clinical impact of Gram stain errors was determined retrospectively by review of the medical chart and pharmacy records. These data were compared to that of a similarly conducted audit from 10/07-09/08. Years of experience of technologists were obtained from human resources records and the schedules during the 2 periods of the study.

RESULTS: From 1/13 to 12/13, 38,745 blood cultures were processed and 3408 (8.8%) were positive. The Gram stains of 51 (1.5%) positive blood cultures were misinterpreted. The rates of interpretation errors were 0/1795 (0%) for Gram-positive cocci, 7/270 (2.6%) for Gram-positive bacilli, 14/1108 (1.3%) for Gram-negative bacilli, 2/2 (100%) for Gram-negative cocci, 0/103 (0%) for yeasts and 28/130 (21.5%) for polymicrobial cultures. Clinical data were available for 40/51 errors. There was a clinical impact in 12/40 (30%) of the cases: 4 with delay in administration of appropriate antimicrobials and 8 with unnecessary antimicrobials. The audit from 10/07 to 09/08 found a significantly lower error rate of 0.9% ($p < 0.05$) with similar types of errors. The proportion of technologists with >5 years of experience decreased from 70% in 2007/08 to 42% in 2013 ($p = 0.016$).

CONCLUSIONS: Although Gram stain reports of positive blood cultures remain highly accurate, there was a significant increase in the Gram stain error rate compared to 5 years ago. This increase in error rate was associated with an increase in the proportion of technologists with <5 years of experience. Training and competency assessment, especially of less experienced staff, should focus on areas with higher error rates such as polymicrobial blood cultures.

SP11

IN VITRO SUSCEPTIBILITY TO FOSFOMYCIN OF ESCHERICHIA COLI AND ENTEROCOCCUS URINARY ISOLATES FROM A CANADIAN TERTIARY CARE HOSPITAL

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OBJECTIVES: To determine the fosfomycin susceptibility rate of urinary isolates of *Escherichia coli* and *Enterococcus* from a university associated tertiary care centre.

METHODS: Consecutive urinary isolates of *E. coli* and *Enterococcus* were collected between February and August 2015, targeting 150 samples of each genus. *In vitro* fosfomycin susceptibility testing was performed using CLSI disc diffusion methods. Although fosfomycin interpretive criteria for *E. faecium* are not defined by CLSI, those for *E. faecalis* were applied for comparison. Patient demographic data were also collected.

RESULTS: Patient demographics for *E. coli* were as follows: 25.3%/74.7% male/female, 43.8% age ≥ 65 ; for enterococci: 40.0%/60.0% male/female, 46.2% age ≥ 65 . Isolates were obtained from inpatients (22.0%), emergency room (34.7%) and clinics (43.3%). Fosfomycin susceptibility rates are presented in Table 1.

TABLE 1

Fosfomycin susceptibility rates

Sample [N (%)]	S [N (%)]	I [N (%)]	R [N (%)]
E. coli			
• Overall (N=146)	140 (95.8%)	3 (2.1%)	3 (2.1%)
• ESBL [N=17 (11.6%)]	16 (94.1%)	0 (0%)	1 (5.9%)
Enterococcus			
• Overall (N=145)	134 (92.4%)	11 (7.6%)	0 (0%)
• <i>E. faecalis</i> [N=126 (86.9%)]	125 (99.2%)	1 (0.8%)	0 (0%)
• VSE <i>E. faecium</i> [N=9 (6.2%)]	5 (55.6%)	4 (44.4%)	0 (0%)
• VRE <i>E. faecium</i> [N=10 (6.9%)]	4 (40.0%)	6 (60.0%)	0 (0%)

CONCLUSIONS: Most *E. coli* urinary isolates, including ESBL-producers, were susceptible to fosfomycin, similar to prior Canadian data. *E. faecalis* had excellent susceptibility rates, while *E. faecium* and VRE exhibited decreased susceptibility. However, a proportion of VRE were susceptible *in vitro*, supporting further evaluation of fosfomycin in the clinical setting for these organisms.

SP12

BINOCULARS TO BIRD FLU: USING CITIZEN SCIENCE TO STUDY THE ECOLOGY OF AVIAN INFLUENZA IN WILD WATERFOWL

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Avian influenza (AI) is a viral disease of poultry and a potential zoonosis. There were multiple outbreaks of highly pathogenic AI in Canada and the USA in 2014-2015, which resulted in over 3.3 billion dollars in economic losses. The source of AI is wild waterfowl, which spread the virus among geographic locations during their migrations. For this reason, wild waterfowl are the focus for most AI surveillance programs. However, there is a paucity of data on the ecology of wild waterfowl in many jurisdictions (i.e., population size, distribution, species composition, behavior etc.), which hinders the development of informed and effective surveillance programs.

OBJECTIVE: To determine whether the citizen science website eBird could be used to obtain data regarding the ecology of wild waterfowl during a local 2014-2015 HPAI outbreak and whether these data could, in turn, help us to understand the ecology of HPAI and to develop a new surveillance method based on screening sediment samples from wetlands. eBird is an expert-moderated, open source, online database in which recreational birders can log the number, location, and date of each bird species they observe.

METHODS: In collaboration with our regional eBird moderator, we collected 10 years' worth of data on local waterfowl in order to detect temporal trends in species abundance and distribution. We also used eBird to identify wetlands that would be optimal for sediment sampling based on the abundance and diversity of waterfowl observed on those wetlands, and their proximity to an infected farm.

RESULTS: Using eBird data we were able to identify 15 local wetlands for sediment screening. AI matrix gene-positive sediment samples were obtained from 9/15 wetlands and whole genomic sequencing is ongoing to characterize the AI strains present. Preliminary analysis of waterfowl data for the region as a whole (2004-2015) identified temporal trends in waterfowl distribution and abundance that might help us to understand the local ecology of AI.

CONCLUSIONS: Our research demonstrates the utility of eBird, and potentially other citizen science based data sources, for studying pathogen ecology, particularly for pathogens with animal reservoirs that are not well studied or understood.

SP13

GROUP B STREPTOCOCCAL STERNOCLAVICULAR SEPTIC ARTHRITIS AND SOFT TISSUE INFECTION: A CASE REPORT AND LITERATURE REVIEW

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OBJECTIVE: To describe an unusual case of group B streptococcal (GBS) sternoclavicular septic arthritis with spread to adjacent muscle and soft tissue, and to contextualize with a review of the literature on invasive GBS infection.

METHODS: English and Spanish language literature was searched using the terms "Group B Streptococcus" or "Streptococcus agalactiae" and "invasive," "sternoclavicular," or "adult." Eight case reports of sternoclavicular septic arthritis due to GBS were identified in addition to our own.

RESULTS: More than two-thirds of invasive GBS infections occur in adults. Risk factors include diabetes mellitus, skin breakdown – both of which our patient had – as well as liver disease and malignancy. Bacterial invasion occurs because of both skin breakdown and decreased immune function. Bone and joint infections represent around 8% of invasive GBS disease. In nine case reports of GBS sternoclavicular arthritis, patient age ranged from 34 to 87 years old. Three patients had diabetes mellitus, three had a history of malignancy, three had skin breakdown, and two had cirrhosis. Where details on antibiotic therapy were available, 7 of 8 patients received a beta-lactam antibiotic with durations ranging from three to eight weeks. Only one patient had residual deformity and pain at the end of therapy. In addition to our case, one other case involved myositis adjacent to the affected joint.

CONCLUSION: This case highlights that GBS can cause severe joint and soft tissue disease in patients with a variety of risk factors and presumed sources. With appropriate antibiotic therapy, prognosis is favourable.

SP14

THE INDIRECT EFFECTS OF CHILDHOOD PNEUMOCOCCAL CONJUGATE VACCINE (PCV) PROGRAMS ON INVASIVE PNEUMOCOCCAL DISEASE (IPD) AND COMMUNITY ACQUIRED PNEUMONIA (CAP) IN ADULTS: A SYSTEMATIC REVIEW

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OBJECTIVES: Non-immunocompromised individuals younger than 2 and older than 65 incur most of pneumococcal diseases' burden in Canada – including invasive pneumococcal disease (IPD) and community-acquired pneumonia (CAP). Therefore, childhood pneumococcal conjugate vaccine (PCV) programs were implemented across Canadian jurisdictions. Indirect effects of childhood PCV programs have been observed in individuals older than 50. This systematic review aims to examine and synthesize the literature on the impact of childhood PCV programs on the incidence of IPD and CAP among individuals older than 50.

METHODS: To identify all relevant articles, a systematic search was conducted in 6 databases using MeSH and free-text search terms. Hand-searches were also conducted. Two researchers independently assessed each study's inclusion eligibility and extracted data. In order to allow for comparisons between studies, details of the PCV program implemented and surveillance system used was ascertained and presented. Heterogeneity assessments were conducted for time since program implementation, method of diagnosis, and surveillance system.

RESULTS: Forty-six studies met inclusion criteria and were included (8 studied the effects on vaccine-type (VT) and/or overall CAP, 38 studied the effects on VT and/or overall IPD). Decreasing incidence of overall CAP was observed in ~88% of included studies (7/8), with changes in the absolute incidence estimates ranging from -202.6/100,000 to 1.5/100,000. Additionally, ~77% of the studies reporting on overall IPD (28/36) estimated decreases in IPD incidence, with changes ranging from

-34.2/100,000 to 10.4/100,000. The trends were observed regardless of length of time following PCV program implementation or method of diagnosis employed.

CONCLUSIONS: While limitations of the data exist, trends toward decreasing incidence of pneumococcal disease among individuals older than 50 were observed following childhood PCV programs. Although causality cannot be established, this supports the evidence that childhood PCV programs have beneficial effects on individuals older than 50.

SP15

THE A-HEMOLYSIN (Hla) GENE KNOCKOUT (KO) IN MRSA USA300 ALTERS THE LOCAL HOST CYTOKINE/CHEMOKINE PROFILE TO LEVELS INDUCED BY MRSA NON-DERMONECROSIS STRAINS IN A MURINE DERMONECROSIS MODEL

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OBJECTIVES: Hla is one of the major virulence factors associated with USA300 dermonecrosis. We constructed a USA300 Hla-KO mutant and explored the role of local host cytokine/chemokine profiles in a mouse dermonecrosis model.

METHODS: Hla-KO was constructed by gene allelic replacement, confirmed by blood agar hemolysis and tested in a *Caenorhabditis elegans* nematocidal model. USA300-Wildtype (WT), Hla-KO, together with control MRSA strains M92 and USA400 (non-dermonecrosis) were compared in our previously established murine skin infection model. Neutrophil infiltration and mobility/recruitment/capillary-crawling were quantified by myeloperoxidase (MPO) assay and spinning disk confocal microscopy, respectively. 32 important cytokines/chemokines were evaluated by luminex assay.

RESULTS: The Hla-KO significantly reduced nematocidal activity compared with USA300-WT ($p < 0.01$). Skin lesions induced by USA300-WT presented as extensive ulcers, whereas Hla-KO, M92 and USA400 caused localized cutaneous infection without dermonecrosis (lesion size 7.0 vs 4.3/3.9/4.0 mm, respectively; all $p < 0.01$). MPO assay confirmed that the Hla-KO, M92 and USA400 induced significantly less neutrophil infiltration than USA300-WT ($p < 0.05$). Live cell imaging also displayed increased neutrophil mobility but decreased recruitment/capillary-crawling in Hla-KO. The Hla-KO altered local host cytokine/chemokine profiles to levels induced by M92 and USA400. Most cytokines/chemokines were increased (7-1584 fold) in infections with all strains when compared with the saline control. The USA300-WT strain induced significantly increased production in those cytokines/chemokines reported to be associated with disease severity (3-40 fold, all $p < 0.05$) but not in those associated with protection when compared with M92 and USA400. The Hla-KO was associated with a reduced severity cytokine/chemokine profile but not a protection profile to the levels seen with M92 and USA400.

CONCLUSION: The Hla KO altered the local host cytokine/chemokine profile in association with the absence of dermonecrosis. These results suggest that the dermonecrosis observed with USA300 associated with Hla may in part be mediated by induction of host responses to cause severe skin lesions, in addition to Hla direct tissue damage. This observation may open new opportunities for therapeutic interventions.

SP16

DETERMINATION OF THE VOLUME OF DISTRIBUTION FOR PYRAZINAMIDE AND ETHAMBUTOL USING SERUM DRUG LEVELS IN THE TREATMENT OF MYCOBACTERIUM TUBERCULOSIS

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OBJECTIVES: There is a paucity of literature to guide optimal dosing for ethambutol (EMB) and pyrazinamide (PZA) in *Mycobacterium tuberculosis* (TB) infections particularly in obese patients. This study aims to review the adequacy of dosing and volume of distribution of EMB and PZA with serum drug levels (SDL).

Abstracts

METHODS: This retrospective review included patients above age 17 with TB infection treated with EMB or PZA and had SDL collected between 1998 and 2013. All SDL were analysed at the National Jewish Health and Research Center (Denver, CO) or at the Infectious Disease Pharmacokinetics Laboratory (Gainesville, FL). Cases were identified through the provincial microbiology laboratory database. Charts were reviewed to obtain baseline characteristics, drug dosing regimens, and peak SDL. Volumes of distribution (Vd) were then calculated and descriptive analyses were performed.

RESULTS: A total of 31 patients with EMB or PZA SDLs were included. The majority of patients were male (84%) and the mean age was 51 years. The average BMI was 20 kg/m². There were 26 patients taking PZA with 2/27 (7%) levels being below the reference range taking a median dose of 1500 mg daily. The average volume distribution was 46.7L. There were 13 patients taking EMB with 3/13 (23%) levels being below the reference range taking a median dose of 1200 mg daily. The average volume of distribution was 384.5L.

CONCLUSIONS: EMB and PZA peak SDL adequacy was achieved in the majority of patients. The Vd of PZA suggests that this drug distributes in the total body water compartment. The Vd of EMB was high, suggesting that this drug distributes into the fat compartment. This may require that body fat be taken into account when dosing EMB particularly in obese patients.

SP17

CLOSE ENCOUNTERS: USING SOCIOMETRIC DEVICES TO MAP AND MEASURE NETWORK INTERACTIONS AND BACTERIA IN A PEDIATRIC EMERGENCY DEPARTMENT

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OBJECTIVES: Healthcare-Associated Infections (HAI) cause an estimated 8,000 deaths per year in Canada. Items worn by healthcare workers such as pagers and identification tags may play a role in HAIs because they carry pathogens, but how social networks influence pathogen transmission is unknown. Sociometric devices (SMDs) were used to map and measure healthcare workers' social networks in a pediatric emergency department and they were also cultured for bacteria. The purpose of this study was to determine if network characteristics and certain demographics influence the presence and number of pathogens found on the SMDs, and to see if these networks could map pathogen flow.

METHODS: SMDs were worn by at least 70% of pediatric emergency staff over eight days. At the end of each shift, SMDs were cultured and the bacteria were identified and quantified. SMD data were analyzed through Sociometric DataLab and visualized through Gephi, a network visualization platform. Multivariate analyses on the type and number of bacteria compared to participant demographics, centrality and number of interactions were carried out using SAS.

RESULTS: Male sex, more years of training, higher degree centrality, higher number of individuals interacted with, and holding a profession other than a staff physician were positively correlated with higher quantities of bacteria found on their respective devices ($P < 0.0001$). Insufficient pathogen counts (13 of 113 devices) prevented further analysis.

CONCLUSIONS: These findings suggest that SMDs can be used to map and measure social networks and bacteria within a health care setting, but their use in modelling pathogen flow requires further investigation.

SP18

HIDDEN RESISTANCE: TREATMENT IMPLICATIONS OF A POSSIBLE INDUCIBLE BETA-LACTAMASE IN *PANTOEA AGGLOMERANS*

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BACKGROUND: *Pantoea agglomerans* is infrequently recognized as a cause of human infection. Only limited data describe this organism's prevalence and clinical significance from human sources. Additionally,

appropriate reporting of its antimicrobial susceptibilities is unclear, given its former association with the *Enterobacter* genus, and the potential presence of an inducible beta-lactamase.

OBJECTIVES: This study aims to describe *P. agglomerans* infections and to determine whether these isolates possess an inducible beta-lactamase.

METHODS: All patients with clinical isolates of *P. agglomerans* presenting to a single academic hospital between 2010-2015 were identified. The medical records of these patients were reviewed to determine whether infection was present. Phenotypic expression of an inducible beta-lactamase was examined among *P. agglomerans* isolates using a disk diffusion method: Imipenem and ceftazidime disks were placed as inducers, where distortion in the zone of inhibition around a central ceftazidime disk indicated the presence of an inducible beta-lactamase. A multiplex PCR assay for plasmid-borne *ampC* genes was performed to further characterize the type of beta-lactamase carried by the isolates.

RESULTS: Eighteen patients with *P. agglomerans* were identified; 12 (67%) met criteria for infection caused by this organism. Four (33%) of the clinical isolates were from blood, 4 (33%) from urine, 2 (17%) from wound swabs, 1 (8%) from dialysate fluid, and 1 (8%) from a tissue biopsy. The mean age of patients was 59.8; 8 (67%) were male. Seven (58%) were inpatients primarily admitted to the general medicine (43%) and urology (29%) services. Most patients (89%) were treated with fluoroquinolones or carbapenems, and appeared to respond to treatment; there were no deaths. Eleven (73%) of 15 *P. agglomerans* isolates had phenotypic expression of an inducible beta-lactamase. PCR testing for plasmid-borne *ampC* genes was negative for all tested isolates, suggesting these enzymes were most likely chromosomal.

CONCLUSIONS: Infection caused by *P. agglomerans* is uncommon; however, the results of this study suggest that most *P. agglomerans* isolates harbour an inducible chromosomal beta-lactamase. This observation may influence the choice of antimicrobial therapy for *P. agglomerans* infections.

SP19

INCIDENCE AND RISK FACTORS OF INFECTION FOLLOWING TRANSCATHETER AORTIC VALVE IMPLANTATION (TAVI)

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OBJECTIVE: Transcatheter Aortic Valve Implantation (TAVI) is a minimally invasive treatment for severe symptomatic aortic stenosis, especially in patients at high or prohibitive surgical risk. We investigated the incidence and risk factors for infection following TAVI at a Canadian centre in hopes of using the information to improve patient care.

METHODS: Data were collected retrospectively from 253 patients who underwent the procedure at a single hospital between Jan. 2012 and Mar. 2015, using standard data collection forms, and standard criteria for infections. Variables were assessed for association with the development of post-operative infections using Fisher's exact and Student's t-tests, as appropriate.

RESULTS: 35 (13.7%) patients developed an infection post-TAVI. Most common infections identified were urinary tract infections (15 cases, 31% of infections) and pneumonia (11 cases, 23%). There were 4 cases of infective endocarditis determined by modified Duke criteria (incidence 1.6%, occurring within 1 year post-TAVI). Almost all (96%) patients received pre-operative antibiotic prophylaxis, but of these, 26% inappropriately received antibiotics more than 1 hour prior to the first incision/arterial access, or after the first incision/arterial access has already occurred. COPD ($p=0.005$) and CHF ($p=0.02$) were comorbidities associated with an increased risk of post-TAVI infections. Procedure related variables that were associated with infections included surgical exposure of femoral artery access site (OR 3.53 [95% CI 1.01– 11.1]; $p=0.02$), post-operative stroke (OR 11.7 [95% CI 2.2–79.4]; $p=0.002$), post-operative bleed with transfusion (OR 2.39 [95% CI 0.84–6.21]; $p=0.06$), and length of hospital stay (95% CI for difference in mean of patients with infection versus no infection –6.7 to 35.1 days; $p=0.003$).

CONCLUSIONS: Infections are a common and important complication of TAVI. Several procedure related variables were associated with increased risk of infections, but additional studies are required to better understand

those risks and to determine effective interventions to prevent infections. Best practice would also indicate that antibiotic prophylaxis should be given within 1 hour prior to the start of the procedure.

SP20

FATAL CASE OF *ASPERGILLUS FUMIGATUS* EMPYEMA NECESSITANS IN A PATIENT WITH CYSTIC FIBROSIS POST DOUBLE-LUNG TRANSPLANT – A CASE REPORT AND REVIEW OF LITERATURE

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BACKGROUND: Empyema necessitans is a rare sequela of empyema/parapneumonic effusion where infection progresses from the pleural space into the soft tissues of the chest wall. We describe the first reported case of *Aspergillus fumigatus* empyema necessitans presenting in a cystic fibrosis (CF) patient following double-lung transplant.

RESULTS: The patient was diagnosed with CF at 2 years of age. Comorbidities included pancreatic insufficiency, diabetes, chronic sino-pulmonary colonization with *Pseudomonas aeruginosa*, and CF-liver disease with stable cirrhosis and portal hypertension. She received a life-saving double-lung transplant at age 39.

Ten years following transplant, she had an exudative, culture-negative right lower lobe parapneumonic effusion successfully treated with cefepime and metronidazole. Over the subsequent year, the patient presented with worsening fatigue, but no change in respiratory status. Chest X-ray showed a moderate right-sided pleural effusion, and the exudative pleural fluid culture grew *Aspergillus fumigatus*. She was treated with voriconazole plus micafungin. VATS was performed, but converted into an open right thoracotomy and decortication. All operative cultures from the pleural fluid, pleural tissue, and chest wall grew *A. fumigatus*.

Despite therapeutic voriconazole serum levels, she developed profound hyperbilirubinemia and acute kidney injury days later. Therapy was changed to a salvage regimen of caspofungin. Unfortunately, due to progressive deconditioning, unremitting hepatic encephalopathy, and acute on chronic kidney injury, she expired 28 days following the identification of her fungal empyema necessitans.

CONCLUSION: Fungal empyema necessitans is a rare and potentially lethal complication which may present many years after lung transplant. We advocate an aggressive medical and surgical approach, as well as consideration for combination therapy with multiple antifungal agents based on recent studies. However, even with aggressive therapy, morbidity and mortality remains high, and outcomes may be heavily influenced by the patient's pre-existing comorbidities.

SP21

MICROBIOLOGY LABORATORY TECHNOLOGIST CLINICAL REVIEW PROGRAM

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OBJECTIVES: Microbiology Medical Laboratory Technologists (MLTs) use their experience and judgment every day to produce accurate and relevant results which help physicians identify the cause of disease. Despite this important role, many MLTs and clinicians are not aware of how these contributions benefit patient care. The objectives of the study were to involve MLTs in patient care and provide insight into the important role their work plays and to improve clinician understanding of the MLT role.

METHODS: Interested MLTs were paired with the ID team on service for one day. The MLT reviewed microbiology results for all ICU patients prior to rounding with the ID team in the ICU or clinical areas and attended Antimicrobial Stewardship rounds. Each MLT was required to complete a pre and post rotation evaluation which was compared using the Wilcoxon signed-ranks test. In addition, they completed a questionnaire evaluating the program.

RESULTS: Evaluations showed a trend toward increased scores for statements 2-5 (Table) and there was a significant increase for the statement "I feel connected to the clinical services provided in the hospital" ($p=0.038$).

Overall the MLTs felt that the rotation gave them insight into the impact their work had on the clinical side (median=5), made them feel proud of what they do (median=4) and all reported that they were glad to have participated.

CONCLUSION: This educational program improved MLT insight into the clinical significance of their work, with minimal increase in workload for all involved. We anticipate that their new insight will improve MLT engagement and their understanding of the importance of timely, accurate patient results.

	Pre-intervention median (IQR)	Post-intervention median (IQR)	p-value
Statement #1: Staff in the hospital are aware of what we do in the lab	3 (2.0-3.5)	3 (2.5-4.0)	0.317
Statement #2: I have a good understanding of the work environment in the ICU	2 (2.0-3.0)	4 (3.5-4.0)	0.059
Statement #3: I feel connected to the clinical services in the hospital	2 (2.0-2.5)	4 (3.0-4.0)	0.038
Statement #4: Communication between the laboratory and clinical areas is good	3 (2.0-3.0)	4 (3.0-4.5)	0.063
Statement #5: I get an appropriate amount of education in my regular work day	3 (1.0-3.0)	3 (2.0-4.5)	0.059

IQR: interquartile range

SP22

THE UTILITY OF BACTEC MYCO/F AND BACT/ALERT MB FUNGAL BLOOD CULTURE BOTTLES FOR THE DETECTION OF INVASIVE FUNGAL INFECTIONS: A 5-YEAR REVIEW AT THE MCGILL UNIVERSITY HEALTH CENTRE (MUHC) IN MONTREAL, QC

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OBJECTIVES: Specific media for isolation of fungi have been introduced on a number of automated blood culture systems. However, their optimal use in a clinical setting is not well defined. We sought to quantify the added value of specialized fungal blood culture media as compared with routine blood cultures and/or fungal antigen testing.

METHODS: An LIS database search was conducted for all fungal blood cultures (BACTEC MYCO/F and BacT/ALERT MB) performed at the MUHC from December 2010-2015. Fungemic episodes, defined as growth of a pathogenic fungus in fungal blood culture media ≥ 7 days from the last known positive fungal blood culture for the same pathogen, were analysed to determine whether they would have been detected by routine blood culture media and/or specialised antigen testing.

RESULTS: Out of a total 3256 fungal blood cultures performed, 90 (2.8%) were positive for a pathogenic fungus, comprising 45 distinct episodes of fungemia. *Candida species* accounted for the majority ($n=39$, 86.7%) of fungemic episodes. Other pathogens isolated by fungal media included 3 (6.7%) *Fusarium species*, 2 (4.4%) *Cryptococcus neoformans*, and 1 (2.2%) *Histoplasma capsulatum*. In 4 (8.9%) episodes of fungemia, routine blood cultures were not performed within 24 hours prior or 72 hours following the fungal blood culture. Overall, 36 (80%) of fungemic episodes were also detected by routine culture media and/or specialised testing. 5 (11.1%) episodes of fungemia, all *Candida spp.*, were detected by fungal blood culture but not other methods. In 3 out of these 5 cases routine blood cultures grew bacteria. The additional cost of fungal blood culture bottles was \$7,280 per additional episode of fungemia detected.

CONCLUSIONS: The majority of fungemic episodes were detected by routine culture and/or specialised testing. Fungal blood culture bottles may be most useful for the detection of mixed fungal-bacterial infections.

SP23

DIRECT CEFOXITIN DISK DIFFUSION TESTING FROM BLOOD CULTURES WITH GRAM POSITIVE COCCI IN CLUSTERS FOR RAPID IDENTIFICATION OF METHICILLIN SUSCEPTIBILITY FOR STAPHYLOCOCCUS AUREUS

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INTRODUCTION: Vancomycin has become the standard empiric treatment for *Staphylococcus aureus* (*S.aureus*) bacteremia due to increasing prevalence of methicillin resistant *S.aureus* (MRSA) in hospital and community settings in Vancouver. However, beta-lactam antibiotics are treatment of choice for methicillin susceptible *S.aureus* (MSSA) infections. Routine phenotypic methods for methicillin susceptibility in *S.aureus* require an additional 24-48 hours after the blood cultures are signalled positive.

OBJECTIVE: To evaluate the use of direct cefoxitin disk diffusion testing (DCDD) for rapid identification of MSSA and MRSA bacteremia directly from positive blood culture broth (BCB).

METHODS: Microbiology laboratory data system was used to identify mono-microbial *S.aureus* bacteremia from January 1, 2013 to December 30, 2015. Only one isolate per patient was included. For DCDD testing, 2 to 3 drops of BCB were used to streak the entire surface of Mueller Hinton agar plate. A 30ug cefoxitin disk was placed and plates were incubated at 35-37°C in ambient air for 18-24 hours. The results were recorded as susceptible (S) or resistant (R) according to current Clinical Laboratories Standards Institute (CLSI) breakpoint values. The results of DCDD testing were compared with the standardized testing methods for identification of MSSA and MRSA isolates.

RESULTS: A total of 401 blood cultures with *S.aureus* were tested by DCDD; 256 (63.8%) were identified as MSSA and 145 (36.3%) as MRSA. The results of DCDD testing were 100% concordant with the standardized susceptibility testing results. Zone size measurements were recorded for 29 isolates. The average zone size was 26mm for MSSA isolates.

CONCLUSION: The DCDD testing is a reliable method to shorten the turn-around-time of reporting MSSA/MRSA directly from blood culture broth. This may also improve time to target beta-lactam therapy and reduce the unnecessary use of vancomycin.

SP24

EXPLOITING PEPTIDE MIMETICS AS NOVEL THERAPEUTICS FOR RESPIRATORY SYNCYTIAL VIRUS

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BACKGROUND/OBJECTIVE: Respiratory syncytial virus (RSV) is a pathogen associated with acute lower respiratory infection, and a leading cause of childhood hospitalizations worldwide. RSV infects almost all children by two years of age, yet there are currently no available vaccines or effective therapeutic treatments. Of the 11 proteins encoded by the negative sense single-stranded RNA virus, the nucleocapsid (N) protein and the phosphoprotein (P) assist in the formation of a RNA-dependent RNA polymerase complex. This interaction is essential for RSV infection, which makes it a potential target for novel therapeutics.

METHODS: The final 21 amino acids of RSV phosphoprotein (P₂₂₀₋₂₄₁) was cloned into a plasmid with a cell penetrating peptide (CPP) and expressed as a recombinant protein for functional analysis *in vitro* using glutathione S-transferase (GST) pull down assays. BEAS-2B cells were incubated with the recombinant peptide, challenged with RSV A virus, and viral loads were assessed by immunofluorescence. Short- and long-term effects of the recombinant protein were evaluated in BEAS-2B cells using cytotoxicity assays in conjunction with cell viability assays.

RESULTS: The GST-pull down experiments demonstrated that the recombinant P₂₂₀₋₂₄₁ specifically binds to RSV's nucleoprotein and is sufficient to prevent nucleoprotein binding with full length phosphoprotein. It can enter into BEAS-2B cells and upon challenge with RSV A, 20 µM

of the therapeutic peptide can inhibit up to 95% of RSV infection *in vitro*. In addition, the therapeutic peptide does not significantly affect cell viability nor exhibit significant cytotoxic effects *in vitro* at 20 µM over a period of 5-7 days.

CONCLUSION: The use of peptide mimetics presents a novel and promising approach in the development of therapeutic treatments against RSV. Further studies are required to evaluate P₂₂₀₋₂₄₁'s affinity for the phosphoprotein and its efficacy *in vivo*.

SP25

DEVELOPING A DENGUE ANTIVIRAL DRUG VIA COMPUTATIONAL-AIDED SCREENING

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INTRODUCTION: Dengue virus is spread through the bite of an *Aedes* mosquito and can cause a range of symptoms from a mild febrile reaction to a fulminant, life-threatening hemorrhagic fever. At present, there are no effective antiviral drugs for dengue virus. Dengue is a flavivirus belonging to the Flaviviridae family, a family that also includes Hepatitis C virus (HCV). As much of the molecular machinery amongst the group is conserved, cross-genus comparisons can often be made. Modelling and experimental studies from HCV's RNA polymerase show that binding to a "thumb" pocket region is able to inhibit the enzyme, rendering the virus incapable of replication (1). Here, inhibition of dengue virus's RNA polymerase is being explored in a similar manner using both computational and experimental work.

METHODS: Using the crystal structure of Dengue-3 RNA polymerase (PDB code 2J7U [2]), a library of previously synthesized compounds available from the ZINC Database online repository was screened, allowing for flexibility of both the "thumb" region residues and the compounds themselves. To enhance confidence in compound selection, two different docking programs were used—AutodockVina and GOLD Suite. The top hits of each program were cross-matched to give a more refined list of compounds to screen. Viral plaque neutralization assays are being performed on the top "hits" using Dengue-2 virus in a Vero E6 cell line. Compounds showing activity are to have further studies to determine IC₅₀ and TC₅₀'s.

RESULTS: Fifteen 'hits' from the computational docking studies were selected for further screening. Subsequent *in vitro* testing of a number of the compounds is being carried out.

CONCLUSION: Through the use of computer-aided rational drug design, dengue antiviral drug candidates are being screened and optimized for their potential to inhibit the virus. If successful, this research will have the potential of creating an effective treatment for a condition for which there is currently none.

This work is further unique in that it has been contrived, initiated and performed by an Infectious Diseases Fellow during training. Supporters/advisors for the work span several different departments and provinces.

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SP26

DOES MOLECULAR TESTING FOR INFLUENZA AND CLOSTRIDIUM DIFFICILE TOXIN B IMPROVE PATIENT FLOW IN THE EMERGENCY DEPARTMENT (ED)?

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BACKGROUND: Molecular diagnostics have the potential to improve patient management and flow in EDs. We undertook a review to determine whether real-time use of Focus Diagnostics Simplexa™ Flu A/B&RSV Direct kit for influenza (FLU) testing and Cepheid Xpert® system for *C. difficile* toxin B (CD) in our laboratory (open 24/7 except 0800-1600 Sat/Sun) provided results that impacted patient management.

METHODS: We reviewed ED visits from 9/2014 to 4/2015 with positive tests, and recorded time from ED registration to results and patient transfer/discharge.

RESULTS: For patients tested for FLU who were not admitted, nasopharyngeal (NP) swabs were obtained in a median of 1.6h (range 0.1-12.2h), and results available in 6.3h (range 2.1 to 39.7h). 26% of results were available prior to discharge. For admitted patients, NP swabs were obtained in 1.8h (range 0.1-20.5h) and results available in 10.5h (range 2.4 to 23.5h). 56% results were available prior to patient transfer to an inpatient ward. For patients tested for CD who were not admitted, stool samples were obtained in 5.3h (range 0.9 to 41.6h), and results available in 13.3h (range 2.9 to 44.6h). 25% of results were available prior to discharge. For admitted patients, stools were obtained in 5.7h (range 0.9 to 20h) and results available in 13.5h (range 2.7 to 24h). 43% results were available prior to patient transfer to an inpatient ward. The median time from specimen collection to lab receipt was 2.8h (range 0 to 23h) for nasopharyngeal swabs and 2.3h (range 0 to 85h) for stools. The median time from lab receipt to results was 2.1h (range 0.3 to 4.6h) for FLU and 1.8h (range 0.9 to 8.0h) for CD.

CONCLUSIONS: Results of molecular tests were available to clinicians in 25% of patients prior to discharge home and in 40-55% of admitted patients prior to transfer to an inpatient unit. The main difference between FLU and CD was time to specimen acquisition. Reducing specimen acquisition, transport and in-lab time might all further improve patient flow.

SP27

A SIMPLE EDUCATIONAL INTERVENTION AIMED AT JUNIOR RESIDENTS DURING A GENERAL INTERNAL MEDICINE ROTATION IMPROVES HAND HYGIENE COMPLIANCE

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BACKGROUND: Health care associated infections affect 1 in 10 hospitalized patients, and the majority of infections are transmitted through health care workers. Compliance with hand hygiene tends to be suboptimal, especially amongst physicians. Interventions to improve hand hygiene can include both individual and organizational level approaches. These are often expensive, and as such, not sustainable. Previous research has established that efficacy of interventions decreases once the intervention is removed.

METHODS: We introduced a simple educational intervention, aimed at residents and medical students during their General Internal Medicine (GIM) Ward rotation, which consisted of a PowerPoint presentation on hand hygiene delivered during the first week of a four-week rotation and an expectation of conducting a brief hand hygiene audit while on the rotation. We compared hand hygiene compliance rates to a sub-specialty medicine ward. The hand hygiene rates were from official AHS (Alberta Health Services) data.

RESULTS: There was a significant improvement in hand hygiene rates on the GIM compared to the subspecialty ward (see Figure 1). Our hand hygiene rates for the experimental wards were 86%, 80%, and 90%, compared to 74% and 76% for the control wards ($p < 0.05$). This was sustained over a one year period. Furthermore, the increase in hand hygiene rates led to a decrease in the number of hospital acquired infections (data currently being analyzed).

CONCLUSIONS: A simple educational strategy to improve hand hygiene is both effective and sustainable. Additionally, this led to a reduced hospital acquired infection rate, resulting in less patient morbidity and mortality.

SP28

REVIEW OF HUMAN PARECHOVIRUS (HPEV)-ASSOCIATED CENTRAL NERVOUS SYSTEM (CNS) INFECTIONS IN INFANTS ADMITTED TO A CANADIAN PEDIATRIC TERTIARY HOSPITAL

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OBJECTIVES: Studies world-wide have identified HPeV CNS infections as a significant cause of infant morbidity, especially in the first 3 months of life. In this study, we aim to examine the prevalence of HPeV infections, based on a newly developed molecular assay, and characterize associated laboratory and clinical parameters in infants <3 months old admitted at our hospital in 2011-2014.

METHODS: One hundred seventy-four available CSF samples collected in 2011-2012 (retrospective panel) and 233 CSF samples collected in 2013-2014 (prospective panel) were tested for the presence of HPeV using a laboratory-developed and validated real time RT-PCR assay. Cell count, protein and glucose measurements and microbiological analysis were reviewed for all samples. Demographic data, clinical presentation and outcomes were obtained through chart review for patients positive for HPeV RNA in CSF.

RESULTS: Four infants (retrospective panel) and 6 infants (prospective panel) had HPeV RNA positive CSFs. Of these 5/10 (50%) were <7 days old; 3/10 (30%) were 7-14 days old; 2/10 (20%) were 14-42 days old; 6/10 (60%) were males. 9/10 (90%) infections occurred during summer/fall. None of the CSF laboratory parameters were significantly different between the HPeV RNA-containing samples and those with no identified pathogen. All of the HPeV-infected infants were term, had no comorbidities and presented with fever >38°C. 7/10 HPeV infected infants had a sick contact, 5/10 had a rash on presentation, 5/10 had a consult from pediatric intensive care unit (PICU) and of those 3 required a PICU admission. All HPeV infected infants survived without neurological sequelae.

CONCLUSIONS: We report ~2% prevalence of CNS HPeV infections in our population with peak incidence in summer/fall. No host predisposing factors, CSF laboratory parameters, or clinical parameters indicative of HPeV infection were identified. Infection outcomes were favourable despite severe presentation in 50% cases. HPeV should be considered in differential diagnosis of CNS infections in infants <3 months age.

SP29

CENTRAL LINE ASSOCIATION BLOODSTREAM INFECTIONS IN QUÉBEC INTENSIVE CARE UNITS: RESULTS FROM THE PROVINCIAL HEALTHCARE-ASSOCIATED INFECTIONS SURVEILLANCE PROGRAM (SPIN)

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BACKGROUND: Following implementation of bundled practices in 2009 in Quebec and recent Canadian intensive care units (ICUs), we describe CLABSI epidemiology during the last 8 years in the province of Québec (Canada) and compare rates with Canadian and American benchmarks.

METHODS: CLABSI incidence and central venous catheter utilization ratios (CVCURs) by year and ICU type were calculated using 2007-2014 data from the *Surveillance Provinciale des Infections Nosocomiales* program

Abstracts

(SPIN). Using American and Canadian surveillance data as benchmarks, we compared SPIN incidence rates (IRs) to rates in other jurisdictions using standardized incidence ratios (SIRs).

RESULTS: A total of 1355 lab-confirmed CLABSIs over 911,205 central venous catheter days (CVC-days) were recorded. The overall pooled IR was 1.49 cases/1000 CVC-days and rates for adult teaching and nonteaching ICUs, neonatal ICUs (NICUs) and pediatric ICUs (PICUs) were 1.04, 0.91, 4.20, and 2.15 cases/1000 CVC-days, respectively. Using fixed SPIN 2007-2009 benchmarks, 2014 CLABSI rates decreased significantly in all ICUs except for PICUs. Rates declined by 55% in adult teaching ICUs, 52% in adult nonteaching ICUs, and 38% in NICUs. Using dynamic American and Canadian CLABSI rates as benchmarks, SPIN adult teaching ICU rates were significantly lower, adult nonteaching ICUs had lower or comparable rates, while NICU and PICU rates were higher compared with Canadian and US rates.

CONCLUSION: Québec ICU CLABSI surveillance shows declining adult ICUs rates. Lack of CLABSI rate decrease in NICUs and PICUs highlight need for continued surveillance and analysis of factors contributing to higher rates in these populations.

SP30

A STUDY OF CLINICAL *STAPHYLOCOCCUS PSEUDINTERMEDIUS* ISOLATED FROM 24 PATIENTS

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BACKGROUND: *Staphylococcus pseudintermedius* is a potential zoonoses associated with dogs and is morphologically and biochemically similar to *S. aureus*. Although human infections with *S. pseudintermedius* are rarely reported, the introduction of highly discriminatory methods such as MALDI-TOF is facilitating their identification.

OBJECTIVE: To provide a microbiological description of human *S. pseudintermedius* isolates recovered by a centralized diagnostic laboratory in Calgary, Alberta.

METHODOLOGY: A total of 27 *S. pseudintermedius* isolates from 24 patients were identified at Calgary Laboratory Services over 12 months beginning in April, 2013. The identity of all isolates was confirmed by sequencing the *cpm60* universal target. Antimicrobial MICs were determined by broth micro-dilution, and methicillin resistance (MRSP) was confirmed by detection of the *mecA* gene. Isolates were typed by MLST. Clinical data was collected through chart review and was analyzed descriptively.

RESULTS: *S. pseudintermedius* most commonly caused skin and soft tissue infections (SSTIs) of the lower limbs and other sites (n=18), but also caused invasive infections including pneumonia, septic arthritis and an arterial line infection with associated bloodstream infection. Six of 27 isolates were methicillin resistant but no resistance to vancomycin, linezolid or daptomycin was identified. A total of twenty three unique sequence types were identified, and notably the European pandemic canine strain ST71 was identified in 4 cases. For cases with data available (22/24), 100% reported canine contact including one patient who was bitten.

CONCLUSION: *S. pseudintermedius* infections may masquerade as *S. aureus* due to the under-recognition of this pathogen. As *S. pseudintermedius* infections are most often zoonotic, a pet exposure history should be obtained in patients infected with this organism.

SP31

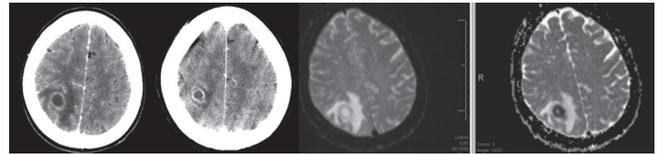
MULTIPLE CEREBRAL ABSCESSSES IN AN IMMUNOCOMPROMISED PATIENT

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OBJECTIVE: To present a case of a patient who presented with multiple large cerebral abscesses, which failed to respond to empiric treatment and required invasive work-up for successful diagnosis and treatment.

CASE: A 64-year-old female with a history of Waldenström's macroglobulinemia presented with a seizure and somnolence. Her first seizure had been 33 days prior. She had no neutropenia, travel history, exposures to animals, or sick contacts. Her initial CT head demonstrated 4 ring enhancing lesions with surrounding edema, felt to be cerebral abscesses, treated empirically with IV ceftriaxone and IV vancomycin at meningitic doses, and oral metronidazole. At presentation her Vital signs were stable and within normal limits. Neurologic examination showed a CGS of 3, increasing to 9 with seizure treatment, no focal neurological deficits and a supple neck. Examination was otherwise unremarkable. A repeat CT showed minimal improvement to her cerebral edema, confirmed with an MRI.



Left: shows CT before and after empirical antibiotics; right: is her MRI this presentation.

Open brain biopsy showed abundant polymorphonuclear white blood cells but no bacteria, fungal elements, or AFB. Cultures were negative for fungi and bacteria. The pathologic slides were stained with GMS stain and narrow branching filamentous organisms were identified. 16s rRNA sequencing showed the organism to be from the *Nocardia* genus, most likely *Nocardia farcinica*. Since no susceptibilities will be available, she has been treated with IV septria, and IV meropenem with good response clinically and on imaging.

CONCLUSION: *Nocardia* must be considered in cerebral abscesses not responding to empiric therapy, particularly in the immune-compromised, and can be very difficult to diagnose and require long treatment courses.

SP32

SMARTENAPP: THE DEVELOPMENT OF A WEB-BASED APPLICATION AS AN ANTIMICROBIAL STEWARDSHIP INTERVENTION: A PILOT PROJECT

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BACKGROUND: Antimicrobial stewardship programs (ASPs) are useful in promoting appropriate antimicrobial use while maximizing patient safety and minimizing cost. Many institutions have implemented such programs but have faced challenges secondary to lack of clinical resources and time and economic constraints. In the era of advancing technology and increasing use of mobile health resources, it is important to look at this avenue as a possible stewardship tool.

OBJECTIVES: To develop and evaluate the utility of a web-based application (app) as an antimicrobial stewardship intervention.

METHODS: A web-based app to assist prescribers with selection of antimicrobial therapy based on local resistance data was developed. The app utilizes four main headings to direct prescribers to the pertinent sections: Clinical Condition, Microbiology, Antibiotics and Location. In March 2014, the app was introduced on to the Internal Medicine Clinical Teaching Units (CTUs). We looked at the uptake and use of the app using web-based statistics. We then did both a comparative and "before/after" analysis of the usage (Defined Daily Doses/1000-patient days) of two targeted antibiotics: piperacillin/tazobactam (TZP) and vancomycin (VAN) on surgical and medical floors at our hospital the year before and after our intervention.

RESULTS: From March 2014 to February 2015, there were 3110 sessions, 16,442 page views, 57.7% returning users and 42.3% new users. There were 5.28 page views and 2.31 minutes per session. Comparing targeted antibiotic usage rates on medical to surgical units from our intervention period - March 2013-February 2014 vs March 2014-February 2015: utilization of VAN was 21% lower on the medical floors (p=0.0001), while TZP showed a non-significant increase of 7% (p=0.4222). This correlated to a decrease

in DDD/1000 pt days of 66 to 55 for VAN and an increase in TZP from 35 to 42 DDD/1000 pt days.

CONCLUSION: A web-based application is a practical, accessible tool for prescribers to aid in antimicrobial selection. Our data suggest a reduction in use of targeted antibiotics is achievable and sustainable.

SP33

EVALUATION OF THE MATRIX-ASSISTED LASER DESORPTION IONIZATION- TIME OF FLIGHT MASS SPECTROMETRY (MALDI-TOF MS) FOR THE IDENTIFICATION OF CYSTIC FIBROSIS PATHOGENS

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OBJECTIVES: To determine the utility of MALDI-TOF MS in the identification of non-fermenting gram-negative bacilli (NFGNB) isolated from patients with cystic fibrosis.

METHODS: Two hundred and forty NFGNB from respiratory cultures of cystic fibrosis patients at the Hospital For Sick Children Microbiology Laboratory, between January 2013 and June 2015, were analyzed using the Burkler Microflex LT MS system and interpreted with the Biotyper software (version 3.1). Organisms included several key cystic fibrosis pathogen groups, such as *Achromobacter* (64), *Acinetobacter* (5), *Burkholderia* [B. cepacia complex (71) and *B. gladioli* (8)], *Chryseobacterium* (16), *Cupriavidus* (8), *Elizabethkingia* (5), *Inquilinus* (18), *Pandoraea* (4), *Pseudomonas* (12), *Ralstonia* (4), *Stenotrophomonas* (5), and *Sphingobacterium* (8). Other groups identified included: *Bordetella* (3), *Comamonas* (1), *Delftia* (1), *Moraxella* (1), *Neisseria* (3), *Pantoea* (1), and *Pseudomonas putida* (3). Identification by MALDI-TOF MS was compared to reference identification by partial 16S rRNA gene amplification and sequencing.

RESULTS: MALDI-TOF MS correctly identified 100% of the NFGNB isolates tested to genus level. All isolates of *B. gladioli*, *Cupriavidus*, *Inquilinus*, *Pseudomonas*, *Ralstonia*, *Stenotrophomonas*, and *Sphingobacterium* species were also correctly identified to species level. Although MALDI-TOF MS provided speciation for some of the *Achromobacter*, *Chryseobacterium*, *Elizabethkingia*, and *Pandoraea* isolates tested, it is difficult to determine their accuracy due to limitations of partial 16S rRNA sequencing in providing identification to species level for these organisms.

CONCLUSIONS: MALDI-TOF MS accurately identified NFGNB which are challenging to identify by conventional methods from cystic fibrosis respiratory specimens to the genus level. Speciation for certain genera, however, will need further evaluation to determine its accuracy.

INCUBATOR POSTER PRESENTATIONS

Thursday, March 31, 2016
Room: Grand Ballroom

IP01

VERIFICATION OF THE RIDA@GENE PERTUSSIS REAL TIME PCR KIT FOR THE DETECTION OF *BORDETELLA PERTUSSIS* AND OTHER *BORDETELLA* SPECIES FROM NASOPHARYNGEAL SWABS COLLECTED IN REGAN-LOWE MEDIA

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BACKGROUND: This study verified the RIDA@GENE pertussis real time PCR (RIDA) assay for the detection of *Bordetella pertussis* (BP), *Bordetella parapertussis* (BPa) and *Bordetella holmesii* (BH) from nasopharyngeal (NP) swabs collected in Regan-Lowe media (RLM).

METHODS: The study included NP swabs collected in RLM, May 2014-November 2015. Due to low volumes of residual primary specimens, clinical samples that were test-positive from IS481 with an in-house real-time PCR assay were pooled for an accuracy panel. Sensitivity and specificity for BP were scored on the ability to detect IS481. Mock-up BH and BPa specimens in RLM were generated from clinical isolates at a range of dilutions. Limit of detection (LOD) panels for BP, BPa, and BH on RLM were generated. The accuracy, sensitivity, specificity, and inter- and intra-run reproducibility were assessed.

RESULTS: 40 clinical and mock-up clinical samples including 21 BP, 9 BH and 10 BPa were tested for accuracy. The sensitivity for IS481, BH and BPa was 100%. The specificity for IS481 was 100%. However, pooled BP positive specimens also contained other targets (non-IS481) for BH (n=3) and BPa (n=1), indicating the presence of these targets in an unknown number of original specimens prior to pooling. LODs were 3.1, 20.5, and 4.2 colony forming units/PCR reaction for BP, BPa and BH respectively. Inter- and intra-run reproducibility was acceptable.

CONCLUSION: The RIDA assay provides a rapid, simple method with high sensitivity and specificity in detection of BP from NP swabs in RLM. Future work will elucidate the prevalence of BH and BPa in clinical specimens from our jurisdiction.

IP02

ENHANCING A CAESAREAN SECTION SURGICAL SITE INFECTION SURVEILLANCE SYSTEM THROUGH AUTOMATED TEXTING AND EMAIL

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BACKGROUND: Surgical site infections (SSI) are the most common healthcare associated infections. As hospital length of stays shorten, post-discharge SSI surveillance (PDS) has become an inevitable challenge for hospitals. Although most hospitals conduct PDS, there is no consensus on the optimal approach. We sought to implement a more automated PDS system to improve case ascertainment, response rates and work efficiency.

METHODS: C/S SSI surveillance started in April 1, 2009. We implemented PDS three years later. In the first year of PDS, we used traditional mail surveys. In the second year, an Infection Control Practitioner (ICP) called patients. In the third year, we initiated email follow-up. This fiscal year, we introduced automated texting/email. We examined SSI rates, response rates and time spent by an ICP. Chi-squared tests were applied to comparisons.

RESULTS: An average of 648 C/S were performed annually. The overall SSI rate in the first three years was 0.36 per 100 procedures. After introducing PDS, overall SSI rate was 1.39 per 100 procedures (p<0.001). Response rates improved from 20% (mail) to 73% (email) Shifting to automated texting/email improved response rates to 80% and decreased ICP time with PDS (46.7 hours to 30.2 hours).

CONCLUSIONS: Automated texting and email is efficient and effective for PDS in our population undergoing C/S. Implementing automated technology ascertained more infections, improved response rates and saved ICP time. Engaging patients using email and texting may have broader health applications.

IP03

CHARACTERIZATION OF NOVEL Γ -LACTAM ANTIBACTERIAL COMPOUNDS AGAINST *CLOSTRIDIUM DIFFICILE* AND DRUG RESISTANT *STAPHYLOCOCCUS AUREUS*

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BACKGROUND: According to the World Health Organization, the prevalence of antibacterial resistance is 83.3% in World Health Regions (as listed by WHO). Furthermore, the number of bacterial strains resistant to existing antibiotics increases every year, necessitating the development of a new classes of antibiotics.

Abstracts

METHODS: Toward developing a novel class of antibacterial compounds, we have created a chemical library by a hybrid approach using chloroquine as a basic scaffold. Screening of the chemical library via disk diffusion method allowed us to confirm antibacterial activity. Tube broth dilution also allowed us to determine the MIC of the novel compound against various strains.

RESULTS: Of the 211 compounds screened, 27 compounds (or 12.7%) were effective against *Escherichia coli* and *Staphylococcus aureus*. Structural analysis of the 27 active compounds revealed the presence of an isatin group and thus being classified under the γ -lactam class of antibiotics. All of the 27 active compounds mimic the β -lactam-based antibiotics while displaying activity against resistant strains of bacteria. The average minimum inhibitory concentration of the 27 compounds (n=3) was comparable to the well-established kanamycin and ampicillin (50 μ g/ mL and 100 μ g/ mL respectively) as determined by a broth dilution method. All of the 27 compounds were also active against ampicillin-resistant, kanamycin-resistant and NDM-1 resistant *E.coli* strains as well as against methicillin-resistant *S. aureus*. However, none was effective against vancomycin-resistant *Enterococcus faecalis*. One compound displayed a better MIC value (50 μ g/ mL) and was chosen for further testing. Our novel compound was also shown to be effective against *Clostridium difficile* as well as *Helicobacter pylori*.

CONCLUSION: Although we have identified novel antibacterial compounds, further studies are being carried out to unravel the mechanism of action of the 27 novel compounds.

IP04

SIMULTANEOUS DETECTION OF COMMON PATHOGENS IN PEDIATRIC EMPYEMA USING LOOP-MEDIATED ISOTHERMAL AMPLIFICATION (LAMP)

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INTRODUCTION: Pleural empyema is a suppurative infection of the pleural space which complicates 3 to 5% of pneumonia in hospitalized children. Despite relatively low mortality rate, empyema has become a heavy burden of health care worldwide. However, in many cases, it is hard for clinicians to verify that the antimicrobial regimen selected is 'appropriate' due to the low sensitivity of traditional culture-based methods. Currently there are no commercially-available or academically-reported application of Loop-Mediated Isothermal Amplification (LAMP) technology in the area of pediatric empyema diagnosis. The overall objective of the present study is to develop a rapid and novel molecular method with high sensitivity and specificity to simultaneously identify common pathogens in pediatric empyema.

METHODS: Primers were designed to simultaneously detect multiple targets in one reaction tube. Internal fragments of *lytA* gene of *Streptococcus pneumoniae*, *dnaseB* gene of *S. pyogenes*, *nuc* gene of *Staphylococcus aureus* and *mecA* genes of methicillin-resistant *S. aureus* (MRSA) were selected as the targets for individual pathogen after broad literature review. Previously frozen clinical isolates were cultured on blood agar and cell suspensions were made with sterile normal saline to 0.5 McFarland ($\sim 1.5 \times 10^8$ CFU/ml) as the primary stock. Negative pediatric pleural fluid samples were spiked with serial dilutions of pathogens (1.5×10^2 to 1.5×10^7) to determine the limit of detection of LAMP method. For LAMP 60 μ l of spiked pleural fluid was mixed with 60 μ l of lysis solution and boiled for 15 min and 5 μ l of clear liquid was used as the DNA template. LAMP was carried out at 65°C for 45 min using a standard reaction mixture. The amplification and annealing temperatures of the amplicons were detected using Genie® II (OptiGene, UK) real-time fluorescence detection instrument.

RESULTS: *S. pneumoniae*, *S. pyogenes* and *S. aureus* were detected by LAMP test with distinctive annealing temperatures. More than 99% of pathogens (120 specimens per pathogen) were detected at the concentration of 10^4 CFU/ml (LOD). Comparing with real-time PCR, LAMP assay

is more cost-effective with about \$5 per test, while \$12 per test for PCR. It is also time-efficient with a turn-around-time of 60 minutes as compared with 2 to 3 hours for PCR test.

CONCLUSION: The LAMP assay successfully identified common pathogens in pediatric empyema, including *S. pneumoniae*, *S. pyogenes* and, both methicillin-sensitive and -resistant *S. aureus* with an excellent sensitivity and specificity.

IP05

PIPERACILLIN-TAZOBACTAM IN ESBL ESCHERICHIA COLI: SHOULD REPORTING BE REVISED?

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BACKGROUND: Controversy exists in the literature regarding the appropriateness of using beta-lactam/beta-lactamase inhibitors (BL/BLIs) to treat infection from Extended Spectrum-Beta Lactamase (ESBL) producing isolates. The Clinical and Laboratory Standards Institute (CLSI) has recommended that PTZ susceptibility be reported as tested and that ESBL screening is not required. Our study evaluated patients with *Escherichia coli* bacteremia to determine whether such reporting leads to potentially inappropriate use of BL/BLIs.

METHODS: A retrospective observational study was performed at the MUHC (917 beds) in Montreal, Canada from April 1, 2010 to June 1, 2015. All cases of adult *E. coli* bacteremia were reviewed. Untreated and duplicate cultures occurring within 14 days were excluded. Susceptibility was determined in accordance with CLSI guidelines. Empiric and definitive therapy were defined as antibiotics given prior to, and after susceptibility results became available, respectively. Univariate comparisons were made using chi-square analysis.

RESULTS: There were 845 *E. coli* bacteremias (Median age 68 & IQR 57 to 81.25) and a 30-day in-hospital mortality of 12.1% (102 deaths). A statistically significant relationship ($p < 0.0001$) was found between ceftriaxone resistance and resistance to all other classes of antibiotics, including PTZ, carbapenems, fluoroquinolones, aminoglycosides and TMP-SMX. Empiric and definitive therapy in ceftriaxone-resistant, PTZ-susceptible isolates are described in Table 1. Among isolates that were ceftriaxone-resistant but PTZ susceptible, PTZ was the most commonly used empiric treatment (65.9%), followed by a fluoroquinolone (34.1%) and a carbapenem (13.6%). Overall, PTZ was used as definitive therapy in 26.2% (11/42) of such cases with all three deaths occurring in patients who received PTZ monotherapy.

CONCLUSION: For ceftriaxone-resistant isolates, PTZ was commonly used if reported as susceptible. Given the debate over the use of BL/BLIs for treating serious infections, microbiology laboratories may need to consider withholding PTZ susceptibility results in invasive ESBL *E. coli* infections pending more definitive evidence on its clinical efficacy.

TABLE 1

Empiric/definitive treatment of ceftriaxone-resistant, piperacillin-tazobactam susceptible isolates

Ceftriaxone Resistant n=44	Empiric (n=44)	Definitive (n=42*)
Carbapenem	6 (13.6%)	21 (50%)
Piperacillin-Tazobactam	29 (65.9%)	11 (26.2%)
Fluoroquinolone	15 (34.1%)	5 (11.9%)
TMP-SMX	0 (0%)	3 (7.1%)
Aminoglycoside	4 (9.1%)	2 (4.8%)
Ceftriaxone	2 (4.5%)	0 (0%)

*2 patients died before susceptibility results were reported. Both received piperacillin-tazobactam as empiric therapy.

IP06 ABSTRACT WITHDRAWN

IP07

MONITORING THE NET CLINICAL IMPACT OF RESISTANCE: COMPOSITE INDICES SHOW IMPROVEMENT IN OUR ABILITY TO COVER SEVERE DEVICE-ASSOCIATED INFECTIONS IN AN ACADEMIC ICU SINCE 2000

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OBJECTIVES: We summarize the net clinical impact of changing antibiotic resistance on empiric therapy of device-associated pneumonias and bloodstream infections in three Toronto academic intensive care units using composite indices.

METHODS: The Empiric Coverage Index (ECI) measures susceptibility of common bacterial infections to available empiric antibiotics as a percentage. The Empiric Options Index (EOI) varies from 0 to "the number of treatment options available", and measures the empiric value of the current stock of antibiotics as a depletable resource. The indices are calculated from 2000-2014 cumulative antibiogram data, and account for drug availability and the relative clinical importance of pathogens.

RESULTS: Since 2000 the prevalence of ESBL-producing Enterobacteriaceae has increased, while multidrug-resistant Staphylococci and *Pseudomonas aeruginosa* have become less common. Overall, we have seen a 3.6% [95% CI 1.3-5.7; p = 0.005] improvement in our ability to empirically cover severe device-associated infections at one site, and no significant change at the other two sites. Our empiric options have increased at two sites ($\Delta\text{EOI}_A = 0.67$ [0.22-1.12; p=0.006], $\Delta\text{EOI}_B = 0.48$ [0.03-0.92; p=0.039]), and remain unchanged at the other.

CONCLUSIONS: Composite indices summarize the net clinical impact of changing resistance, putting alarming changes in perspective. In these units, our ability to empirically cover severe device-associated infections has improved or remained the same since 2000 because increasing prevalence of ESBLs has been offset by less resistant Staphylococci and *P. aeruginosa*. Adaptation, stewardship and infection control efforts appear to be helping, and we hope these results encourage further efforts.

IP08 ABSTRACT WITHDRAWN

IP09

PCR-BASED DISCRIMINATION OF VACCINE-PREVENTABLE SEROTYPES OF *STREPTOCOCCUS PNEUMONIAE*

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BACKGROUND: The reference for *Streptococcus pneumoniae* serotyping is the Quellung reaction, which uses serotype-specific antibodies to classify isolates based on differences in capsular antigens. PCR-based serotype deduction has been introduced as an alternative; however, the capsular biosynthesis (*cps*) genes on which it relies fails to discriminate certain serotypes, and thus limits its use for pneumococcal surveillance.

OBJECTIVES: This study aimed to identify and validate novel PCR targets located outside the *cps* loci that can accurately discriminate vaccine-preventable serotypes of *S. pneumoniae*.

METHODS: Next generation sequencing and comparative genomics was used to identify unique PCR targets for each serotype within the following "non-discriminated" groups obtained with traditional PCR that contained a vaccine-preventable serotype (underlined): 6A/6B/6C/6D; 7E/7A; 9V/9A, 9N/9L, 11A/11D, 12F/12A/12B/44/46; 15B/15C; 18C/18F/18A/18B; 22E/22A, and 33F/33A/37. Each novel target was evaluated for its ability to

discriminate the desired serotype, and specificity was tested against 82 *S. pneumoniae* serotypes characterized by Quellung and 32 other members of the *Streptococcaceae* family.

RESULTS: To date, 16 of the 28 desired serotypes can accurately be discriminated: 6A, 6B, 6C, 9A, 9L, 9V, 11D, 12A, 12B, 12F, 15C, 18C, 18F, 33F, 44, and 46. No significant cross-reactions were observed.

CONCLUSIONS: This study provides the proof-of-principle that PCR targets outside the *cps* loci can be used to accurately discriminate vaccine-preventable serotypes of *S. pneumoniae*. The novel PCR assays could be used in an algorithm, following a positive screening result with the traditional PCR-based serotype deduction methods. Since serotyping of *S. pneumoniae* is important to monitor its epidemiology and to determine the proportion of pneumococcal disease is vaccine-preventable, this study represents a significant technological advance in pneumococcal disease surveillance.

IP10

A POTENTIAL NOVEL TREATMENT FOR MALARIA INFECTIONS: MAGNETIC EXTRACTION OF PARAMAGNETIC PARTICLES FROM A FREE FLOWING SYSTEM

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BACKGROUND: With the spread of resistance to antimalarial chemotherapies, the management of malaria epidemics is becoming increasingly difficult and the need for new therapies effective on both chemotherapy resistant and sensitive strains is growing. One important trait of certain intra-erythrocytic parasites, such as malaria, is that they create a paramagnetic pigment known as hemozoin, as a method to detoxify the heme molecules released during their digestion of haemoglobin. The current work investigates a potential new antimalarial therapy, the purification of a patient's blood of malaria infected erythrocytes using magnetic extraction from a continuously flowing system.

METHODS: β -hematin, the synthetic form of hemozoin, was synthesized from bovine hemin using previously published protocols. It was characterized with MALDI-TOF mass spectrometry and Fourier Transform Infrared Spectroscopy. The paramagnetism of the molecule was qualitatively demonstrated. The magnetic extractor, a sheath flow cuvette, was fabricated using polydimethylsiloxane with integrated channels moulded using polyimide coated capillaries. A 0.5 T rare earth magnet was placed in contact with the sheath flow cuvette to create the magnetic field for extraction. Laminar flow of a buffer stream within a sheath liquid was then demonstrated within the cuvette. The β -hematin, suspended in a phosphate buffer, was injected into the cuvette and encased in a sheath buffer fluid. The magnetic separation of the pigment from the sample stream into the sheath buffer stream was demonstrated microscopically. A model of malaria infected erythrocytes, paramagnetic latex microspheres, were suspended in a phosphate buffer and separated within the sheath flow cuvette using a similar procedure.

RESULTS: The β -hematin had similar physical properties to previously published data, including its paramagnetism. When flowing through the sheath flow cuvette, the course of the pigment was redirected out of the sample stream and into the sheath fluid, extracting the pigment magnetically. Similarly, the model malaria infected erythrocytes, were also pulled out of the sample stream and into the buffer stream within the sheath flow cuvette.

CONCLUSIONS: These results suggest that a clinically relevant magnetic extractor may be a potential avenue of treatment for malaria infections, capable of extracting malaria infected erythrocytes from a patient's bloodstream.

IP11

NOT YOUR USUAL APPENDICITIS

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HISTORY: 32-year-old, G2P2 with recurrent abdominal pain for 2 years, presented to the emergency department with acute onset of excruciating right sided, abdominal pain. She was afebrile with two days of nausea and

Abstracts

vomiting prior to presenting. She denied any urinary symptoms. She left the Philippines, where she was born, in 2008, her last trip there, being in 2013/14. Her presentation was most compatible with acute appendicitis. She had a laparoscopic appendectomy and specimen was sent for pathology evaluation.

INVESTIGATIONS: Slides shown in Figures 1, 2 reveal findings from her appendectomy. The patient's *Schistosoma* serology was negative. She had no peripheral eosinophilia.

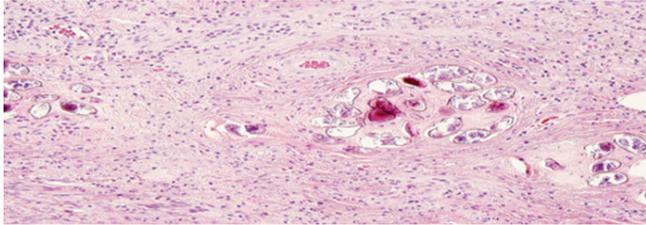


Figure 1) Hematoxylin-eosin stain

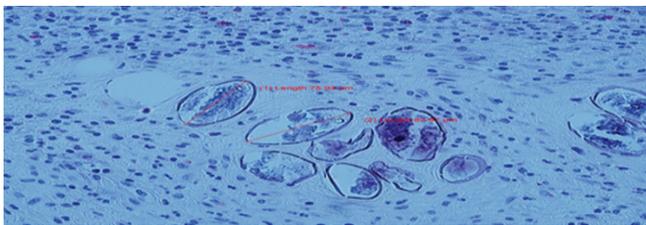


Figure 2) Trichrome stain

Slides show a transmural acute inflammation with multiple foci of oval shaped 80um parasitic eggs embedded within muscularis propria. Moderate eosinophils are noted in the background. The morphology most consistent with eggs from *Schistosoma* species

DIAGNOSIS: Based on pathology reports, and confirmation parasitology expert the diagnosis of *S. Japonicum* causing appendicitis was made. She was treated with Praziquantel 60mg/kg divided TID x 1 day.

TAKE HOME POINTS: Appendicitis can be caused by parasites including *Schistosoma*. Without pathological specimens we would not likely have been able to diagnose her condition. *S. japonicum* can embolize to the central nervous system in 5% of cases, therefore care should be taken when examining and treating these patients. With increased globalization it is important that practitioners be aware that parasitic infections can present with appendicitis.

IP12

USING REAL-TIME COMPUTER-GENERATED ALERTS TO IDENTIFY INTERVENTIONS AND OPTIMIZE ANTIMICROBIAL STEWARDSHIP

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OBJECTIVES: The implementation of antimicrobial stewardship programs (ASP) is challenging with limited physician and pharmacist time. A multi-disciplinary approach (clinical pharmacists, medical microbiologists, infectious diseases, information technology) was undertaken to integrate information technology within our ASP, with alerts to identify potential interventions.

METHODS: A new Clinical Decision Support System (CDSS) software "Antibiokos" was developed and implemented in a regional hospital with 230 acute-care beds, to enable our ASP team to track interventions, using real-time data from interfaces connected with pharmacy, microbiology laboratory and admission-discharge-transfer. Electronic algorithms included core elements of ASP such as: time-sensitive stop orders (3 days for IV, 7 days for oral), overlapping spectra, switch from intravenous to oral, drug optimization according to culture results, formulary restriction and pharmacokinetics (PK). Real-time metrics (DDD, DOT, Costs) were provided.

RESULTS: During the first 4 months, a total of 7348 DDD were observed among inpatients, and 1004 electronic alerts were generated in 686 patients. The alerts were time-sensitive stop orders 55%, restriction 12%, PK 10%,

optimization according to culture 6%, switch IV to oral 6%, overlapping spectra 6%, other 4%. A total of 184 interventions were done in 135 patients, mainly on Quinolones 23%, Pip-Tazo 21%, Cephalosporins 17%, Carbapenems 9%, Macrolides 5%, Antifungals 4%, Antivirals 3%. Suggestions were: no change 65%, replacement 23% and stop 12%. High acceptance rate of suggestions (95%) was observed. In comparison to the previous year, DDD were reduced by 14% and costs by 34%. The software provided significant time-reduction with estimates: >95% to get the metrics (DDD or DOT), and >50% to target and perform interventions.

CONCLUSIONS: Real-time alerts from the CDSS 'Antibiokos' provided a powerful tool to our ASP team, saving time and generating significant reductions of antimicrobial consumption and cost.

IP13

THE CLINICAL IMPACT OF A UTI MANAGEMENT BUNDLE IN A TERTIARY CARE TEACHING HOSPITAL

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OBJECTIVES: Antibiotics are often inappropriately prescribed for asymptomatic bacteriuria (AB). The aim of this study is to assess the impact of an institutional UTI management bundle to reduce AB treatment and improve diagnosis and treatment of symptomatic urinary tract infection.

METHODS: The UTI management bundle consisted of nursing education, prescriber education, modification of the reporting of positive urine cultures, and review of antimicrobial choice by the hospital pharmacy team, if possible. A retrospective chart review of consecutive inpatients with positive urinary cultures was performed before and after implementation of the management bundle.

RESULTS: Prior to the implementation of the management bundle, 278 patients met eligibility criteria for chart review. Of these, 61.2% (170/278) were found to have AB, of which 70% (119/170) were treated with antimicrobials. 299 patients met eligibility criteria for post-intervention chart review. Of these, 49.8% (149/299) were found to have AB, of which 19.5% (29/149) were treated with antimicrobials. This represents a 72.1% reduction in AB treatment. Educational components of the bundle resulted in a substantial decrease in non-physician directed lab sample submission, and an overall reduction in urine bench workload by 38% when compared to the same time period the year before. Adherence to an institutional best practice algorithm improved substantially in the intervention period, with a notable decrease in fluoroquinolone prescription for empiric UTI treatment.

CONCLUSIONS: An institutional stewardship bundle resulted in a dramatic improvement in the management of urinary tract infection, in particular a significant reduction in the treatment of AB. Empiric management of symptomatic urinary tract infection was improved, and the intervention led to a reduction in lab resource utilization.

IP14

OPTIMAL ANTIMICROBIAL PRESCRIBING – THERE'S AN APP FOR THAT!

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BACKGROUND: Appropriate selection and prescription of antibiotics can be convoluted and perplexing. Choosing wisely requires harmonizing information from a patchwork of mismatched sources. Even when complete, information available to the prescriber is often cluttered with far more information than is needed or misses important nuances of interpretation. Frustration often leads to initial over-prescribing. Failure to order appropriate diagnostic testing discourages narrowing of antimicrobial spectrum at appropriate opportunities.

METHODS: The problems in antibiotic prescribing and diagnostic testing are well suited to computer-based solutions. We are developing an application through which physicians can quickly and definitively acquire both the narrow and broad antimicrobial prescription picture when confronted with a clinical puzzle. To facilitate regional variances, institutions can customize

their antibiogram, current empiric therapy recommendations, and educational information to best suit their local conditions.

RESULTS: We present an approach that presents information in a user-centered, visually intuitive format and includes a printable treatment plan (including criteria for stepping-down and stopping antibiotics), and information for patients in plain language. Data tracking will allow the stewardship team to recognize which topics users most access to target educational opportunities.

CONCLUSIONS: It is possible to create a system that allows prescribers to access the most up-to-date information available for the institution and infection in question and promotes appropriate microbiology sampling to encourage narrowing. Further support in management can be achieved with detailed treatment plans. Patient education is possible through printable plain-language information sheets. When successfully implemented and widely adopted, we anticipate an improvement in prescription compliance with stewardship guidelines.

IP15

PHARMACIST LED BETA-LACTAM ALLERGY SKIN TESTING (BLAST) TO REDUCE USE OF ALTERNATE SECOND-LINE THERAPY AMONG PATIENTS WITH REPORTED BETA-LACTAM ALLERGY

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OBJECTIVE: Reported allergy to beta-lactam antibiotics frequently results in selection of alternate second-line antimicrobial therapy that are associated with worse patient outcomes. The aim of this study was to evaluate the use of beta-lactam allergy skin testing (BLAST) at the point-of-care to improve the use of preferred beta-lactam therapy among patients encountered on the Infectious Diseases consultation service.

METHODS: Following a 3-month baseline period, clinical pharmacists were trained to perform BLAST for patients with history of beta-lactam allergy who would otherwise receive alternate therapy due to severity of their allergy. Patients with prior history of non-IgE mediated reactions, expected short duration of therapy (<2 days), recent reactions (<3 months) or who declined BLAST, were excluded. The primary outcome was the proportion of patients with a clinical indication for beta-lactam therapy who did not receive preferred beta-lactam therapy due to their reported allergy. Days of therapy of alternate second-line antimicrobials were measured before and during the 3-month intervention period.

RESULTS: At baseline, the proportion of patients receiving alternate second-line therapy due to their reported beta-lactam allergy was 30.6% (22/72) corresponding to 21.5% (149/692) of overall days of therapy. Following availability of BLAST, use of alternate therapy decreased to 13.8% (8/58) of patients (risk ratio with BLAST, 0.45 [95% CI 0.22–0.92]; $p=0.02$) corresponding to 7.2% (66/918) of overall days of therapy ($p<0.001$). All patients undergoing BLAST had negative tests and tolerated preferred beta-lactam therapy without any adverse effects ($n=8$).

CONCLUSIONS: The use of BLAST at the point-of-care is a promising antimicrobial stewardship strategy to preserve the use of beta-lactam therapy among patients with reported allergy. A larger multicentre evaluation is needed to determine safety and cost-effectiveness of this intervention.

IP16

AN ELECTRONIC HEALTH SYSTEM TO ENHANCE ACCESS AND DELIVERY OF HEALTH CARE TO URBAN SLUM DWELLERS AND OTHER NEGLECTED POPULATIONS

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OBJECTIVE: Electronic health systems have proven to increase efficiency, reduce redundancy and improve patient care in health care systems worldwide. The Kenyan Medical Record Initiative (KMRI) aims to deliver these advantages to neglected populations, primarily those living in urban slums who often do not have any form of a medical record. The initiative also aims to improve on the functionality of electronic health systems by

allowing real time electronic report generation and integrating geomatic information systems. Doing so will facilitate health referral networks, public health programs and research initiatives.

METHODS: Using a multidisciplinary team involving physicians, nurses, Kenyan Ministry of Health, computer programmers, networking consultants, GIS specialists, non-governmental organizations, field researchers, an open source primary care electronic medical software system using OpenMRS was built. Hardware and networking capabilities were installed in three pilot clinics found in Kenya's largest slum, Kibera. An informational campaign was launched to provide education about electronic medical records and qualitative surveys were launched to understand perceptions and concerns about such a system.

OUTCOMES: A primary care electronic medical record with patient demographics, a cashier, inventory system and specific forms for adult, pediatric, HIV, and maternity was installed in all three clinics. Barriers identified during implementation included power stability, server safety and maintenance, clinic staff reluctance to transition from paper to electronic medical records, and the absence unique patient identifiers.

FUTURE DEVELOPMENTS: Demographic information on patients will be expanded to include biometrics for unique identification and approximate GPS coordinates of their dwellings. This will facilitate the generation of geographical maps with the distribution of symptoms or disease within urban slums and other geographical areas to inform public health interventions. The electronic health system will be expanded to mobile health workers and more clinics to grow the established referral network.

IP17

CREATION OF A NOVEL PROVINCE-WIDE ANTIMICROBIAL STEWARDSHIP PRECEPTORSHIP PROGRAM – AN INNOVATIVE CAPACITY BUILDING STRATEGY FOR STEWARDSHIP IMPLEMENTATION

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OBJECTIVES: Increasing capacity for antimicrobial stewardship (AS) is a priority for acute care hospitals across Canada since Accreditation Canada's 2013 Required Organizational Practice on establishing AS programs to optimize antibiotic use. We developed a novel Antimicrobial Stewardship Preceptorship Program (ASPP) as a capacity building strategy to address province-wide AS implementation challenges.

METHODS: A province-wide multidisciplinary group with expertise in infectious diseases, pharmacy, administration, education and clinical practice collaboratively developed core ASPP principles including: learning objectives, preceptee/preceptor expectations, reading lists, project outcomes, preceptorship activities, and an evaluative framework. An online open document service (Microsoft SharePoint 2013) was used for development, with formal meetings occurring via unified communications platform (Microsoft Lync 2010). Consensus was achieved through multiple iterative feedback phases, and an independent external review.

RESULTS: Self-identified preceptees from sites without an AS program completed mandatory pre-program activities including: core readings, online infectious diseases training modules and an introductory AS presentation. Preceptors were recruited from sites with an established AS program. Intense, on-site two week preceptorships focused on prospective audit and feedback services. Preceptees initiated planning for an AS project at their home site, attended educational events and received ongoing feedback from preceptors. Preceptors actively integrated the preceptees into daily AS patient care activities specific. The inaugural preceptorships were completed in December 2015 and January 2016. Qualitative self-assessments pre- and post-preceptorship (immediate and 6 months) will be used to inform process improvements.

CONCLUSION(S): We describe a novel and innovative program to expedite the implementation of stewardship initiatives across an entire province, allowing potential penetration into all acute care sites. We believe that this model may serve as a useful strategy for other jurisdictions across Canada.

IP18 ABSTRACT WITHDRAWN

IP19

BLASTOMYCOSIS IN NORTHWESTERN ONTARIO, 2004 TO 2014

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BACKGROUND: Blastomycosis is an invasive fungal disease caused by *Blastomyces dermatitidis* and the recently discovered *Blastomyces gilchristii*. The Kenora region of northwestern Ontario has the highest reported incidence of blastomycosis in the world. Thunder Bay, Ontario is the largest city in northwestern Ontario and provides health services to a large surrounding rural catchment area that contains a substantial Aboriginal population. The objective of this study was to analyze blastomycosis disease in patients presenting at the Thunder Bay Regional Health Sciences Centre (TBRHSC).

METHODS: The medical charts of 64 patients with confirmed cases of blastomycosis that presented at the TBRHSC from February 1, 2004 to January 31, 2014, were retrospectively reviewed for clinical and demographic data. To determine whether the Aboriginal patients had a statistically significant increased proportion of comorbidities compared with non-Aboriginal patients, a contingency table was used to test for significance using the χ^2 distribution; statistical significance was determined to be $P < 0.05$.

RESULTS: 64 cases of blastomycosis were diagnosed over a 10 year period. Aboriginals were observed to be disproportionately represented in the patient population. Of the patients whose smoking status was known, 71.4% had a history of smoking. 59.4% of patients had underlying comorbidities and a higher comorbidity rate was observed among Aboriginal patients. The case-fatality rate from direct complications of blastomycosis disease was calculated to be 20.3%.

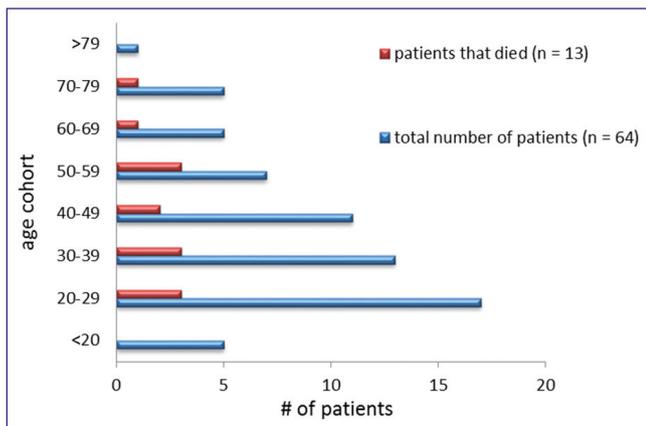


Figure 1) Age distribution of all blastomycosis patients and blastomycosis patients that died.

TABLE 1

Age, sex, aboriginal heritage, and case-fatality rate among 64 patients with blastomycosis

Age group (years)	No. of patients					
	Age group total*	Male	Female	Aboriginal heritage	Death count	Case-fatality (%)
<20	5 (7.8)	4 (80)	1 (20)	3 (60)	0	0.0
20-29	17 (26.6)	9 (52.9)	8 (47.1)	11 (64.7)	3	17.6
30-39	13 (20.3)	10 (76.9)	3 (23.1)	7 (53.8)	3	23.1
40-49	11 (17.2)	8 (72.7)	3 (27.3)	5 (45.4)	2	18.2
50-59	7 (10.9)	3 (42.9)	4 (57.1)	3 (42.9)	3	42.9
60-69	5 (7.8)	4 (80.0)	1 (20.0)	2 (40.0)	1	20.0
70-79	5 (7.8)	2 (40.0)	3 (60.0)	1 (20.0)	1	20.0
>79	1 (1.6)	1 (100.0)	0 (0.0)	0 (0.0)	0	0.0
total	64	41	23	32	13	20.3

Number of patients (percent of age group); *percent of total patients

TABLE 2

Comparison of comorbid status between Aboriginal and non-Aboriginal patients diagnosed with blastomycosis

Status	Aboriginal	Non-Aboriginal	Total
Comorbid	22	16	38
Non-comorbid	8	17	25
Total	30	33	63

Of the 64 patients in the present study, race was specified in 63 patients. Of the Aboriginal patients, 73.3% were comorbid, compared with 48.5% of the non-Aboriginal patients, and the difference was statistically significant (Pearson's $\chi^2 = 4.054$, $df = 1$, $P = 0.044$)

CONCLUSIONS: Aboriginals are disproportionately affected by blastomycosis disease which may be explained by the higher rate of comorbidities observed. The number of blastomycosis diagnoses per year in Ontario has increased considerably compared with the number of cases diagnosed per year before 1990 (when blastomycosis was removed from the list of reportable diseases in Ontario). The case-fatality rate of direct complications from blastomycosis at the TBRHSC is the highest ever to be reported in Canada and more than double that of previously published Canadian studies.

IP20 ABSTRACT WITHDRAWN

IP21

CLINICAL OUTCOMES OF STAPHYLOCOCCUS AUREUS BACTEREMIA FOLLOWING INTRODUCTION OF MANDATORY INFECTIOUS DISEASE SPECIALIST CONSULTATION

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OBJECTIVES: To investigate if mandatory infectious disease (ID) consultation as a hospital policy leads to improved clinical outcomes in patients with *Staphylococcus aureus* bacteremia.

METHODS: A pre- and post-intervention study design was used to compare process and outcome measures before and after a quality-improvement strategy. The pre-intervention population consisted of two cohorts: one group that received infectious disease consultation (IDC) after positive *S. aureus* blood culture and the other group that did not receive ID consultation (NIDC). Intervention was the implementation of mandatory ID consultation at three academic hospitals for patients ≥ 18 years of age with ≥ 1 positive blood culture for *S. aureus*. Post-intervention population were patients with positive *S. aureus* culture between December 2014 and May 2015. Patients were excluded if within 2 days of blood culture they: died, were deemed palliative, or left against medical advice. Electronic medical records were assessed using a standardized data collection form.

RESULTS: In the pre-intervention population, 506/847 (59.7%) received ID consultation (IDC) versus 341/847 (40.2%) did not (NIDC). In the post-intervention group, 112 patients with *Staphylococcus aureus* bacteremia were identified, of which 108 (96%) received ID consult. In the pre-intervention group, the IDC cohort had an in-hospital mortality rate of 21% versus 29% in the NIDC group. In the post-intervention group, in-hospital mortality was 22/112 (19.6%). After the intervention, there was also increased use of process measures, notably echocardiogram use; compared to the pre-intervention cohorts, 73% of IDC receiving echocardiography and 56% of NIDC, in the post-intervention group, 96 (85%) received an echocardiography.

CONCLUSION: Mandatory ID consultation for *S. aureus* bacteremia as a quality improvement strategy resulted in reduced in-hospital mortality and improved adherence to certain process measures.

IP22 ABSTRACT WITHDRAWN

POSTER PRESENTATIONS

Friday, April 1, 2016
Room: Grand Ballroom

P01

DYNAMICS OF SERUM QUANTITATIVE HEPATITIS B SURFACE ANTIGEN TESTING IN ASSESSING NUCLEOS/TIDE ANALOG TREATMENT RESPONSE AND DISEASE PHENOTYPE IN CHRONIC HEPATITIS B PATIENTS IN CANADA

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BACKGROUND: Quantitative hepatitis B surface antigen (qHBsAg) levels have been reported as a useful marker of chronic hepatitis B (CHB) disease phenotype and in assessing response to nucleoside analogues (NA) treatment. A cut-off qHBsAg of <2 log₁₀ IU/ml has been associated with a low risk of relapse after NA treatment cessation though most published studies were conducted in cohorts with a more limited HBV genotype distribution and using older generation NA.

OBJECTIVE: To determine the clinical value of qHBsAg monitoring in a large Canadian cohort of CHB patients.

METHODS: In this retrospective review, we included treatment-naïve or NA treated patients who underwent qHBsAg testing (Abbott Architect). All patients had HBV DNA testing by kinetic PCR (Roche TaqMan or Abbott m2000) and ALT or AST levels within 3 months of qHBsAg testing. CHB disease phases were classified according to current guidelines.

RESULTS: 429 CHB patients (230 [54%] male, median age 44 y [IQR 36-56], 302 [72%] Asian) underwent qHBsAg testing, including 187 (44%) with serial tests (median follow up 1.3 yrs [IQR 0.6-3.7]). HBV genotyping was done in 151 (35%) and was: A in 20 (14%), B in 43 (29%), C in 53 (36%), D in 22 (15%) and E in 10 (7%). In the treatment naïve group, 21 (5%) were immune tolerant, 36 (8%) immune intolerant, 109 (25%) inactive carriers, and 119 (28%) had HBeAg negative CHB. The corresponding mean log qHBsAg levels were 4.55 (IQR 3.39-4.92), 3.94 (IQR 3.32-4.49), 2.92 (IQR 1.80-3.80), and 3.24 (IQR 2.69-3.95), respectively; p<0.05 for all comparisons except immune tolerant versus immune intolerant. 193 (45%) received NA (58 [30%] entecavir and 135 [70%] tenofovir) for a median duration of 4.45 years (IQR 3.20-5.70) with a median on treatment qHBsAg of 3.20 (2.65-3.70). NA treated patients showed a modest decline in qHBsAg levels (median -0.07 [IQR -0.20 to 0.01]). There was no statistical difference between TDF and ETV treated patients. In patients on long-term ETV or TDF, 39 (22%) had qHBsAg levels < 2_{log(10)} IU/mL, of which three cases to date have stopped NA (follow-up < 6 months after treatment cessation).

CONCLUSIONS: In this large Canadian cohort study, qHBsAg was associated with CHB disease phase and declined slowly in patients receiving potent NA. A significant number of patients on therapy had low qHBsAg levels of which some may be eligible for therapy discontinuation.

P02

NOT SUCH A LONELY PLANET: TRAVELERS WITH HAND, FOOT, AND MOUTH DISEASE AFFECTING LIMBS, TRUNK AND FACE

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OBJECTIVES: To highlight the emergence of an atypical hand, foot, and mouth syndrome associated with global enterovirus epidemics, especially coxsackievirus A6.

METHODS: Case presentation and commentary.

RESULTS: We present two paediatric cases of atypical hand, foot, and mouth disease occurring in the confounding context of international travel. In both cases the differential diagnosis of fever and rash was wide, including numerous acute life-threatening conditions.

CONCLUSION(S): Atypical hand, foot, and mouth syndrome characterised by polymorphous erosive and/or vesiculobullous eruptions should be considered in travellers with fever and rash. Awareness of this condition should lead to faster diagnosis, limit unnecessary investigations and empirical treatment.

P03

TIME TO REPORTING OF POSITIVE BLOOD CULTURES FOR PEDIATRIC PATIENTS ASSESSED AT A CHILDREN'S HOSPITAL EMERGENCY DEPARTMENT

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BACKGROUND: When infants are admitted to the hospital with a diagnosis of 'rule out sepsis', the optimal duration of hospitalization for observation pending blood culture results remains uncertain. We investigated whether 24 hours of observation would be sufficient to detect children with bacteremia at a hospital that lack microbiology services 24/7.

METHODS: This study was carried out at the Children's Hospital in Winnipeg, Manitoba. The microbiology laboratory at this institution is not staffed overnight. Laboratory records were retrospectively reviewed to identify all children who had a positive blood culture obtained at the Children's Hospital Emergency Department (CHER) between January 1 and June 30, 2014. Time to positivity of blood cultures was determined from a BacT/ALERT® instrument (BioMérieux, Durham, North Carolina). Time of collection was obtained from the specimen requisition, and time of reporting to a responsible physician was determined from review of the laboratory information system. Blood cultures that grew a potential contaminant were excluded from further analysis. The primary outcome of interest was the percentage of positive blood cultures reported to a responsible physician within 24 hours of sample collection.

RESULTS: 1444 blood cultures from CHER were received by the microbiology laboratory during the study period (mean patient age of 3.9 years). A significant pathogen was recovered from 35.94.3% of these had a time to positivity of <26 hours on the BacT/ALERT® instrument. However, time from blood culture collection to physician notification was <24 hours for only 63% (22/35). Further, time from collection to physician notification was >30 hours in 25.7% (9/35). Delays in reporting were primarily related to cultures arriving overnight or going positive overnight.

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CONCLUSIONS: These data suggest that for a hospital lacking 24/7 microbiology services, absence of reported blood culture positivity 24 hours following sample collection is not sufficient to guarantee safety for patient discharge.

P04

DETECTION OF VIRAL RNA FRAGMENTATION AS A SURROGATE MEASURE OF VIRUS VIABILITY FOR ENVIRONMENTAL SURVEILLANCE PROJECTS

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OBJECTIVE: The 2014/2015 West African Ebola outbreak resulted in an unprecedented number of Ebola patients and management centres. In these settings, ebolavirus environmental contamination presents inherent nosocomial risks to patients and personnel. Efforts to detect environmental contamination have been hampered by the inability to perform in-field ebolavirus culture. Alternative techniques using viral nucleic acid amplification proved sensitive but are poor predictors of viability. This study aims to identify whether sunlight exposure, a common Ebola field decontamination technique, causes measurable RNA damage and whether it inversely correlates with virus viability.

METHODS: Vesicular stomatitis virus (VSV), an ebolavirus surrogate, was exposed to natural sunlight and aliquots were frozen at several time points. The aliquots were divided for RNA extraction and viral isolation. RNA fragmentation was assayed using reverse transcription (RT) followed by separate quantitative PCR (qPCR) reactions amplifying regions 150, 800 and 1200 base pairs (bp) downstream of the RT primer 3' end.

RESULTS: The VSV culture titre decreased with increasing sunlight exposure, with no viable virus detected after two hours. When RT and amplification steps were separated, positive amplification of viral RNA by qPCR was detected using the 150 and 800 bp primers irrespective of virus viability. In contrast, amplification was detected at the 1200 bp primer only when the virus was viable. When used in one-step PCR reactions, all three primer/probe sets amplified efficiently.

CONCLUSION: As expected, increasing sunlight exposure led to a decreasing VSV titre. This correlated well with the loss of PCR signal from our 1200 bp primer/probe set. This may be due to RNA fragmentation preventing long transcript formation during the RT reaction, resulting in the absence of the distal primer/probe target sequence. Our data suggest that this approach can act as an alternative to viral culture for the detection of viable virus in the field setting.

P05

TRENDS OF ANTIMICROBIAL RESISTANCE OF *NEISSERIA GONORRHOEA* STRAINS IN QUEBEC FROM 2010 TO 2014: EMERGENCE OF SEQUENCE TYPE, ST-10567 ASSOCIATED WITH AZITHROMYCIN RESISTANCE

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BACKGROUND: Multidrug resistant *N. gonorrhoeae* (NG) is a major public health threat. In Quebec, the overall reported gonorrhoea cases (cultures and molecular-based assays) increased from 2010 (n=2319) to 2014 (n=3292). Quebec's NG treatment guidelines recommend a third generation cephalosporin (3GC) and empirical *Chlamydia trachomatis* azithromycin treatment. Monotherapy with azithromycin 2 g is recommended in case of severe penicillin allergy.

OBJECTIVES: In this study, we described the antimicrobial susceptibility rates between 2010 and 2014 as well as the molecular typing of emergent azithromycin-resistant NG strains in the province of Quebec.

METHODS: All NG strains (men 3016 [73.4%], women 1075 [26.2%], unknown 18 [0.4%]) collected in the province of Quebec, as part of the

surveillance program (2010, n=920; 2011, n=797; 2012, n=772; 2013, n=714; 2014, n=906) were tested for ciprofloxacin, ceftriaxone, cefixime and azithromycin using agar dilution method described by CLSI. Molecular typing was performed using NG multi-antigen sequence typing method (NG-MAST).

RESULTS: The proportion of strains with azithromycin resistance (MIC ≥ 2 mg/L) was <2% from 2010 to 2013 and increased to 6.7% in 2014. In 2014, 87% (n=53) of the azithromycin resistant strains were isolated from men and 57% (35/61) of these belonged to a newly described ST profile: ST-10567. During this period, an increase of 3GC (cefixime and ceftriaxone) MICs was observed: while the proportion of strains with reduced susceptibility (MIC 0.12 mg/L) to ceftriaxone was less than 0.5% between 2010 and 2013, it increased to 3.9% (35 strains) in 2014.

CONCLUSION: The year 2014 was marked by an increase of azithromycin-resistant NG strains in the province of Quebec along with increased MICs to ceftriaxone. Half of these azithromycin resistant strains (57%) were assigned to a novel sequence type, ST-10567 not previously reported in the international database. Monitoring of azithromycin susceptibilities in NG is crucial to support STI treatment guideline recommendations.

P06

USING SIGNAL-TO-CUTOFF RATIOS TO IMPROVE REVERSE SEQUENCE ALGORITHM FOR SYPHILIS DIAGNOSIS

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OBJECTIVES: 1) To correlate the magnitude of signal-to-cutoff (S/CO) ratios of 6 commercial kits used in Quebec with syphilis infection confirmation results; 2) To establish a S/CO value above which treponemal confirmation would not be required.

METHODS: Between January 2014 and April 2015, serum samples from previously undiagnosed individuals, reactive by EIA/CLIA and either negative RPR or reactive with a low titer (1:1-1:4), were included in the study. All samples were tested with TPPA and, if negative or inconclusive, with a line immunoassay (LIA). Syphilis infection confirmation was defined by a reactive TPPA or LIA. Logistic regression analysis was used to determine S/CO values (95% CI=0.98) above which confirmation would not be required. Kits used by the 27 participating laboratories were Architect (n=14), Bioplex (n=1), Syphilis EIA II (n=5), Trepsure (n=4), Immulite (n=1) and Vitros (n=2).

RESULTS: Of the 2723 EIA/CLIA specimens tested, 1796 (66%) were confirmed as true syphilis cases. Confirmation rate was significantly higher in samples with low-titer positive RPR (91%) than with negative RPR samples (54%); p<0.01. S/CO values above which a confirmation would no longer be needed for the Architect, Bioplex and Trepsure kits are shown in the table. No S/CO values could be established for the Syphilis EIA II, the Immulite and the Vitros kits.

EIA/CLIA	All samples		Negative RPR		Low-titer RPR	
	S/CO	No confirmation	S/CO	No confirmation	S/CO	No confirmation
Architect	16.4	136/668 (20%)	20.3	22/441 (5%)	13.9	121/227 (53%)
Bioplex		No S/CO identified			7.4	333/442 (75%)
Trepsure	24.6	42/293 (14%)	28.8	11/227 (5%)	34.7	5/66 (8%)

CONCLUSIONS: S/CO values could be used with some of the commercial kits to identify sera not requiring extra treponemal confirmation. Obviating the need for confirmation in 14 to 20% of EIA/CLIA reactive sera with negative or low titer RPR, and in up to 75% of sera with low-titer RPR, would improve cost-effectiveness of the reverse sequence algorithm.

P07

ENHANCED SELECTIVITY FOR TARGETED KILLING OF *STREPTOCOCCUS MUTANS* BY A PHEROMONE-GUIDED ANTIMICROBIAL PEPTIDE

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BACKGROUND: A major challenge using antibiotics to treat infectious diseases is that these agents may indiscriminately kill the resident organisms, resulting in ecological disruption or other negative clinical consequences. To circumvent this problem, we have developed a new class of antimicrobial peptides, called pheromone-guided antimicrobial peptides (PG-AMP), which can selectively bind to the target cells and initiate rapid killing.

METHODS: In this study, we evaluated a newly designed peptide HP30 by examining its selective killing activity against *S. mutans* and other related species.

RESULT: The results revealed that nearly 80% of *S. mutans* cells in planktonic cultures lost their viability following exposure to HP30 (5.0 mM) for 15 min. Only 20% of *S. sanguinis* or *S. gordonii* and 5% of *Actinomyces naeustlundii* were killed following the same exposure. A *S. mutans* mutant lacking the ComD receptor only showed 22% of killing by HP30, while a ComD overexpression strain showed 92% of killing. The results suggest that HP30 predominantly binds to the ComD receptor to mediate selective killing. Similar results were observed in dual-species biofilms that consisted of two closely related species. In addition, a combination of HP30 with 2 mM of a chelating agent EDTA significantly enhanced the target killing of *S. mutans* cells grown in biofilms. Our work showed that HP30 retained its killing activity in the presence of physiological salt concentrations. The peptide was also relatively stable in the presence of human saliva containing 2 mM EDTA and it did not cause any hemolysis.

CONCLUSION: The data indicate that HP30 shows an improved selectivity for targeted killing of *S. mutans* cells when compared with a previously reported peptide IMB-2. This novel PG-AMP shows promise for further development as a target-specific antimicrobial agent.

P08 ABSTRACT WITHDRAWN

P09

THE PERFORMANCE OF DIRECT DISK DIFFUSION FOR COMMUNITY-ACQUIRED BACTEREMIA DUE TO GRAM-NEGATIVE BACILLI, AND ITS IMPACT ON PHYSICIAN TREATMENT DECISIONS

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BACKGROUND: Direct disk diffusion susceptibility testing provides results within twelve to eighteen hours after blood culture detection, as compared to forty eight hours for standard microtitre susceptibility. This result may impact patient outcome in sepsis if it is accurate, and if physicians use the information to promptly and appropriately change antibiotic treatment.

OBJECTIVE: To compare the performance of direct disk diffusion against standard susceptibility, and to consider physician decisions in response to these early results, for community-acquired bacteremia with Gram-negative bacilli.

METHODS: Retrospective observational study of all positive blood cultures with Gram-negative bacilli collected over one year (2014) was conducted. Direct disk diffusion and standard susceptibility correlation were reported using percent agreement and the rates of very major, major, and minor errors were determined. Physician antibiotic treatment decisions were assessed by an infectious diseases physician based on information available to the physician at the time of the decision.

RESULTS: 2452 blood culture bottles grew Gram-negative bacilli, from which 89 bottles were included in the analysis. Direct disk diffusion agreement with standard susceptibility varied widely. In 47 cases (52.8%), the physician should have changed to a narrower spectrum but did not, in 18 cases (20.2%), the physician correctly narrowed from appropriate broad coverage, and in 8 cases (9.0%), the empiric therapy was correct.

CONCLUSION: Because inoculum is not standardized, direct susceptibility results do not agree with standard susceptibility results for all antibiotics. Physicians do not act on direct susceptibility results. Direct susceptibility should be discontinued in clinical microbiology laboratories.

P10

COMPARISON OF TWO CHROMOGENIC MEDIA AND AN ENHANCED BLOOD PLATE METHOD FOR THE PURPOSE OF GBS DETECTION FROM BROTH ENRICHED VAGINAL/RECTAL SAMPLES

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OBJECTIVES: The CDC has recommended that laboratories maximize recovery of GBS, including atypical strains, by using a broth sub-cultured to a Blood agar or chromogenic plate. Unless manufacturers suggest specific reading times, all plates must be incubated 48 hrs if negative at 24 hrs. The Thermo-Fisher chromogenic plate Brilliance GBS with Inhibigen™ BRI requiring a read once only at 18-24 hrs. was compared in its performance to chromogenic Bio-Rad Strep B Select SEL and a Thermo-Fisher Oxoid blood agar BAP with an added 10 µgm. gentamicin disc applied to second quadrant to differentiate non-hemolytic GBS and Enterococcus.

METHOD: 1) 300 pre-natal vaginal/rectal samples received for GBS detection were inoculated into a Thermo-Fisher Oxoid LIM broth and incubated 18-24 hrs. To each BAP 2nd quadrant, a 10 µgm. gentamicin disc was added. All plates were incubated for 18-24 hrs. and read for GBS colonies (BRI - pink; SEL- turquoise; BAP- typical grey, hemolytic and growth up to gent disc.) . SEL (and BAP) were reincubated for additional 24 hrs. as per manufacturer and/or CDC. Confirmation was via PathoDxtra B latex agglutination. PYR Catalase, gram used as necessary. A positive GBS was defined as agglutination etc. positive from any one or combination of positive plates. 2) 44 known positive broths were subbed to each plate and incubated as above. Recovery and mixed growths were noted.

RESULTS: 1) 80 samples recovered GBS (27%). BRI detected 79; SEL:76; BAP:70 with respective sensitivities of 98%, 95%, and 87.5%. 7 of SEL and 8 BAP samples required reincubation or subculturing to achieve useable growth for testing. All GBS growths detected at 18-24 hrs. Specificity was BRI: 84%; SEL:97 %; BAP:95%. 2) All 44 pos. recovered on BRI (100%); 41 on SEL (93%) and 40 on BAP (91%). BRI 30% mixed; SEL 79% mixed; BAP 100% mixed with breakthrough flora. 6 GBS strains were deemed non-hemolytic with recovery on all plates.

CONCLUSIONS: Sensitivity BRI>SEL>BAP. Specificity SEL>BAP>BRI. All typical BRI results can be released 24 hrs earlier than SEL and BAP. TAT BRI<SEL=BAP. Colony size BRI>SEL>BAP. Breakthrough growth BRI<SEL <BAP. All grew non-hemolytic GBS well. Non haemolytic GBS, unlike Enterococcus, shows growth up to gentamicin disc on BAP.

P11

THE USE OF MATRIX ASSISTED LASER DESORPTION IONIZATION-TIME OF FLIGHT MASS SPECTROMETRY (MALDI TOF MS) TO DETERMINE SUSCEPTIBILITY OF *CANDIDA GLABRATA* TO CASPOFUNGIN

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BACKGROUND: *Candida glabrata* is a significant cause of candidemia among hospitalized patients. As *C. glabrata* are often resistant to azoles, the echinocandins, specifically caspofungin, is the drug of choice for treatment. Caspofungin resistance is increasingly being observed necessitating a rapid, accurate method for determination of susceptibility. **OBJECTIVE:** To demonstrate whether MALDI-TOF MS can be used as an inexpensive, accurate, rapid method to detect caspofungin resistance in *C. glabrata* isolates.

METHODS: Ten well-characterized isolates of *C. glabrata* with confirmed susceptibility/resistance to caspofungin (assessed by microbroth dilution (MBD) and FKS sequence analysis) were tested: 5 susceptible and 5 resistant isolates. For the MALDI-TOF MS assay, isolates were incubated in RPMI media with a range of caspofungin concentrations (0.015 mg/L - 8 mg/L) and

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a negative control for 16 hours. Spectra were obtained using the Bruker Microflex LT MS system. Spectra were analyzed using the Biotyper software (version 3.0, Bruker Daltonics, Germany) to generate individual Composite Correlation Index (CCI) scores, a method which allows for comparison of spectral data. CCIs can be used to determine, MPCCs, which are the lowest drug concentration at which the spectra is more similar to that observed at the maximum drug concentration than that observed at the null drug concentration. MPCCs have been demonstrated to approximate MICs by other groups. Here, an MPCC value of ≥ 0.5 mg/L was interpreted as resistant in keeping with the CLSI guidelines on antifungal susceptibility testing.

RESULTS: Based on our analysis of 10 strains, there was 90% categorical agreement between the MBD method and MALDI-TOF MS method. The single discordant isolate had low-level resistance by MBD but was non-resistant by MALDI-TOF-MS. In most cases, the MPCC was within 1 serial dilution of the MIC.

CONCLUSION: Here, we demonstrated that MALDI-TOF MS can be used to detect caspofungin resistance among *C. glabrata* isolates with a high degree of accuracy. Although inexpensive, this method is not more rapid than the current gold-standard, MBD.

P12

HIDING IN PLAIN SIGHT: HOW DO PRESCRIPTION PRACTICES AND CLINICAL OUTCOMES DIFFER BETWEEN KNOWN AND POTENTIAL EXTENDED-SPECTRUM BETA-LACTAMASE PRODUCING ORGANISMS?

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BACKGROUND: Widespread usage of third-generation cephalosporins has resulted in the emergence of organisms that possess an extended-spectrum beta-lactamase (ESBL) enzyme. Certain organisms, including *Serratia*, *Proteus (non-mirabilis)*, *Providentia*, *Acinetobacter*, *Citrobacter*, *Enterobacter* and *Morganella* (SPACE-M) may carry a gene (AmpC) that allows them to over-express this enzyme 10 to 100 fold above their normal levels during treatment with a beta-lactam.

OBJECTIVE: To explore prescription practices and clinical outcomes among SPACE-M bloodstream infections (BSI) treated with different beta-lactam and non-beta-lactam therapies, and to compare these with proven ESBL *E. coli* infections.

METHODS: We retrospectively reviewed all adult SPACE-M and ESBL *E. coli* BSI from April 1, 2010 to June 1, 2015 at the McGill University Health Centre. Antibiotic susceptibilities were determined in accordance with the Clinical & Laboratory Standards Institute guidelines. Basic patient demographic data and clinical outcomes were collected from the laboratory information system and the patients' charts.

RESULTS: There were 284 unique episodes of SPACE-M bacteremias. Compared with established ESBL *E. coli* bacteremias, patients were less likely to receive definitive treatment with a carbapenem (30.99% vs. 50%; $p=0.0081$), but received equal amounts of PTZ (23.55% vs. 26.2%; $p=0.3557$). Among all SPACE-M isolates, there were no statistically significant differences in ICU admission, relapse, or mortality among patients who were treated either empirically or definitively with PTZ vs. other classes.

CONCLUSION: Despite theoretical risks of failure, a similarly elevated proportion of blood stream infections caused by SPACE-M and ESBL *E. coli* isolates were treated with PTZ, with no apparent differences in clinical outcomes. Further research is warranted to determine if it is an acceptable treatment.

P13

DIRECT MALDI TOF IDENTIFICATION AND VITEK® 2 ANTIBIOTIC SUSCEPTIBILITY TESTING OF ENTERIC GRAM NEGATIVE BACILLI FROM BLOOD CULTURES

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BACKGROUND: Recent studies have demonstrated direct testing on blood cultures (BC) improves the time to effective antibiotics, leading to reductions in mortality and length of stay. To reduce time to reporting identification (ID) and antibiotic susceptibility testing (AST), we verified direct testing methods in our laboratory.

METHODS: From September 2014-2015, BC positive for enteric GNB were tested if they were positive from 800 to 2300. Blood was inoculated into 2 serum separator vacutainer tubes (SST), centrifuged at 450xg for 15 minutes, then serum was removed, with the remaining pellet left intact. Pellet material from one SST was used to inoculate the MALDI TOF target while the second pellet was used to inoculate a Vitek® 213 card. ID scores and AST results were recorded and compared to results obtained with conventional methods. MALDI TOF scores were analysed to create an algorithm for accepting direct IDs from BC. Vitek® 2 results were analysed for categorical and essential agreement, with minor, major and very major errors calculated using CLSI breakpoints.

RESULTS: In total, 105 GNB underwent direct MALDI TOF testing with an ID obtained in 98/105 (93%), of which 95 (97%) were correct. The 3 isolates with incorrect IDs had scores <1.3. An algorithm for accepting direct MALDI TOF IDs was created with this data. In total, 110 enteric GNB underwent direct Vitek® 2 AST, including 13 unique isolates resistant to ceftriaxone. Minor, major and very major errors were below established thresholds for all antibiotics except cefazolin, cephalexin and nitrofurantoin. Only cefazolin is reported routinely on BC in our lab so we developed an algorithm for its testing and reporting to ensure accurate results from direct testing methods.

CONCLUSIONS: Direct MALDI TOF ID and Vitek® 2 AST on BC with enteric GNB provided reliable results compared to conventional testing.

P14

OUTBREAK OF A VARIANT STRAIN OF CMRSA-5 IN A NEONATAL INTENSIVE CARE UNIT

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BACKGROUND: An MRSA outbreak was identified in a level III NICU and discharge/transfer screening initiated as part of outbreak management. Two patients who were MRSA negative by PCR on discharge screening were found to be MRSA culture positive on admission screening at two other regional hospitals. Subsequent investigation identified that an additional 5 patients were MRSA negative by PCR but positive by culture. An investigation was initiated to determine the cause of the false negative PCR MRSA screens.

METHODS: All NICU MRSA cultures and screens were reviewed. Following identification of the false-negative PCRs, subsequent point prevalence studies of NICU patients were done by PCR and culture. Prior to PCR (Roche LightCycler® MRSA advance Test), swabs were incubated overnight in an MRSA selective broth. For culture, all selective broths were subcultured to a chromogenic agar (Bio-Rad). MRSA isolates were typed using variable number tandem repeat (VNTR) PCR and MALDI-TOF. For 10 isolates the MRSA genotype was confirmed by PFGE at the Public Health Ontario Laboratory. The presence of *mecA* gene was confirmed by PCR.

RESULTS: A total of 16 NICU patients had culture positive, PCR negative MRSA detected. The negative PCR result was confirmed by testing isolated colonies from the broth subculture. All isolates were identical by VNTR and MALDI-TOF and found to be related to CMRSA-5. PFGE confirmed the relatedness of the outbreak strains as being a variant of CMRSA-5. All isolates carried the *mecA* gene.

CONCLUSION: The MRSA outbreak in the NICU was due to a strain related to CMRSA-5 that failed to be detected by a commercial screening PCR assay. This strain may contain variability in the right junction of the SCC_{mec} genetic element that prevented detection and further investigation is ongoing. This outbreak highlights the limitations of molecular based screening methods and reliance on PCR for MRSA detection.

P15

MANAGEMENT OF MALARIA IN [LARGE CANADIAN CITY]: A MULTI-FACETED QUALITY ASSURANCE PROJECT REVIEWING 2010-2013

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BACKGROUND: Malaria is a blood-borne parasite transmitted by *Anopheles* mosquitoes in endemic countries. It is estimated that in 2013, approximately 198 million people were infected with malaria, with 584,000 deaths (1). With the increasing travel and immigration to and from malaria endemic areas, tropical diseases like malaria are becoming more frequently encountered in our practice setting. At the same time, these events are still rare enough that many physicians encountering these patients either do not recognize the condition or understand its serious sequelae, if inappropriately treated. The following work acts as a quality assurance study for the management of malaria in the acute care setting in [a large Canadian city] from 2010-2013.

METHODS: Cases were identified by positive malaria smears through [our centralized laboratory system]. Demographics of the patient (age, country acquired, reason for travel, etc) and parasite (species, parasitemia), location of first smear request (outpatient clinic, emergency department or inpatient), and severity criteria as per the Canadian Malaria Network (and WHO) were collected. Also assessed were timing of multiple facets including specimen transport, lab diagnosis, treatment decision, pharmacy processing and delivery of antimalarial. Further scrutiny was given around management of the cases, including repeat smears and involvement of infectious diseases consultants. Overall assessments were made for time taken for the patient to receive the first dose of appropriate antimalarial.

RESULTS: There were 125 unique adult malaria cases during the study period. Over 50% were diagnosed in the outpatient setting; 12% after admission to hospital. Thirteen percent of cases had parasitemias >2% (severe, by current guidelines). Of the cases managed in the acute care setting (ER or inpatient), 61% of cases received their first dose of antimalarial within 6 hrs of having their first smear drawn. There were no malaria-related deaths during the study period.

CONCLUSIONS: The appropriate management of malaria in non-endemic settings depends on the integration of several factors from physician recognition to specimen transport to laboratory diagnostics to timely administration of effective drug. Assessing each of these components individually can help identify areas for focus and improvement.

REFERENCE

1. World Health Organization. World Malaria Report, 2014.

P16

COMPARISON OF FOUR DIFFERENT SEROLOGICAL ASSAYS FOR DIAGNOSIS OF HEPATITIS C VIRUS INFECTION

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BACKGROUND: The prevalence of Hepatitis C Virus (HCV) infection in the Canadian population is estimated at 0.8% (242,500). Of those, a predicted 21% are unaware of their infection. Recent availability of improved therapeutics for treatment of HCV infection has prompted international discussions regarding population based screening to identify the undiagnosed population. Here we assess the performance of four commercial assays to identify HCV infection in the Alberta population.

METHODS: 151 serum samples previously characterized by serology (anti-HCV, Abbott Diagnostics), NAT (RT HCV RNA, Abbot Molecular) and genotype (RT HCV Genotype II, Abbott Molecular) were run in parallel on the Evolis Monolisa Anti-HCV PLUS V2 (Bio-Rad), the Evolis Monolisa HCV Ag-Ab ULTRA V2 (Bio-Rad), the Elecsys Anti-HCV II (Roche), and the Centaur aHCV (Siemens) platforms. Discordant results were confirmed by INNOLIA (Fujirebio). All testing was performed according to the individual manufacturer's instructions.

RESULTS: True clinical diagnosis (TCD; including HCV NAT and INNOLIA results) was used as the gold standard to which each assay was measured. Sensitivity, specificity, positive and negative predictive values (%) were calculated for all assays as follows: Bio-Rad PLUS (99, 98, 99, 98), Bio-Rad ULTRA (100, 100, 100, 100), Roche (99, 86, 93, 98) and Siemens (99, 100, 100, 98) respectively. A total of 9 samples were discordant by at least one assay. Seven discordant samples were considered false positives when compared to the TCD (Bio-Rad PLUS (1), Roche (7)), while two different genotype 3 samples were missed by at least one assay (Bio-Rad PLUS (1), Roche (1) and Siemens (1)).

CONCLUSION: The best overall performance was observed with the Bio-Rad HCV Ag-Ab ULTRA and the Siemens Centaur. While the Roche Elecsys assay has very high sensitivity, a second enzyme immunoassay may be needed for final confirmation to avoid false positive results.

P17

ALERE I INFLUENZA A&B ISOTHERMAL MOLECULAR ASSAY PERFORMANCE IN DIRECT FLUORESCENT ANTIBODY INDETERMINATE AND FALSE NEGATIVE SAMPLES IN A PEDIATRIC SETTING

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BACKGROUND: The Direct fluorescent antibody (DFA) test is relatively rapid and accurate for diagnosis of Influenza. The Alere i influenza A&B™ is the first Health Canada approved rapid (~ 15 minute) molecular assay for influenza A/B. We evaluated this assay by testing stored influenza A or B RT-PCR positive samples, previously found by DFA to be either negative or indeterminate due to non-specific fluorescence (NSF), or insufficient cells (IC).

METHODS: All samples submitted to BC Children's Hospital Virology Laboratory for influenza A or B RT-PCR between September 2009 and November 2015 were reviewed. All RT-PCR positive samples that were DFA negative, or indeterminate were tested with the Alere i influenza A/B assay after retrieval from -80C storage. Any sample negative on the Alere assay was retested with RT-PCR to control for significant nucleic acid degradation.

RESULTS: 43 samples were identified that were RT-PCR positive and DFA negative or indeterminate (37 influenza A / 6 Influenza B). Of the 37 Influenza A PCR positive samples, DFA was negative for 14, NSF for 16, and IC for 7. There were 6 Influenza B PCR positive (2 DFA negative, 4 NSF). Testing results in Table 1.

TABLE 1

Comparison of Alere i and DFA testing for Influenza A and B

	DFA result	Alere i influenza A&B result		
Flu A PCR + (n=37)	Neg=14	Pos=3	Neg=10	Invalid=1
	NSF=16	Pos= 12	Neg=3	Invalid=1
	IC=7	Pos= 4	Neg= 3	
Flu B PCR+ (n=6)	Neg=2	Pos=1	Neg= 1	
	NSF=4	Pos=4		

CONCLUSIONS: Using RT-PCR as gold standard, the Alere i influenza A&B assay correctly identified 56% additional samples that DFA testing had found falsely negative or indeterminate. Most of the additional positives detected by the Alere assay were NSF on DFA testing. The Alere assay appears to be a rapid alternative to DFA testing that may result in fewer indeterminate results.

P18

FACILITY CHARACTERISTICS INCORPORATION IN STANDARDIZED INCIDENCE RATIOS FOR CENTRAL-LINE ASSOCIATED BLOODSTREAM INFECTIONS (CLABSI)

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BACKGROUND: Benchmarking using standardized incidence ratios (SIR) for CLABSI in intensive care units (ICUs) is currently stratified only on hospital type and year. We incorporated other facility characteristics such as device utilization ratio, and occupancy in predicting expected number of CLABSI.

METHODS: Using the Surveillance Provinciale des Infections Nosocomiales (SPIN) CLABSI data from 2007 to 2014, Poisson regression analysis was used to predict expected number of CLABSIs in adult ICUs in Québec. Covariates of interest included device utilization ratio (DUR), type of ICU (teaching or nonteaching), average occupancy in patient-days per bed, and surveillance year. Percent errors were used to evaluate accuracy of predicted incidence rates compared to actual yearly incidence. SIRs were subsequently obtained by dividing observed CLABSI cases by the calculated expected number of cases.

RESULTS: The percent error of predicted rates ranged from 1 to 59% for adult nonteaching ICUs (average percent error 21%), and from 1 to 54% for adult teaching ICUs (average percent error 15%) during 2007 to 2014. SIRs from predicted rates show significantly lower SIRs for adult nonteaching ICUs in 2013 (0.60 (0.34, 0.97)) and 2014 (0.41 (0.21, 0.72)). SIRs for adult teaching ICUs were significantly lower in 2011 (0.73 (0.55, 0.94)), in 2013 (0.75 (0.58, 0.96)), and in 2014 (0.46 (0.33, 0.62)).

CONCLUSION: Poisson regression modeling incorporating ICU facility characteristics for predicting expected incidence can be utilized to achieve benchmarking for calculating SIRs. These results corroborate with SIRs derived from the most recent 3 years of CLABSI incidence surveillance stratified by teaching status, further supporting the declining rate of CLABSI over the study periods' latter years.

P19

EFFECTS OF STORAGE TIME AND TEMPERATURE ON THE ABILITY OF HOLOGIC'S APTIMA HPV ASSAY TO DETECT HPV IN CERVICAL SAMPLES COLLECTED IN SUREPATH PRESERVATIVE

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OBJECTIVES: Hologic's Panther system with the Aptima human papillomavirus (HPV) assay is Health Canada approved for use with cervical samples collected in Thin-Prep, but not in Surepath. Storage conditions for Surepath samples are not defined in the product insert. We assessed the impact of storage time and temperature on the ability of Hologic's Aptima HPV test to detect HPV E6/E7 mRNA in cervical samples collected in Surepath preservative.

METHODS: 202 unprocessed samples were split equally with one aliquot stored at room temperature (RT) and the other at 4°C. Weekly, for 4 weeks, these aliquots were re-processed and tested by Aptima HPV assay. 500µl of the vortexed original sample was aliquotted into an Aptima transfer tube, treated with a solution of proteinase K and formaldehyde scavengers, and heated to 95°C for 15 min prior to testing.

RESULTS: There was good agreement between the initial results and the 2, 3 or 4 week results regardless of storage condition. The lowest overall agreement was observed for samples stored at 4°C for 2 weeks (93.7% k=0.86) and the highest overall agreement was 96.5% k=0.93 for samples stored for 3 weeks at 4°C. Despite the strong agreement, significant discrepancies were observed between initial results and the samples stored at RT for 4 weeks (3.47% p=0.0391).

CONCLUSIONS: Hologic's Panther system with the Aptima HPV test is able to detect HPV in cervical samples collected in Surepath and stored for at least 4 weeks post collection at 4°C or RT. From this data we conclude that while storage at 4°C is preferable, short term storage at room temperature (≤4 weeks post collection) will not significantly affect overall agreement. This could extend the pre-treatment time required by Aptima to as long as 4 weeks and allow for service to remote areas.

P20

A NEW BRUNSWICK CASE OF CALIFORNIA SEROGROUP VIRUS INFECTION ASSOCIATED WITH PROBABLE ENCEPHALITIS AND COGNITIVE IMPAIRMENT

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BACKGROUND: California serogroup viruses (CSG) such as Jamestown Canyon (JC) and snowshoe hare (SSH) viruses are wide ranging mosquito-borne pathogens which can cause both febrile and neurological disease. Human exposures to these agents have been described across Canada, however, significant numbers of infections are likely being undetected. In this case report we described a laboratory confirmed case of neuroinvasive disease involving a New Brunswick patient infected with a CSG virus.

CLINICAL HISTORY & RESULTS: In July 2015, a 73-year-old male was admitted to hospital with febrile illness, confusion and lack of coordination. His state quickly deteriorated and was diagnosed with delirium and encephalitis. The patient later became afebrile but with persistent delirium and an ongoing cognitive disability was demonstrated. Serological testing ruled out a number of possible causes of encephalitis by infectious disease agents including Herpes Simplex, Bartonella, Borrelia Coxiella, Anaplasma, and Powassan. Additional serological testing was performed for detecting CSG virus antibody. Serum samples collected at 2 and 4 weeks post-symptom onset demonstrated seroconversion to Jamestown Canyon virus indicating that the patient's illness was associated with an acute infection by this virus.

CONCLUSIONS: Although most CSG infections result in mild disease this case further highlights that these viruses can be etiological agents of neuroinvasive disease. Patients from New Brunswick and other provinces with possible mosquito exposure and febrile and/or encephalitic clinical symptoms should be considered for CSG virus testing. JC and SSH viruses should be considered in the differential diagnosis during the spring, summer and fall seasons.

P21

CONTINUING HOSPITAL EXPOSURE DESPITE ACTIVE SURVEILLANCE FOR INFLUENZA

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OBJECTIVE: To determine the burden of hospital exposure to patient influenza and the rate of transmission from patients with laboratory-confirmed influenza (LCI) to their hospital roommates, and to identify factors associated with this.

METHODS: Prospective data collected from consenting patients with LCI (rtPCR or culture) matched to infection control charts for patients with LCI and their roommates for the 2012/13-2014/15 influenza seasons.

RESULTS: Of the 661 patients with LCI (age: 1wk-103yr), 557 were placed on Additional Precautions at admission and 104 only had symptoms detected after admission: 57 with symptom onset within 72 hours of admission (CA) and 47 with symptom onset after 72 hours (nosocomial), including 11 outbreak-associated. 78 of these 104 patients were admitted to double/multibed rooms and exposed 149 roommates of whom 8 (5.4%) acquired influenza. Factors associated with transmission were: exposure on day 1/2 of symptoms (P=0.001), larger number of roommates exposed (P=0.01), and being part of an outbreak (P=0.046). Of 637 patients with available data, 25%, 57%, and 70% met PHAC and CDC influenza-like illness (ILI) definitions and the Provincial Infectious Diseases Advisory

Committee (PIDAC) febrile respiratory illness definition, respectively. Among the 56 patients with CA-influenza detected after admission, 12.5%, 23.2%, and 33.9%, respectively, met PHAC, CDC, and PIDAC classification at admission.

CONCLUSIONS: In a setting with careful adherence to infection control guidance 1 in 6 patients with influenza were not diagnosed until patients and HCWs had been exposed for >24 hours. Only 1 in 3 patients with CA-influenza detected after admission met the most inclusive definition on admission. Sporadic nosocomial influenza cases are not rare.

P22

WHAT IMPACT DOES PLASMA STORAGE TEMPERATURE HAVE ON HIV-1 VIRAL LOAD QUANTIFICATION?

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BACKGROUND: In HIV-1 viral load testing, the normal protocol has been to use plasma or sera stored at ultralow temperatures (-80°C). There has been little information regarding the impact of other storage temperatures on viral load quantification. The NLHRS used group data from its HIV-1 viral load proficiency testing program to examine the effect of four alternate storage temperatures compared to the standard -80°C (-20°C for 13 months, 8 months, 35 days and 5 freeze/thaws).

METHODS: One HIV-1 RNA subtype B sample diluted to ~1000 copies/mL was aliquoted and stored in duplicate under the various storage temperatures. Canadian and international labs tested the samples on either the Roche COBAS® AmpliPrep/COBAS® TaqMan® HIV-1 Test, v2.0 and the Abbott RealTime HIV-1 assay over 2 years in 3 proficiency test events.

RESULTS: On the Roche assay, samples at all storage temperatures including -80°C, generated a viral load range >0.5 log. Conversely, only samples stored at -20°C for 13 months had a >0.5 log range on the Abbott assay. The Roche assay did not show a significant difference for any of the storage temperatures compared to storage at -80°C ($p>0.11$) but the intra-sample variation was high. While the Abbott assay showed a significant difference for storage at -20°C for 8 months and 5 freeze/thaws compared to storage at -80°C ($p<0.02$), the intra-sample variation was still within 0.5 log. Overall, the viral load results on the Abbott assay ran slightly lower than the Roche assay and generally had a tighter range.

CONCLUSIONS: Our data suggests that samples stored at -20°C for up to 8 months will still yield HIV-1 RNA results within 0.5 log of samples stored at -80°C on the Abbott assay which is consistent with commonly used HIV viral load testing guidelines. This may be beneficial in resource limiting settings where laboratories may not have access to ultra-low freezers and/or inadvertently stored samples below -80°C. The wide range within samples (>0.5 log) on the Roche assay at all storage conditions is troublesome as acceptable variation is generally ≤ 0.5 log. Further investigation in storage methods is warranted based on the findings of this study.

P23

QUALITATIVE AND QUANTITATIVE ASSESSMENT OF WHOLE GENOME AMPLIFICATION KITS FOR NEXT GENERATION SEQUENCING OF SCARCE DNA

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INTRODUCTION: In the emerging field of microbial forensics, methods to exploit trace biological material are a necessity. A key issue with whole genome sequencing (WGS) is the input necessary to prepare libraries of acceptable quality to give informative data for analysis. During our validation process for WGS, we investigated the utility of four whole genomic amplification (WGA) kits by multiple displacement amplification (MDA) for this purpose.

MATERIALS AND METHODS: The REPLI-g UltraFast Kit (Qiagen), REPLI-g Mini Kit (Qiagen), REPLI-g Single Cell Kit (Qiagen), and Illustra GenomiPhi V2 DNA Amplification Kit (GE Healthcare) were compared for performance using *Bacillus anthracis* and *Yersinia pestis* reference DNA over a range of 0.01 – 10 ng. The Illumina Nextera XT library

kits and MiSeq platform were completed as per manufacturer's instruction. All bioinformatics data analysis was performed using custom workflows within Galaxy via a variety of metrics to compare kits including: estimated coverage (total # bp sequenced / reference genome size), average coverage (total # bp mapped / reference genome size as a measure of uniformity), % mapped to reference genome (as a measure of specificity), number of non-covered bases and GC bias.

RESULTS AND DISCUSSION: The GE proved to be the best kit for our needs. The upfront time and input for the GE and UF kits is less than that required by the MN and SC kits (1.5 hr vs > 8 hrs and 1 uL vs 2.5 uL respectively), moreover, the GE kit was also cheaper and resulted in better overall yield than the UF kit. Input of 0.01 ng produced enough DNA to generate excellent libraries displaying a normal distribution with a median fragment size of 500 bp to 600 bp. All runs had clustering ranging from 1100 – 1700 k/mm², >50% total reads >Q30, and a total error rate <4. Downstream bioinformatics demonstrated that regardless of input, all samples had >40× coverage, >93% reads mapped to the reference strain and little difference was observed for max contig length nor number of contigs during *de novo* assembly. SNP analysis revealed no SNP differences across the range tested, thus, the MDA kits did not introduce SNPs. Furthermore, as MDA reactions can potentially introduce bias we examined for GC bias and did observe a bias towards GC balanced segments of the genome. This experiment confirmed the ability to sequence limited samples using MDA kits and will be applied to future work in metagenomic processes.

P24 ABSTRACT WITHDRAWN

P25

A 63-YEAR-OLD MAN WITH AN UNUSUAL AETIOLOGY OF COUGH

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BACKGROUND: *Entamoeba histolytica* is an intestinal protozoan parasite transmitted through the faecal-oral route. Up to 90% of *E. histolytica* infections are asymptomatic or associated with mild symptoms. Most cases in Canada are from residents of, or travellers from areas of high endemicity although autochthonous cases have been reported amongst the men who have sex with men (MSM) and Canadian native populations.

CASE: A 63-year-old previously healthy MSM Canadian man, living in China since 2012, presented to hospital with fever, weight loss, and haemoptysis. Six weeks prior to presentation, he reported malaise, fatigue, night sweats and fever. He subsequently developed non-bloody diarrhoea, for which he was hospitalized in Beijing. One month later, he developed haemoptysis in addition to ongoing constitutional symptoms. Failing to improve, he sought medical attention in Montreal, Quebec. On presentation, he was cachectic, had evident decreased air entry to his right lower lobe, but no abdominal pain. Laboratory investigations revealed leukocytosis and an elevated C-reactive protein. Human immunodeficiency virus testing was negative. Chest radiograph demonstrated a large mass-like lesion in the right lung base. A thoracic computed tomographic scan revealed a heterogeneous multi-lobulated lesion suggestive of a necrotic mass in the right lower lobe of the lung communicating with the right lobe of the liver. An aspirate of the liver lesion was negative on bacterial culture. Sputum bacterial culture and staining for acid fast bacilli were negative. Stool culture and ova and parasite were negative. Given his epidemiological risk factors, *E. histolytica* serology was sent and was strongly positive. Since, in the convalescent phase, the sensitivity of serology exceeds 90%, a diagnosis of invasive amoebiasis was made. The patient was successfully treated with drainage followed by a 14-day course a tissue amoebicide targeting trophozoites, metronidazole.

CONCLUSION: We present an uncommon case of amoebic liver abscess with diaphragmatic perforation and intrapulmonary extension. Amoebic liver abscesses are infrequently seen outside of endemic areas, rarely extend outside the liver and should be suspected in cases of unexplained fever even in the absence of signs, symptoms, or basic blood tests suggestive of liver pathology.

P26 ABSTRACT WITHDRAWN

P27

RAPID IDENTIFICATION OF BACTERIA RECOVERED DIRECTLY FROM POSITIVE BLOOD CULTURES USING THE MALDI-TOF MASS SPECTROMETER (VITEK®-MS, BIOMERIEUX)

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BACKGROUND: Decreasing time to bacterial identification (ID) from positive blood cultures can significantly improve patient outcomes. We evaluated a method of bacterial ID using bioMerieux Vitek®-MS directly from positive blood culture (BC) bottles using a Serum Separator Tube (SST).

METHODS: Positive aerobic/anaerobic BC bottles (BacT/ALERT® charcoal-free culture media, bioMerieux) received at the Regina General Hospital Microbiology Laboratory between September 15 and November 28, 2015, were included in the study. 5 mL of blood from each positive BC bottle was inoculated into an SST tube. SST tubes were centrifuged for 5 minutes, the supernatant was aspirated, and a small amount of pelleted bacteria was removed for Vitek®-MS target plate preparation.

Direct from blood MALDI ID results were compared to MALDI ID obtained from cultures after 18-24 hours of incubation as per lab protocol.

RESULTS: 219 positive blood culture bottles were evaluated. 138 Gram positive organisms, 71 Gram-negative organisms, and 3 yeast were identified. 6 bottles contained polymicrobial growth.

59% (n=130) of direct IDs had confidence values of 99.9 and correlated with culture IDs to the species level. 26% (n=57) of direct IDs yielded 'No Identification'. 12% (n=27) of direct IDs had confidence values <95 and were discrepant with culture ID results. 4 direct IDs yielded confidence values between 95 and 99.8 and were discrepant with culture ID results: (i) *Listeria grayi* confirmed to be *Staphylococcus epidermidis*, (ii) *Staphylococcus haemolyticus* confirmed to be *Staphylococcus aureus*, (iii) *Streptococcus salivarius* confirmed to be *Streptococcus dysgalactiae*, and (iv) *Rhizobium radiobacter* confirmed to be *Providencia rettgeri*.

CONCLUSIONS: 59% of direct from BC MALDI IDs correlated with standard culture IDs. Protocol in our laboratory does not release IDs with confidence values less than 99.9. Thus, none of the 219 BCs, including those with polymicrobial growth or yeast, resulted in incorrect IDs that would have been reported out.

P28

INCREASED PARVOVIRUS B19 ACTIVITY IN NEWFOUNDLAND AND LABRADOR (NL), CANADA IN 2015

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BACKGROUND: Parvovirus B19 affects approximately half of the population before adulthood. Although most common in children, testing targets those at higher risk of potentially serious complications like pregnant women and immunocompromised patients. Canadian information regarding parvovirus infection is limited and largely focused on seroprevalence.

METHODS: Serum specimens positive for B19V-IgM antibodies (Euroimmun, Germany) were sent from the NL PHL to NML for confirmation by PCR (RealStar B19 PCR, Altona Diagnostics, Germany) and capture IgM EIA (Biotrin, Ireland). Phylogenetic analysis of the NS/VP1 unique region junction of B19 genome was performed.

RESULTS: At NL PHL during 2010-13 annual average of 440 patients underwent B19 testing; approximately 3.3% were acute infections. In 2014-15, testing and the number of acute cases increased, however significant false-positivity was observed. Of 545 samples (January-October, 2015), 71 (13%) were diagnosed as acute based on the B19V-IgM EIA. NML testing showed that 8.3% were true positive for markers of acute infection, representing a 250% increase from the average annual incidence (2010-2013). Most cases were adult women, (24-50 years of age) with 14% children, 4-14 years old. Women in child-bearing age (24-36) were 53%

and the majority (95%) were 46 years old or younger. We amplified the NS/VP1 unique region junction (994 nucleotides) of 43 B19 strains from NL and 17 from three other provinces. All Canadian B19 isolates belonged to subgenotype 1a, but their spatio-temporal distribution showed the existence of two lineages. All 2014-15 NL isolates clustered in lineage 1a1, while older isolates (2012-13) from Alberta (AB) and Nova Scotia belonged to lineage 1a2. The majority of AB isolates from 2014 were classified within lineage 1a1. Most NL strains could be grouped into 4 subclusters comprised of identical and/or very similar sequences. However, even within these groupings the sequence homology was very high (98.4-98.8%). Such minor genetic heterogeneity strongly indicates that the majority of acute B19 cases in late 2014-15 were caused by the same strain.

CONCLUSION: Increased incidence of acute parvovirus infection was observed in NL in 2014-15. The pronounced genetic relationship between the isolates suggests that a single strain was responsible for most of the acute cases in this first documented B19 outbreak in Canada.

P29

IMPLEMENTATION OF CENTRALIZED IGRA TESTING IN BRITISH COLUMBIA PARTNERING WITH LABORATORIES ACROSS BRITISH COLUMBIA

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BACKGROUND: The Interferon Gamma Release Assay (IGRA) is well-known for its use to identify patients with latent TB infection. BC is the first Province in Canada to offer IGRA testing. The TB rate is higher in BC compared to the rest of Canada. Centralized testing is challenging because geographically, BC is one of the largest mountainous provinces with an area of 944,735 square kilometres and population of 4.631 million (July 1, 2014).

METHODS: The Zoonotic Diseases & Emerging Pathogens Lab, BCCDC Public Health Laboratory (BCPHL) took the lead and partnered with BCCDC TB Services and several hospital laboratories throughout the province for collection and pre-processing of Quantiferon TB (QFT) samples. Since 2009, we have established 9 sample collection sites, 6 of which are also pre-analytical processing sites. Samples are shipped to BCPHL where testing is performed. Protocols were developed and shared among all partners to have quality assured testing and results reported for physicians' use.

RESULTS: TB IGRA tests (QFT and TB T-Spot) were validated and implemented jointly by BCPHL, Vancouver and New Westminster BCCDC TB Clinics. Then the 7 distant hospital QFT sites were added; St Paul's Hospital (Vancouver), Kelowna, Prince George, Surrey, Victoria, Nanaimo and Whitehorse General Hospital (Yukon). Four more hospital QFT sites in BC will be added gradually throughout 2016. From December 2009 to December 2015, 2269 patients were positive from 8628 QFT samples, and 508 of 3803 samples were positive by the TB T-Spot test. Sample rejection, unsatisfactory test results, repeats and equivocal results will be determined as a quality measure.

CONCLUSIONS: Our combined efforts proved that centralized testing is feasible utilizing distant hospital laboratories as pre-processing sites. This approach will provide budget sensible and quality assured testing. Currently we are working to further expand TB IGRA testing to dialysis and transplant populations.

P30

EVALUATION OF A NEW ZEUS VLSE-1/PEPC10 IGG/IGM LYME ELISA ON THE DYNEX DS2 AUTOMATED PLATFORM

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OBJECTIVE: There are many ELISA kits available for Lyme disease screening but C6 peptide based ELISAs demonstrate greater sensitivity. Recently a combination ELISA utilizing both VLSE-1 (C6) and pepC10 (part of OspC) has been reported to have higher sensitivity for all stages of Lyme infection, including early stages. As the screening test currently used by our laboratory was changing from a polyvalent to two separate assays, the decision was made to evaluate a more sensitive polyvalent test and a new automated platform.

METHODS: The Zeus (Alere Canada) Borrelia VLSE-1/pepC10 IgG/IgM ELISA was compared to our laboratory's current Lyme screening method, VIDAS Lyme IgG/IgM whole cell antigen immunofluorescent assay (Biomerieux) and confirmatory MarDx Western Blot. Previously stored characterized panels from CDC (n=48) and New York Public Health (n=23) labs were tested, as well as samples received for routine Lyme disease testing (n=678) using the Zeus manual ELISA. Favourable results were obtained and a further 627 routine and characterized samples were tested using the Zeus kit on the Dynex DS2 automated EIA platform. Potential cross-reacting samples (n=96) were tested and reproducibility was also evaluated.

RESULTS: The sensitivity of the Zeus test was determined to be 100% when compared to MarDx IgG Western blot, both by manual EIA and on the automated Dynex DS2 platform. Specificity was lower, but considered acceptable using a two-tiered testing approach. Reproducibility results were also good.

CONCLUSIONS: The Zeus Borrelia VLSE-1/pepC10 IgG/IgM ELISA performed well. The Dynex DS2 automated platform also performed well and eliminated manual pipetting. Sensitivity was excellent and preliminary data suggests that fewer blots will be performed due to the higher specificity of the Zeus kit compared to the whole cell product based Biomerieux VIDAS kit. As a further advantage, the Zeus kit can also detect European Lyme antibodies.

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CLINICAL FEATURES OF INFLUENZA- AND RESPIRATORY SYNCYTIAL VIRUS-POSITIVE ADULT CASES DURING THE 2014-2015 WINTER SEASON: A RETROSPECTIVE COHORT STUDY FROM A TERTIARY MEDICAL CENTRE IN QUÉBEC

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OBJECTIVE: A retrospective cohort study was performed comparing clinical features as well as complications and outcomes of confirmed influenza and respiratory syncytial virus (RSV) adult cases from a heart and lung institute (HLI) during the 2014-15 winter season.

METHODS: Qualitative reverse-transcriptase polymerase chain reaction using the Simplexa Flu A/B and RSV assay was performed on nasopharyngeal swabs from patients consulting for flu-like illnesses at the emergency room of the Quebec City HLI, affiliated to Université Laval, from December 2014 to April 2015. All RSV-positive cases as well as a subset of influenza A-positive samples were selected for analysis. Electronic medical records were reviewed and information was collected for both populations.

RESULTS: RSV-positive patients (n=33) had statistically more pulmonary co-morbidities than influenza-positive cases (n=36) (72.7% vs 47.2%; p=0.032). A greater proportion of RSV cases were former smokers (48.5% vs 22.2%; p=0.022) and they presented more frequently with dyspnea at initial evaluation compared to influenza cases (78.8% vs 47.2%; p=0.007). Only influenza-positive cases developed leucopenia (13.9% vs 0%; p=0.026). Remarkably, complications as well as clinical outcomes were comparable between RSV and influenza groups, including hospitalization rates and duration, ICU admission rates and duration, need for mechanical

ventilation and oxygen supplementation, and in-hospital mortality. Most patients (90.6% and 72.2%) received antibiotics (AB) and the duration of AB treatment was longer for RSV cases (8.1 days vs 5.8 days; p=0.044). RSV-positive patients required more frequently bronchodilators than influenza-positive patients (72.7% vs 55.6%; p=0.023)

CONCLUSION: This study highlights the important burden of RSV infection in adult population during the 2014-15 winter season. Our results also emphasize the usefulness of a rapid PCR assay detecting both influenza and RSV in adult patients consulting at a tertiary medical centre. Finally, our results argue for the development of an effective antibiotic stewardship program targeting seasonal respiratory viral infections.

P32

QUALITY OF DESIGN AND REPORTING OF STUDIES OF COMMERCIAL POINT-OF-CARE DIAGNOSTIC TESTS

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BACKGROUND: Point-of-care diagnostic tests for infectious diseases may improve patient outcome, however design and reporting of commercially sponsored studies of new point-of-care tests are generally poor. Weak study quality may influence performance interpretation and implementation policy.

OBJECTIVE: To evaluate adherence to QUADAS-2 and STARD criteria for published reports between 2004-2015 describing point-of-care commercial diagnostic tests for group A *Streptococcus* (GAS), *Streptococcus pneumoniae* urinary antigen (PUAg) and influenza (INF). A survey of study quality for these tests has not been performed previously.

METHODS: PubMed articles meeting inclusion criteria were analyzed for adherence to STARD and QUADAS-2 criteria. Each author abstracted data independently and discrepancies were resolved.

RESULTS: Of 37,174 articles, 102 (0.27%) met inclusion criteria (GAS (n=23), PUAg (n=19), INF (n=60)). All studies had weaknesses identified by QUADAS-2 and STARD criteria. Most commonly, articles demonstrated bias in index test performance (high = 16.7%, unclear = 50%), unclear patient selection design (51%), and reference standard interpretation bias (high = 33.3%). Reports lacked blinding of index and reference test (80.4%), training and expertise of those executing the tests (87.3%), methods for calculating reproducibility (94.1%), and flow of patients throughout study (72.5%). No articles reported adverse events related to testing. Quality of study design differed significantly by organism (p=0.014). There was no significant difference in quality of reporting between test groups (p=0.152) or by year (p=0.279).

CONCLUSIONS: Reports of point-of-care diagnostic tests lacked adherence to QUADAS-2 and STARD criteria. More stringent requirements from journals may enhance the quality of publications.

P33

DESCRIPTIVE EPIDEMIOLOGY OF HIV POINT-OF-CARE TESTING (POCT) IN MANITOBA FROM 2011 TO 2014

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BACKGROUND: HIV POCT has been available in Manitoba since 2008. This study evaluated the program's effectiveness in identifying individuals with previously unknown HIV status, its effects on clinical outcomes, and the characteristics of the populations being reached.

METHODS: A retrospective database review was conducted at Cadham Provincial Lab for individuals who received HIV POCT from 2011 to 2014. Time to linkage to care and viral load suppression was compared between individuals who tested positive for HIV using POCT and a control group identified as positive through standard screening methods. Testing outcomes for women with previously unknown HIV status accessing POCT through the Women's Hospital's Labour & Delivery Unit (LDU) was also assessed.

RESULTS: Of 3204 individuals receiving HIV POCT (1055 females [32.9%] and 2149 males [67.1%]), POCT was the first recorded HIV test for 2205 [68.8%]. Males were more likely to access POCT as their first recorded HIV test (OR 1.40). Between the two main test sites (Main Street Project [MSP] and Nine Circles), MSP tested a higher proportion of females (OR 1.27) as well as all age groups over the age of 30 (OR of 1.83, 2.51, and 3.64 for age groups of 30-39, 40-49, and >50, respectively). There was no difference in the time to linkage to care ($p=0.3449$) or viral load suppression ($p=0.4046$) between the POCT and standard screening cohorts. Of 215 women presenting to LDU with unknown HIV status, 1 was identified as HIV positive.

CONCLUSIONS: HIV POCT in Manitoba has been successful at identifying individuals with previously unknown HIV positive status. The differences in demographics between the two main testing sites support the notion that this intervention is reaching unique populations. Given that there is no significant difference in time to clinical outcomes, it is reasonable to continue to use HIV POCT as a targeted intervention.

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EVALUATION OF THE LUMINEX® MAGPIX® NXTAG™ RESPIRATORY PATHOGEN PANEL

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OBJECTIVES: The BCCDC Public Health Laboratory (PHL) currently uses a combination of the Luminex 200 xTAG® Respiratory Viral Panel (RVP) fast assay and in-house developed real-time PCR assays for the detection of viral respiratory pathogens and atypical bacterial agents. We evaluated the performance of the new MAGPIX® NxTAG® Respiratory Pathogen Panel (RPP) assay for simultaneous detection of respiratory viruses and atypical bacteria from upper and lower respiratory specimens extracted by the MagMAX™ Express-96 Magnetic Processor.

METHODS: Manufacturer-provided cultures were used to verify assay performance and limit of detection (LoD). Direct ($n=188$) and diluted ($n=63$) respiratory samples were used for retrospective evaluation. In-house PCR and/or xTAG® RVP fast assays were used as comparator methods. Extraction methods (manual column-based, bioMérieux NucliSENS® easyMag®, MagMAX™ Express-96) were evaluated in parallel. Hands-on time and assay run-times were measured.

RESULTS: The NxTAG® RPP LoD for most targets were within one log of manufacturer expected values. The sensitivity of the NxTAG® RPP assay was 100% for most viruses, including for all influenza A, influenza B and RSV samples diluted to achieve high in-house PCR cycle threshold (Ct) values. However, only 9/10 parainfluenza 4, 8/9 human metapneumovirus, and 6/8 adenovirus were detected. For atypical bacteria, the sensitivity of the NxTAG® RPP assay for *Chlamydia pneumoniae*, *Legionella pneumophila*, and *Mycoplasma pneumoniae* was 100% for specimens with in-house PCR Ct values of <40. Of the negative specimens tested, parainfluenza 1 was detected by the NxTAG® RPP assay in 1 case. No significant differences were identified between easyMag® and MagMAX™ extraction methods. The NxTAG® RPP assay reduced labour time by 70 minutes for 96 samples when compared to xTAG® RPP.

CONCLUSIONS: The MAGPIX® NxTAG® RPP assay provides high-throughput and accurate detection of multiple respiratory pathogens in a simple to use, labour saving format. Investigation of discordant results and a head-to-head, prospective analysis of methods and discrepancies between specimen types is underway.

P35

EXTENDED-SPECTRUM BETA-LACTAMASE-PRODUCING ENTEROBACTERIACEAE ARE NOT ASSOCIATED WITH DECREASED SURVIVAL IN PATIENTS WITH BLOODSTREAM INFECTIONS

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OBJECTIVES: Factors impacting mortality risk among patients with Enterobacteriaceae bloodstream infections (BSIs) are not well defined. Controversy exists whether extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae are independently associated with increased mortality compared to non-ESBL-producing Enterobacteriaceae among inpatients with BSIs. This study determined seven and 30-day mortality rates along with mortality risk among inpatients with ESBL-producing Enterobacteriaceae compared to non-ESBL-producing Enterobacteriaceae BSIs.

METHODS: This was a retrospective matched cohort study involving four tertiary care hospitals from November 2005 to November 2012. All adult inpatients with ESBL-producing Enterobacteriaceae BSIs during the study period ($n=162$) were matched (1:1) to inpatients with non-ESBL-producing Enterobacteriaceae BSIs ($n=162$). Seven and 30-day mortality rates were determined. Mortality risk was assessed using time to death, censored at 30 days, as the main outcome measure for the Cox regression analysis.

RESULTS: Seven-day mortality rates for the ESBL and non-ESBL groups were 20/161 (12.4%) and 19/160 (11.9%), respectively (odds ratio [OR] 1.1 [95% CI 0.5–2.2]; $p=0.86$); 30-day mortality rates were 35/152 (23.0%) and 32/153 (20.9%), respectively (OR 1.3 [95% CI 0.7–2.5]; $p=0.38$). Using Cox regression analysis, controlling for inadequate therapy, nosocomial-association and Charlson comorbidity index, mortality at 30-days was not statistically different between patients with ESBL or non-ESBL-producing Enterobacteriaceae BSIs (HR=1.0; $p=0.91$).

CONCLUSIONS: Patients with ESBL-producing Enterobacteriaceae BSIs do not have an independent increased mortality risk compared to those with non-ESBL-producing Enterobacteriaceae BSIs. When assessing mortality risk amongst patients with Enterobacteriaceae BSIs, emphasis should be placed on clinical factors such as adequate therapy, nosocomial-association and comorbidities.

P36

DECREASING TIME TO ANTIMICROBIAL SUSCEPTIBILITY TESTING RESULTS USING A NOVEL LYSIS CENTRIFUGATION METHOD DIRECTLY FROM POSITIVE BLOOD CULTURES

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OBJECTIVES: Reducing the time to bacterial identification and susceptibility testing from positive blood cultures enables timely delivery of appropriate antimicrobial therapy leading to improved patient outcomes. However, laboratories generally rely on lengthy culture-based methods for organism isolation, identification, and antimicrobial susceptibility testing (AST). This study evaluated the utility of a novel lysis centrifugation pelleting method for rapid bacterial isolation and characterization directly from positive blood cultures.

METHODS: 187 culture negative BacT/Alert SA Standard Aerobic blood culture (BC) bottles (bioMérieux) were spiked with Gram-positive and -negative organisms and incubated in the BacT/ALERT (bioMérieux) BC system. Blood extracted from positive bottles was both pelleted and sub-cultured to facilitate method comparison. Susceptibility profiles were generated from sub-cultured and pelleted isolates using the Vitek2 (bioMérieux) AST system and AST-GP67 (Gram-positive) or AST-N220 (Gram-negative) cards. Additionally, 48 *Staphylococcus aureus* isolates were

assessed for methicillin resistance (MRSA) using the MRSA Latex Test kit (Denka Seiken), while 85 *Enterobacteriaceae* were assessed for extended spectrum beta-lactamase (ESBL)-production using the β LACTA Test kit (Bio-Rad).

RESULTS: A total of 3075 antibiotic comparisons were evaluated, with an average \pm twofold dilution agreement of 98.2% (1650/1681) and 98.6% (1375/1394), and categorical agreement of 98.6% (1628/1651) and 98.5% (1373/1394) for Gram-negative and -positive cards, respectively. Major error rates fell below 5% for all antibiotics tested except for MRSA which was falsely reported as oxacillin sensitive 17.2% (10/58) of the time. Pelleting reduced the time from Gram-stain result to Vitek2 AST report from 41.6 to 11.6 hours compared to the sub-culture method. Lastly, the sensitivity and specificity of the MRSA Latex Test was 94.7% (36/38) and 90.0% (9/10) respectively, while the ESBL β LACTA Test was 90.3% (65/72) and 100.0% (13/13), respectively.

CONCLUSIONS: The lysis centrifugation approach makes possible same-day AST reporting from positive blood cultures, while providing information regarding MRSA and ESBL resistance as early as 1-2 hours post-positivity. Such rapid results will improve patient outcomes through prompt delivery of targeted antibiotic therapy.

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BLINDED COMPARISON OF PERFORMANCE AND COST EFFECTIVENESS OF CHROMOGENIC AND DIRECT LATEX METHODS FOR DETECTION OF GROUP B *STREPTOCOCCUS*, WITH IN-HOUSE PCR AND LAMP AS REFERENCE STANDARDS

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BACKGROUND: Group B *Streptococcus* (GBS) testing during pregnancy prevents neonatal GBS infection. New testing methods may be more accurate and cost effective than conventional culture methods.

OBJECTIVE(S): To compare three chromogenic agars and two direct latex agglutinations after carrot broth enrichment, to determine performance and cost efficiency, using in-house PCR and LAMP as reference standards.

METHODS: 285 consecutive vaginal-rectal swabs were enriched with carrot broth and then blindly tested using conventional *Streptococcus* selective agar (SSA), ChromAGAR Strep B (Colorex) [Alere ULC, Ontario, Canada], ChromID Strepto B [bioMérieux Canada, Quebec], Brilliance GBS [Oxoid Company Inc, Ontario, Canada] and two latex agglutination kits: PathoDxtra Strep Grouping Reagent Kit (ThermoFisher Scientific, Oxoid Company, Ontario, Canada) and MEDStrep (Alere ULC, Ontario, Canada). In-house PCR and LAMP were performed on frozen carrot broth.

RESULTS: Of the 285 samples received, 244 samples were analyzed by in-house PCR and 195 samples were analysed by LAMP. SSA is less sensitive than PCR, but is equally specific. Chromogenic agars were equally or more sensitive than SSA, and cost equal or greater than SSA. Direct latex antigens were less sensitive and specific than SSA, and cost less than SSA. In-house PCR was more sensitive than LAMP.

CONCLUSION(S): The performance of chromogenic media was approximately equal to SSA, but costlier. Direct latex agglutination methods do not achieve adequate performance. The ideal limit of detection for PCR is unknown since the risk to the newborn of maternal carriage of a low inoculum of GBS is unknown.

P38

COMPARISON OF MONOPLEX AND DUPLEX RT-PCR ASSAYS FOR THE DETECTION OF MEASLES VIRUS

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BACKGROUND: Measles virus (MeV) infection is of significant public health concern. Diagnostic methods for MeV include RT-PCR, and the National Microbiology Laboratory (NML) uses two monoplex reactions targeting the nucleoprotein (N) and hemagglutinin (H) genes.

OBJECTIVES: This study aimed to compare the analytical and clinical performance of the H and N gene monoplex RT-PCRs to a duplex RT-PCR reaction using both targets, in order to reduce testing cost.

METHODS: The HN duplex RT-PCR used the same oligonucleotides as the NML monoplex reactions, but differed in reagents and amplification conditions. Analytical sensitivity was assessed using 10-fold serial dilutions of MeV strain Edmonston (ATCC VR-24). Analytical specificity was tested against MeV genotypes (A, B3, D8, D9, and H1) and various other viruses, which included paramyxoviruses (respiratory syncytial virus, parainfluenza viruses 1 to 4, mumps virus, and human metapneumovirus). Clinical performance was evaluated using 33 throat swabs, 43 nasopharyngeal swabs, and 53 urine specimens (of which 3, 13, and 23 were positive, respectively).

RESULTS: Using a reference MeV strain, the analytical sensitivity was found to be equivalent for all assays, and no cross reactivity was observed. Concordance in clinical specimens was 100% between the duplex and N gene monoplex. The H gene monoplex failed to detect MeV genotype B3 in four urines, one throat, and one nasopharyngeal swab, resulting in a clinical sensitivity of 83%.

CONCLUSIONS: While the H gene monoplex failed to detect genotype B3, both the HN duplex and N gene RT-PCRs were able to accurately detect all MeV genotypes evaluated. Recently, the NML has validated an alternate H gene primer/probe combination that enables detection of genotype B3, yet the HN duplex RT-PCR described in this study provides a suitable alternative for MeV detection. Future analyses will evaluate the benefits of the novel NML H gene oligonucleotides in a duplex RT-PCR with N gene.

P39

PNEUMONIA IN THE ICU: COMPARING CRITERIA FOR PNEUMONIA DIAGNOSIS AND TREATMENT IN ICU PATIENTS AT HAMILTON HEALTH SCIENCES

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BACKGROUND: The diagnosis of pneumonia is challenging, and utilizes both clinical and radiographic evidence. This is particularly true in patients with other underlying non-infectious etiologies that may mimic signs and symptoms of pneumonia. Overdiagnosing pneumonia may increase inappropriate antimicrobial use in the hospital setting. We analyzed diagnostic parameters met prior to antibiotic treatment of patients with a clinical diagnosis of pneumonia in two intensive care units (ICUs).

METHODS: Patients with a clinical diagnosis of pneumonia were identified by the intensivist at antimicrobial stewardship rounds at two tertiary care ICUs in Hamilton, ON, with 20 and 30 beds, respectively. For this study, definite pneumonia was defined as having ≥ 2 SIRS criteria and a change in the chest x-ray (CXR) consistent with pneumonia. VAP patients were analyzed separately with modified SIRS criteria.

RESULTS: We included 90 patients treated with antibiotics for pneumonia (43 and 47 at the two sites, respectively); 63% were male, and the average age was 67. For non-VAP cases, SIRS criteria and changes in the CXR were each observed in 59 cases (80%), but only 48/74 (65%) met both criteria of our definition of definite pneumonia. This was more frequently the case in one of the two ICUs (79% vs. 47%; odds ratio 4.15 [95% CI 1.51–11.44]; $p < 0.001$). The most common SIRS criterion met

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was a respiratory rate of ≥ 20 (61/74 [82%]). Only 5/16 (31%) patients treated for VAP met our definition of definite pneumonia.

CONCLUSIONS: One-third of patients with a clinical diagnosis of pneumonia in the ICU did not meet our definition of SIRS criteria and changes in the CXR consistent with pneumonia, whereby the threshold to start treatment for suspected pneumonia seems to be lower at one of the sites, which may be explained by differences in antimicrobial stewardship cultures or in patient population.

P40

COMPARISON OF TWO AUTOMATED INSTRUMENTS FOR EPSTEIN BARR VIRUS (EBV) SEROLOGY TESTING

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BACKGROUND: Serology remains the mainstay for diagnosis of Epstein-Barr virus (EBV) infection, and EBV panels are now available for automated instruments to help streamline EBV testing.

OBJECTIVES: This study aimed to compare two automated serology platforms (BioRad Bioplex 2200 and the Abbott Architect i2000) for testing of three EBV serological markers: viral capsid antigen [VCA] IgM, VCA IgG, and EBV nuclear antigen-1 [EBNA-1] IgG.

METHODS: Pedigreed specimens previously tested by Euroimmun IgM (n=37), IgG (n=38), and EBNA (n=40) were used to compare the automated instruments. Discrepant results were resolved with IgM immunofluorescence testing using Merifluor IFA VCA EBVM, or enzyme immunoassays using the Zeus EBV IgG and EBNA kits. Each automated method was compared to a modified gold standard defined as two of three concordant results between the automated system (Bioplex or Architect), Euroimmun, and the discrepant analysis.

RESULTS: Compared to the modified gold standard, Bioplex testing resulted in 100% sensitivity and specificity for all targets. The overall concordance between the Bioplex and Architect was 98.2%, and there were two discordant results. First, a falsely reactive VCA IgG on the Architect i2000 (signal 1.10 vs. cutoff 1.0) was obtained in a patient who was IgM and IgG negative by all tests (including discrepant analysis), thus resulting in a specificity of 93.3%. Second, a false negative EBNA result was noted for Architect i2000, where a positive result was obtained for Euroimmun, Bioplex 2200, and Zeus EBNA, thus resulting in a sensitivity of 96.1%.

CONCLUSIONS: This study demonstrated that both automated systems for EBV serology had good performance; however, the Bioplex 2200 had better sensitivity for EBNA and specificity for VCA IgG. Since the patient population tested at our institution is primarily adults, an algorithm-based approach with Bioplex EBV serology testing was implemented where EBNA is tested first, and if negative, VCA IgM and IgG are performed. This decreased turnaround times and reduced test order errors.

P41

IMPACT OF A URINARY TRACT INFECTION MANAGEMENT BUNDLE ON MICROBIOLOGY LABORATORY WORKLOAD

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OBJECTIVE: A comprehensive review of 300 inpatients with positive urine cultures, at the Moncton Hospital, revealed that 61% of patients had asymptomatic bacteriuria, and 71% of these patients received unnecessary antibiotics. Ciprofloxacin was by far the most common antibiotic prescribed. The high inappropriate use of ciprofloxacin and treatment of asymptomatic patients led to the development of a urinary tract infection (UTI) management bundle. We determined the impact of an institutional UTI management bundle on microbiology laboratory workload.

METHODS: An institutional UTI management bundle was implemented on selected floors from February 16 to September 16, 2015. The major components of this bundle included education of nursing staff, physicians,

and pharmacists; no longer routine reporting of positive urine results from study floors; and pharmacy prospective audit and feedback for all positive urine cultures. We measured the urine bench workload by determining the number of specimens processed plus the number of identifications and susceptibilities performed. The workload from February 16 to September 16, 2014, served as control.

RESULTS: During the study period 581 specimens were submitted; 56/138 isolates were identified by Vitek2 and 120 strains were tested for their susceptibilities. In the control period 863 specimens were processed; 84/241 isolates were identified by Vitek2 and susceptibilities were performed on 218 isolates. The material cost was \$635.36 for the study period compared to \$1,273.52 for the control period. These measures reduced the urine bench workload by 38% and realised a savings of 50.1% in material cost. During the study period there were 62836 patient days on the study floors compared to 61404 patient days in the control period.

CONCLUSION: A UTI management bundle is an effective tool at least over a short period to ensure proper use of laboratory resources.

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SUSCEPTIBILITY RESULTS OF URINARY STRAINS OF *E. COLI* ISOLATED FROM FOUR DISTINCT OUTPATIENT GROUPS

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BACKGROUND: Uncomplicated urinary tract infections (UUTI) are a common occurrence in sexually active women. Therapeutic guidelines recommend treating UUTI empirically without culture. It is essential to know the susceptibility pattern of *Escherichia coli* in the community in order to choose empiric antimicrobial therapy. This study was undertaken to determine the susceptibility of *E. coli* in 4 population groups.

METHODS: *E. coli* strains isolated from female non-pregnant outpatient urine samples were saved. The patients were classified in 4 groups according to their age and history of UTI. Groups 1 and 2 consisted of patients 16 to 50 and ≥ 51 years of age, respectively with no history of UTI within the last 6 months. Patients in groups 3 and 4 were 16 to 50 and ≥ 51 years old, respectively but had at least one positive urine culture within the last six months. All strains were tested by the CLSI disk diffusion method for susceptibility to ampicillin (Amp), amoxicillin/clavulanic acid (Amx/Clav), cefazolin, SXT/TMP, nitrofurantoin (Nitro), ciprofloxacin (Cip), and fosfomycin (Fos).

RESULTS:

Antibiotic	Group 1 (n=100)	Group 2 (n=100)	Group 3 (n=36)	Group 4 (n=75)
Amp	51 (51%)	47 (47%)	17 (47.2%)	21 (26%)
Amx/Clav	78 (78%)	76 (76%)	27 (75%)	48 (64%)
Cefazolin	72 (72%)	80 (80%)	20 (55.5%)	32 (42.6%)
Cip	92 (92%)	94 (94%)	33 (91.6%)	58 (77.3%)
SXT/TMP	88 (88%)	88 (88%)	27 (75%)	54 (72%)
Nitro	100 (100%)	100 (100%)	36 (100%)	71 (94.6%)
Fos	98 (98%)	99 (99%)	35 (97.2%)	73 (97.3%)

CONCLUSIONS: Susceptibility of *E. coli* strains varied by patient group. Antimicrobial resistance was associated with older age and history of previous urinary tract infection. In our institution *E. coli* remained highly susceptible to fosfomycin in all four groups studied. Published susceptibility data should be differential and specific to the population for which it will be used.

P43

EVALUATION OF CHROMAGAR™ CAMPYLOBACTER (CAC)

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BACKGROUND: Campylobacter Blood Free agar (CBFA) is commonly used for primary isolation of Campylobacter species. However, final culture results require incubation for 72 hours and break through of non-Campylobacter organisms is common. CAC agar was evaluated to determine if performance could be improved.

METHOD: Growth and colonial morphology were evaluated with known Campylobacter organisms. Breakthrough growth was evaluated with non-Campylobacter organisms. Clinical specimens were inoculated in parallel

to CBFA and CAC, and incubated microaerophilically at 42°C. CAC were examined at 24, 48 and 72 hours. CBFA were examined at 48 and 72 hours. Organisms were identified using the bioMerieux Vitek®-MS.

RESULTS: 10 clinical isolates of *C. jejuni* and 1 of *C. fetus* grew easily identifiable red colonies on CAC at 24 hours. Isolates of *C. albicans*, *E. faecium*, *Salmonella*, *Enterobacter*, *Proteus*, *S. aureus*, *S. epidermidis*, and *E. coli* were totally inhibited. *Klebsiella* grew as teal green colonies. *P. aeruginosa* grew as red colonies.

182 clinical stool specimens were inoculated onto both plates. *C. jejuni* was isolated from 2 specimens: 1 on both CBFA and CAC, and 1 on CAC alone. Both isolates on CAC were identified at 24 hours. 8% of CAC plates had breakthrough of non-Campylobacter red colonies.

CONCLUSION: The CHROMagar™ Campylobacter produced distinct red colonies at 24 hours that identified directly with the bioMerieux Vitek®-MS, and if implemented, would reduce the final TAT by 24 hours.

P44

EXPLORING THE NEXT GENERATION SEQUENCE ANALYSIS PIPELINE FOR LYME DISEASE CAUSING AGENT

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OBJECTIVES: Lyme disease, caused by *Borrelia burgdorferi* (Bb), is one of the most common vector-borne diseases in North America. The causative agent, *B. burgdorferi*, has a unique and complex genome structure with a linear chromosome, and several linear and circular plasmids. The nature of both linear and circular plasmids can vary in different isolates. This mosaic genomic content can make sequence assembly and other bioinformatics analyses challenging, therefore we compared various genome assemblers to evaluate which tools produced the best/most informative sequence assembly of this complex genome.

METHODS: Cultures of five Bb isolates acquired from different vectors, hosts, locations and years were selected. DNA was extracted using the Qiagen QIAamp DNA extraction kit. Whole Genome Sequencing was performed using a Nextera XT DNA library preparation kit, and 150nt paired-end reads were generated using the Illumina® MiSeq benchtop sequencer. Bowtie2 was used to align raw reads to genomes downloaded from Pathosystems Resource Integration Centre to find the most suitable Bb reference. Sequence assembly was then performed using A5 pipeline, Velvet, AbySS, and SPAdes with default parameters.

RESULTS: For the reference selection, the top three hits of Bowtie2 reference selection are all clustered in the same lineage on the whole genome phylogenetic tree. For the *de novo* assembler comparison, from the score of 8 assembling quality indicators, we found SPAdes and A5 scored higher than others.

CONCLUSIONS: Bowtie generated consistent results and the program could serve as a dependable reference genome selection tool. SPAdes and A5 scored the highest on all indicators despite differences among *Borrelia* isolates. They are the two most suitable *de novo* assemblers for Bb, and we plan to use them in parallel for future pipeline setup.

P45

PHYSICIAN AND PHARMACIST PERCEPTIONS OF AN ANTIMICROBIAL STEWARDSHIP PROGRAM (ASP) THAT USES SYNDROMIC PATHWAYS IN ADDITION TO AUDIT AND FEEDBACK ROUNDS

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OBJECTIVE: To determine staff physician, resident and pharmacist perceptions of an Antimicrobial Stewardship Program (ASP) that uses syndromic pathways and audit and feedback (AF) rounds at a tertiary-care, university-affiliated hospital. The following pathways were available and promoted: community acquired pneumonia (CAP) from March 2013, chronic obstructive pulmonary disease exacerbation (COPDE) from May 2014, and urinary tract infection (UTI) from Jan 2015.

METHODS: We distributed a 16-item survey in May 2014 to staff physicians, residents and pharmacists with whom the ASP team had rounded on General Internal Medicine (GIM), Intensive Care, Respiriology and Family Medicine services from September 2013. The survey was redistributed to the GIM service in August 2015. In each survey, we asked respondents to respond to a 5-point Likert scale, indicating their level of satisfaction with various aspects of the ASP experience and the utility of the syndromic pathways. Likert scale responses were analyzed as interval data (1-5), allowing parametric statistical tests of differences in means (E.g. ANOVA, t-test).

RESULTS: 156/431 (36%) of those surveyed in 2014 and 2015 responded. 87% of respondents felt that the ASP had a positive impact on patient care, though residents were more likely than staff physicians to agree with this statement (mean resident Likert 4.35, mean staff physician Likert 3.85; p=.012). Mean Likert responses for the syndromic pathways were CAP 4.18, COPDE 4.18, UTI 4.21; GIM residents were more likely than GIM staff physicians to feel that the pathways were useful (CAP, p=0.003; COPDE, p=0.002; UTI, p=0.016).

CONCLUSIONS: Our survey results indicate physician and pharmacist satisfaction with an ASP focused on AF and syndromic pathways, with 87% of respondents agreeing that the ASP had a positive impact on patient care. Residents perceived the positive impact of the ASP and utility of the syndromic pathways more highly than staff physicians. These data support the continued use of AF and syndromic pathways for uptake and expansion of the ASP, as well as additional research and measures to increase staff physician satisfaction with the ASP.

P46

PCR IS USEFUL AS A SUPPLEMENTAL TEST IN THE REFERENCE LABORATORY TO ASSIST WITH DIAGNOSIS OF AMOEBIASIS IN LIVER SAMPLES

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BACKGROUND: Amoebic dysentery is a serious illness caused by the eukaryotic amoeba *Entamoeba histolytica*. *E. histolytica* can also cause serious invasive extraintestinal disease endemic in tropical areas around the world. An ELISA confirmatory test is available for distinguishing *E. histolytica* from *Entamoeba dispar* from stool samples but is not recommended for liver samples. Liver amoebiasis is occasionally suspected in returning travellers and immigrants to Canada, which prompts a need for a test for liver samples. In the last few years, the BCCDC Public Health Laboratory (BCPHL) has adopted a sensitive nested PCR test that specifically targets *E. histolytica*, which can detect and differentiate *E. histolytica* from *E. dispar*. The test can be used for liver or other sample types. It is currently used as a supplemental test to other standard laboratory tests for *E. histolytica*.

METHODS: The BCPHL Parasitology Laboratory receives liver samples (usually aspirates) for microscopic examination of *E. histolytica* from hospitals throughout the province. The laboratory uses a nested PCR test targeting *Entamoeba* small subunit rRNA. The outer PCR for *E. histolytica/dispar* will generate a 910bp amplicon with the primer set E-1 and E-2. The outer PCR amplicon is then used as template for the subsequent two inner PCR reactions which are run in parallel. The first primer set EH-1/EH-2 specific for *E. histolytica* and the second ED-1/ED-2 specific for *E. dispar*.

RESULTS: *E. histolytica* in liver samples is often a difficult diagnosis to make due to lack of sensitivity as well as requiring high expertise to confirm by microscopy. In comparing *E. histolytica* PCR test result data to corresponding microscopy, serology and ELISA on 21 samples, the PCR test is found to be highly sensitive and specific.

CONCLUSIONS: The *E. histolytica* PCR test has proven to be an excellent supplemental test for the diagnosis of *E. histolytica* from liver samples.

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PAN-HOSPITAL PARTICIPATION WITHIN A SINGLE METROPOLITAN REGION IN THE GLOBAL POINT PREVALENCE SURVEY OF ANTIMICROBIAL CONSUMPTION AND RESISTANCE (GLOBAL-PPS) – A TOOL FOR IDENTIFICATION OF TARGETS FOR QUALITY IMPROVEMENT (QI) IN ANTIMICROBIAL STEWARDSHIP (AS)

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OBJECTIVE: Given the importance of AS in acute care hospitals across Canada, and with pan-hospital participation in the GLOBAL-PPS, a unique opportunity was provided to use the data collected to identify targets for QI at individual hospitals.

METHOD: A point prevalence survey was conducted between February-April 2015, in all wards of all 5 tertiary hospitals (4 adult /1 paediatric) serving a large metropolitan region (population 1.4 million). Detailed data were collected using a standardized method (www.global-pps.com) for surveillance for all inpatients receiving an antimicrobial on the day of the PPS. Antimicrobials were surveyed according to the WHO Anatomical Therapeutic Chemical classification. Surveyors were comprised of infection control practitioners, and infectious diseases physicians and pharmacists.

RESULTS: Overall, 30% of all patients in our health region were receiving at least one antimicrobial (31% adult, 24% paediatric). Of 666 adult and 66 paediatric patients, 55% and 33% respectively, were receiving at least one antibiotic via the oral route. For adult and paediatric patients (excluding neonates), the most common diagnosis prescribed for each antimicrobial was lower respiratory tract infection. Seventeen percent of adult patients were receiving an antimicrobial for a hospital-acquired infection. Four percent of adults were being treated for *C. difficile* associated diarrhea, of whom 33% received oral vancomycin. Eleven percent of adult patients were receiving cefazolin as surgical prophylaxis, and of those, 32% received >3 days duration. Regarding broad-spectrum drugs, 13% of adult patients received piperacillin+tazobactam (39% for hospital-acquired; 84% empiric) while 3% of adult patients received meropenem. Eight percent of adult patients received parenteral vancomycin while 1.4% received linezolid. For 83% of adult patients, and 94% of paediatric patients, a reason was given (in the medical record) for at least one of the antimicrobials.

CONCLUSION: The standardized GLOBAL-PPS was a valuable process and captured several key variables for future QI in all our urban acute care sites. It not only allowed comparison with other global sites but also identified areas for QI initiatives, including prolonged surgical prophylaxis in adults, and parenteral vancomycin use.

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CONFIRMATION OF NEISSERIA GONORRHOEAE POSITIVE NAAT RESULTS: ARE PRESERVATION AND TRANSPORT MEDIA COMPATIBLE ACROSS ASSAYS FOR VALIDATION PURPOSES?

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Commercially available NAATs are more sensitive than culture for detection of *N. gonorrhoeae* (NG). However, they are not approved for use on pharyngeal and rectal specimens. Results obtained on extra-genital specimens should be validated by a second assay that makes use of different primer/probe sets. Before undertaking such a study, we wanted to determine the compatibility of preservation and transport (P&T) media between commercial platforms.

METHODS: We inoculated serial dilutions of NG (ATCC 49226; final dilutions 10⁶ to 10⁰), as well as 2 non-gonococcal *Neisseria* spp. into 6 sets of P&T media. Dilutions of NG prepared in each of Abbott RealTime, GenProbe Aptima Combo 2 (AC2), Roche Cobas 4800, BD Probetec ET, BD ProbeTec Qx Viper and Cepheid Xpert CT/NG P&T media were tested by each commercial assay. A P&T kit was considered compatible (C) with the commercial platform if a positive result was obtained at ± 1 dilution compared to the result obtained with the P&T media specifically sold with the commercial platform; compatible with reduced sensitivity (RS) if the first positive result was obtained at 2 dilutions below, and not compatible (NC) if obtained at >2 dilutions below.

RESULTS:

Platform	P&T media					
	Cobas		ProbeTec ET	ProbeTec Qx	RealTime	Xpert
	AC2	4800				
AC2	-	RS	RS	RS	RS	C
Cobas 4800	NC	-	C	C	C	C
ProbeTec ET	NC	NC	-	NC	NC	NC
ProbeTec Qx	NC	C	C	-	C	C
RealTime	C	C	C	NC	-	C
Xpert	NC	C	C	C	C	-

Platforms reported negative results for *N. perflava* and *N. cinerea* inoculated samples.

CONCLUSIONS: Compatibility of P&T media across commercial platforms is variable. These results will prove useful when deciding the combination to be used for a prospective validation study on pharyngeal and rectal specimens.

P49

A RETROSPECTIVE OBSERVATIONAL COHORT STUDY OF HCV RE-INFECTION IN HIGH-RISK PEOPLE WHO INJECT DRUGS

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OBJECTIVE: People who inject drugs constitute the majority of cases of HCV infection in Canada. The rate of HCV reinfection after achieving Sustained Virologic Response (SVR) has exceeded 5% in clinical practice and clinical trials in this population. Ongoing engagement in care may contribute to reducing this rate.

METHODS: We have documented 31 cases of SVR following HCV therapy, in which patients continued high-risk behaviour for HCV acquisition following SVR. A cohort of 68 individuals who achieved SVR was also followed. HCV RNA testing was done every 6 months following SVR to document recurrent viremia. The endpoint of this analysis was a positive HCV RNA test.

RESULTS: Within the cohort of 31 active drug users treated for HCV, 84% were male, 61% genotype 1, 84% previously treatment naive, 29% co-infected with HIV, 65% used heroin, 71% cocaine, and 58% were on opiate substitution therapy. With a mean of 18 months of follow-up, there were no cases of recurrent viremia. Among the 68 patients, 65% were male, 13.2% were HIV co-infected, 62.9% genotype 1, and 92.5% previously treatment naive. In a mean of 5.95 person-years of follow-up/subject, 4 cases of reinfection were noted, all of which were co-infected with HIV. The only factor associated with an increased risk of re-infection was use of stimulants.

CONCLUSION: In our cohort, HCV re-infection rates were much lower than previously reported in this population. The program of long-term engagement in care, offered at our centre, serves to reduce the level of risk associated with ongoing injection drug use. Interventions such as this should be considered as the availability of HCV treatment is expanded in this population.

P50

SURVEILLANCE OF INVASIVE *STREPTOCOCCUS PYOGENES* IN SOUTHWESTERN MANITOBA

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INTRODUCTION: *Streptococcus pyogenes* (group A streptococcus, GAS), is an important human pathogen responsible for more than 500,000 deaths per year globally. Its clinical presentation, ranges from pharyngitis to life threatening streptococcal toxic shock and necrotizing fasciitis. In Manitoba, invasive GAS is a reportable disease. An annual surveillance study of invasive GAS was initiated to monitor both the number of isolates and their *emm* gene typing for southwestern Manitoba.

METHODS: From June 2, 2004 to December, 7, 2015 all sterile fluid/site specimens that were submitted to DSM, Westman Regional Laboratory for culture work-up and grew *S. pyogenes* were submitted to the National Microbiology Laboratory for serotyping/*emm* typing, via Cadham Provincial Laboratory. All invasive GAS were also reported to Manitoba Communicable Disease Control.

RESULTS: During this time, 115 patients from 41 communities, had 115 specimens submission, all were blood specimen except for 21 joint fluids, 6 deep tissue and 3 abscess aspirates. The age range of patients varied from 1 month to 94 yrs, with an average age of 50 yrs. Of these patients, 76 were in-patients, 19 were out-patient/ER, and for 15 patient status was unknown at the time of specimen submission. More males than females had invasive GAS disease. There was a general increasing trend of invasive GAS. There were varied M/*emm* types seen through the years with M/*emm* type 1 seen most years.

CONCLUSIONS: Invasive GAS disease is more common in older male adults. Since 2004 there has been a general increasing trend for invasive GAS and although there are varied M/*emm* types through the years, M/*emm* type 1 was seen most years throughout the study period. M/*emm* type 1 has been reported to be the most prevalent type in Canada, since the early 1990s.

P51

CHALLENGES IN DEVELOPING A REAL-TIME PCR ASSAY FOR HEPATITIS C VIRUS GENOTYPING

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OBJECTIVES: Genotyping of Hepatitis C virus (HCV), including subtyping of genotype (Gt)1, is necessary for determining the optimal drug treatment regimen. Genotyping by a reverse hybridization line probe assay (LiPA), the most common commercial method, is expensive and time consuming. Given a recent increased demand for HCV genotyping, we investigated the use of a laboratory-developed real-time (q)PCR assay as an efficient approach to identifying HCV infections with Gt1a, Gt1b, and Gt3a, the predominant genotypes in British Columbia.

METHODS: HCV-positive blood specimens previously tested at the BCCDC Public Health Laboratory (PHL) were used to evaluate qPCR assays with primers and probes targeting the HCV core and NS5B genes. The performance of locked nucleic acid (LNA) versus minor groove binder (MGB) probes was compared. Melt curve analysis with SYBR green and TaqMan chemistry based qPCR assays were performed on an ABI 7500 Fast system. The reverse hybridization VERSANT HCV Genotype 2.0 LiPA was used as the comparator method.

RESULTS: Initial screening revealed that qPCR with LNA-probes provided the best sensitivity for HCV genotype detection. Further, melt curve analysis and qPCR using MGB probes were unable to differentiate between the three genotypes. The best performing primer and LNA-probe combinations were evaluated on 223 samples using multiplex qPCR: 96.7% (119/123) Gt1a, 75% (21/28) Gt1b, and 100% (43/43) Gt3a samples were successfully identified. Four samples gave discrepant results due to cross hybridization between oligomers. This multiplex PCR reduced labour time by approximately 5 hours for 94 specimens when compared to the LiPA, and cost approximately \$1.50 per sample in reagents and consumables.

CONCLUSIONS: Successful development of a multiplex qPCR assay for HCV genotyping requires careful design of primers and probes that target non-overlapping regions. Due to the low cost, an in-house qPCR assay can provide a rapid, cost-effective screen to identify the most prevalent HCV genotypes and reduce the reliance on more expensive commercial assays. Future work will evaluate assay performance on greater sample numbers and on other HCV genotypes as well as on mixed genotype infections.

P52

DEVELOPMENT OF A FAST TRIPLEX REAL-TIME RT-PCR FOR THE DETECTION OF NOROVIRUS GENOTYPES I AND II IN RNA EXTRACTS FROM STOOL AND VOMITUS SPECIMENS

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OBJECTIVES: The BCCDC Public Health Laboratory (PHL) currently uses an in-house developed triplex real-time RT-PCR (qRT-PCR) assay to detect *Norovirus* genotypes I and II (GI and GII) and an exogenous internal positive control (IPC) to detect inhibition in BioMerieux NucliSENS easyMag extracts of stool and vomitus samples. We replaced the original 2 GI probes with a single degenerate probe and the original GII probe with one that also detected the Sydney GII.4 strain efficiently. We modified probe fluorophores to improve signal to noise ratios, re-optimized the assay to run in fast cycling mode and evaluated performance of the newly-optimized "NoroFast" qRT-PCR against the assay in use.

METHODS: After optimizing the NoroFast qRT-PCR and confirming constituent reactions to be as efficient as those in the current method, 50 archived clinical RNA extracts (20 GI, 20 GII and 10 *Norovirus* negative) were tested by the NoroFast assay and cycle threshold (Ct) values obtained were compared to those of the original assay, using a threshold of 0.1 in all cases. Specificities and sensitivities of the NoroFast method were determined against the assay in use, as were differences in Ct values for GI and GII targets.

RESULTS: Sensitivities and specificities for GI and GII in the NoroFast qRT-PCR were 100% with respect to the assay in use. NoroFast GI and GII reaction efficiencies were similar to those obtained in the current method and respective GI, GII and the IPC Ct values differed, on average, by less than one cycle from the existing method. Aside from workflow efficiencies that reduced the labour invested in assay performance, the NoroFast qRT-PCR method reduced cycling time from approximately 120 to 50 minutes. **CONCLUSIONS:** The newly-optimized NoroFast qRT-PCR assay detects *Norovirus* genotypes I and II in a single 20 µL fast reaction and maintains the existing assay's sensitivity and specificity with moderate cost savings and significant workflow efficiencies.

P53

DEVELOPMENT OF A FAST MULTIPLEX REAL-TIME PCR FOR THE DETECTION OF *CHLAMYDOPHILA PNEUMONIAE*, *LEGIONELLA PNEUMOPHILA* AND *MYCOPLASMA PNEUMONIAE* IN DNA EXTRACTS FROM ATYPICAL PNEUMONIA SPECIMENSD Eisler¹, A McNabb¹, L Janz¹, A Paccagnella¹, N Prystajec^{1,2}, P Tang³, L Hoang^{1,2}¹British Columbia Centre for Disease Control Public Health Laboratory, Provincial Health Services Authority; ²Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC; ³Department of Pathology, Sidra Medical and Research Center, Doha, Qatar

OBJECTIVES: The BCCDC Public Health Laboratory (PHL) currently uses an in-house developed real-time PCR (qPCR) assay consisting of 1 singleplex and 2 duplex reactions for the detection of *Chlamydomphila pneumoniae*, *Legionella pneumophila*, *Mycoplasma pneumoniae* and inhibition and extraction controls, in Qiagen QIAamp spin column extracts of lower respiratory samples. To improve cost- and workflow-efficiencies, we redesigned the assay as a fast multiplex qPCR ("CLM-4plex") for the detection

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of the 3 bacterial targets and the human β -globin gene (an endogenous sample quality and inhibition control) in one tube and evaluated its performance against the assay in use.

METHODS: After optimizing the CLM-4plex qPCR and confirming that constituent reactions were as efficient as those in the routine assay, 91 archived DNA extracts from 87 samples submitted to the PHL for detection of *C. pneumoniae*, *L. pneumophila* and *M. pneumoniae* between 2007 and 2014 were tested blindly using the CLM-4plex. Post-run analysis of these multiplex reactions was performed with a threshold of 0.1 and results were compared to those from the current method. Specificities and sensitivities of the CLM-4plex qPCR were determined against the assay in use, as were differences in crossing threshold (Ct) values for the bacterial targets. Time and materials efficiencies were noted.

RESULTS: Sensitivities in the CLM-4plex were 100% for all bacterial targets and specificities were 98.8% for *C. pneumoniae* and 100% for *L. pneumophila* and *M. pneumoniae*, reflecting detection of an additional *C. pneumoniae* positive when compared to the current qPCR assay. CLM-4plex qPCR amplified *C. pneumoniae*, *L. pneumophila* and *M. pneumoniae* by an average of 6.7, 2.5 and 4.1 cycles earlier, respectively, than the currently-used method. The CLM-4plex assay decreased the estimated per sample qPCR cost from \$15 to \$2, reduced cycling time from approximately 120 to 40 minutes and decreased labour using a more efficient workflow.

CONCLUSIONS: The newly-optimized CLM-4plex qPCR assay detects *C. pneumoniae*, *L. pneumophila* and *M. pneumoniae* in a single 20 μ L fast reaction, it is at least as sensitive as the current 3-tube assay and incorporates several efficiencies to decrease test cost and improve workflow.

P54 ABSTRACT WITHDRAWN

P55

USE OF GENOME SEQUENCING TO INFORM DIAGNOSTIC ASSAY DEVELOPMENT FOR *STREPTOCOCCUS PNEUMONIAE* AND *S. PSEUDOPNEUMONIAE*

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OBJECTIVE: 16S gene sequencing is used routinely for organism identification. However, it is not able to separate species within the *S. mitis* group (*S. mitis*, *S. pneumoniae* and *S. pseudopneumoniae*). Genome sequencing was used to aid in development of in-house laboratory diagnostic tests to differentiate *Streptococcus pneumoniae* and *S. pseudopneumoniae*.

METHODS: The pan-genome of clinically relevant *Streptococcus* spp. was mined for species-specific markers that could reliably differentiate *S. pneumoniae* from *S. pseudopneumoniae*. Nearly 4,800 genomes were included in the analysis, including six *S. pseudopneumoniae* strains isolated in British Columbia.

RESULTS: Initially a genome-wide comparison of twelve *S. pseudopneumoniae* genomes to twenty-seven *S. pneumoniae* genomes identified 29 unique genes specific to *S. pseudopneumoniae* and 49 genes specific to *S. pneumoniae*. These targets were further evaluated against ~4,800 publicly available genomes, which included *S. pseudopneumoniae*, *S. pneumoniae* and *S. mitis*, to determine species-specificity. These markers could be used as targets for a qPCR assay for rapid identification between *S. pneumoniae* and *S. pseudopneumoniae*.

CONCLUSIONS: Genome sequencing provided useful information for informing the development of diagnostic qPCR assay to rapidly differentiate between closely related *Streptococcus* spp. Genomic data provided insights to the genetic content of these organisms, allowing us to initially pull out 29 and 49 potential species specific markers for *S. pseudopneumoniae* and *S. pneumoniae*, respectively. The specificity of each marker was further screened in against a diverse set of approximately 4,800 *Streptococcus* genomes. New diagnostics assays can be designed taking into account the diversity of a genus or species using *in silico* methods. Caution, however, is heeded as not all publicly available genomes are what they claim to be; vigilance is important.

P56

COMPARISON OF FOUR ASSAYS FOR DETECTION OF *CLOSTRIDIUM DIFFICILE* TOXIN

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OBJECTIVE: The purpose of this study is to look retrospectively at the performance characteristics of 4 different assays for the detection of toxigenic *Clostridium difficile* in a pediatric population compared to the standard Cell Cytotoxin assay.

METHODS: The study included residual liquid/loose stools from patients ≤ 16 years old, but ≥ 1 year old (exception: Hirschsprung's disease) submitted to the BC Children's and Women's Microbiology Laboratory for *C. difficile* toxin testing. These stools were previously tested by the Cell Cytotoxin assay, and were then retrospectively tested using 4 different methods: Cepheid Xpert™ *C. difficile* assay (GeneXpert), Illumigene™ *C. difficile*, Meridian Bioscience Inc, BD GeneOhm™ Cdiff assay, and, Toxigenic *C. difficile* Culture. Residual stool samples were thawed and suspended in sterile buffer and split into 3 tubes and stored at -80 °C. Subsequently, each tube was thawed and tested using one of the 4 methods. True positives were defined as positive by ≥ 2 methods or positive only by Toxigenic Culture.

RESULTS: A total of 249 residual stool specimens were retrospectively tested, of which 96 were positive and 153 were negative based on the result of the Cell Cytotoxin assay. The cumulative testing results from the 4 different assays concluded that there were 89 true positives and 160 true negatives.

	Cytotoxin Assay			BD GeneOhm™	Toxigenic Culture
	GeneXpert™	Illumigene™	GeneOhm™		
Sensitivity (%)	95.5	97.8	83.1	88.8	92.1
Specificity (%)	93.1	98.1	98.1	99.4	100
PPV (%)	88.5	96.7	96.1	98.8	100
NPV (%)	97.4	98.7	91.3	94.1	95.8

CONCLUSION: Based on our comparative study of different *C. difficile* toxin testing platforms our institution implemented the Cepheid Xpert™ *C. difficile* assay (GeneXpert) as our routine diagnostic test for *C. difficile* toxin in children.

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IMPLEMENTING THE BD BACTEC™ FX IN THE ER DEPARTMENT – A LAKERIDGE HEALTH LEAN INITIATIVE

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BACKGROUND & OBJECTIVES: Lakeridge Health is a hospital servicing a community of >600,000 people. The ER collects ~50% of blood cultures. When cultures were loaded 24/7 into the BD BACTEC™ FX Blood Culture System in the Core Laboratory, an average delay of 2.48 hours was noted from collection to loading. The implementation of a satellite BACTEC™ FX and EpiCenter™ Data Management System in the ER provided an opportunity to reduce time to detection and reporting results.

METHODS: Pre- and post-install time to incubate (TTI) data was collected from LIS and BACTEC plots (n=76, 29 positives) and LIS and EpiCenter – Specimen Registration (n=120, 51 positives), respectively. Data was extracted to excel and analyzed for improvement in TTI.

RESULTS: Following implementation, an 82% decrease (2.02 hours) in TTI for all ER blood cultures was observed with an 84% reduction (2.14 hours) for positive cultures. The largest improvement was noted during the night shift: from 2.57 hours to 27 min. EpiCenter monitored instrument status, capacity, contamination, positivity rates and blood volume.

CONCLUSION: This study demonstrates that placement of a blood culture incubator close to the site of collection can dramatically reduce TTI allowing for alignment with best practices and improved patient care. In a recent survey:

1. More than 50% of Canadian physicians indicated they weekly encounter a patient with suspected sepsis.
2. Blood culture with subsequent identification/susceptibility was rated as the two most important lab tests for detection, antibiotic optimization and improved patient outcomes.*
3. Delays in TTI are inherent in many institutions.*
4. To reduce time to pathogen identification and improve outcomes for patients with sepsis; guidelines recommend cultures should be incubated within 2 hours from draw.**

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P58

DEVELOPMENT OF ANTIMICROBIAL STEWARDSHIP ONLINE RESOURCES BY PUBLIC HEALTH ONTARIO

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BACKGROUND: Many hospitals require guidance to initiate or advance an antimicrobial stewardship program (ASP). Numerous antimicrobial stewardship tools, interventions and activities (collectively termed “strategies”) are described in the literature. Each requires different levels of resources, expertise and time to implement and has varying impact on improving antimicrobial prescribing and patient outcomes. The ASP team at Public Health Ontario (PHO) identified that institutions have difficulty prioritizing and determining which antimicrobial stewardship strategies are best suited to their needs and resources. To address this gap, our goal was to develop a consolidated online resource to assist hospitals in selecting and implementing antimicrobial stewardship interventions most appropriate for their institution.

METHODS: Phases of the project included: 1) identifying individual antimicrobial stewardship strategies; 2) creating summary documents; 3) soliciting examples of supporting tools from consulting institutions; 4) assigning each strategy a priority and difficulty rating; 5) summarizing the evidence for five stewardship outcomes; and 6) creating templates and supplementary documents to accommodate the strategies on PHO’s website.

RESULTS: PHO identified, summarized and prioritized 32 antimicrobial stewardship strategies. Examples of supporting tools created by various institutions were provided for most of the strategies. These resources have been posted on PHO’s website, with capabilities to filter by priority rating, difficulty level, stage of program, type of intervention and evidence for certain antimicrobial stewardship outcomes.

CONCLUSION: The new resources on PHO’s website can provide valuable and needed direction for institutions building their ASPs. Health care institutions can use the consolidated strategy documents to identify, prioritize and implement antimicrobial stewardship strategies most suited to the facility’s needs and resources.

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A SURVEY OF CURRENT PRACTICE FOR DETECTION OF GASTROINTESTINAL PATHOGENS IN CANADIAN MICROBIOLOGY LABORATORIES

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Over the last decade, with increasing laboratory amalgamations and advancements in molecular-based identification methods, practices for testing gastrointestinal pathogens have changed.

OBJECTIVE: To determine the current methods and outcomes for enteric pathogen testing across Canadian laboratories.

METHODS: Laboratories across Canada were invited to complete a self-administered survey that questioned their current (December 2014–November 2015) practices for testing enteric pathogens.

RESULTS: Of the 100 labs contacted thus far 29 completed the survey. Overall the number of stool samples received for testing ranged from 115,500 at community diagnostic labs to 600 at community hospital labs; tertiary hospital labs averaged approximately 3500 samples. Of those, 550-23,000 samples were tested for bacterial pathogens (excluding *C. difficile*). Routine testing for *Salmonella* spp., *Campylobacter* spp., *Yersinia* spp., *E. coli* 0157 and *Shigella* spp. was common (100%, 100%, 100%, 96% and 88% respectively). The majority of labs identified bacterial pathogens by culture, and only 10% by molecular diagnostics (MD), resulting in 0.07-9% positive in-patient samples and 1.5-4% positive out-patient samples. Stools tested for *C. difficile* toxin ranged from 339-5578 of which 8.7-16.4% were positive overall. To identify *C. difficile*, 33% of labs tested for toxin, 27% tested by MD and 40% used a combination of toxin and MD. Of the labs that responded to the survey 42% tested for viral and 42% for parasitic pathogens with testing volumes of 288-5398 and 30-88,402 samples respectively. Norovirus, rotavirus, adenovirus, and enterovirus, were routinely tested (80%, 78%, 55%, 55% respectively) resulting in positivity rates of 2.5-8.8% for both in and out-patients combined. On average 50% of these labs reported using electron microscopy to identify viral pathogens and 50% incorporated MD. Enteric parasites routinely tested for included *Giardia lamblia*, *Cryptosporidium* spp., *Cyclospora* and *Entamoeba histolytica* (89%, 89%, 79%, and 79%). Of these samples 1.2-16.8% were positive overall, with concentration and permanent staining being the most common detection and identification methods. Up to 25% of labs indicated they were considering adopting MD in the future.

CONCLUSION: Pathogen identification has become more centralized but few labs have adopted MD methods for enteric pathogen testing as of yet.

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GENETIC CHARACTERIZATION OF THE INFREQUENT CLINDAMYCIN-RESISTANT/ERYTHROMYCIN-SUSCEPTIBLE (CR/ES) PHENOTYPE IN GRAM-POSITIVE COCCI

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BACKGROUND: Clindamycin is a lincosamide that inhibits protein synthesis by blocking the peptidyltransferase site of the 50A ribosomal subunit. Resistance is usually due to 23S ribosomal RNA methylation leading to co-resistance to macrolide, lincosamide and streptogramin B antimicrobials. Isolated lincosamide-resistance [reflected as (CR/ES)] is infrequently seen with two implicated gene families that have not been studied in depth: *hnu* and *lsa*. The *hnu* gene family encodes lincosamide nucleotidyl-transferases including *hnu(B)* and *hnu(A)* in *Staphylococcus aureus* and *hnu(B)* in *Streptococcus agalactiae*. The *lsa* gene family encode ABC transporters that efflux lincosamides, streptogramin A, and pleuromutilin including *lsa(C)* in *S. agalactiae* and *lsa(E)* upstream to *hnu(B)* in *S. aureus*.

METHODS: Clinical CR/ES Gram-positive cocci isolated from clinical and surveillance samples over a 10-yr period in a tertiary-care clinical microbiology laboratory were studied. Isolates were subcultured twice from -80°C and confirmed to have CR/ES by disk diffusion following CLSI. DNA was extracted using a Triton X100 protocol. *hnu(A)*, *hnu(B)*, *lsa(C)*

and *lsa(E)* were amplified by PCR using primers previously published. Amplicons were sequenced to confirm specificity.

RESULTS: A total of 60 CR/ES Gram-positive cocci were reported from the clinical laboratory during the study period. There was no trend of increasing resistance over the study period. 13 isolates (7 *S. agalactiae*, 5 methicillin-susceptible *S. aureus*, 1 *S. pneumoniae*) were available for testing and confirmed to have CR/ES [exception: 1 *S. agalactiae* was CR but had intermediate susceptibility to erythromycin (CR/EI)]. 5/7 *S. agalactiae* carried *lsa(C)*; 1 carried *hnu(B)* and *lsa(E)*, and the 1 CR/EI isolate carried *hnu(A)*. 1/5 *S. aureus* carried *hnu(B)* and *lsa(E)*. 4/5 *S. aureus* and 1/1 *S. pneumoniae* did not carry any of *hnu(A)*, *hnu(B)*, *lsa(C)* and *lsa(E)*.

CONCLUSIONS: The infrequently CR/ES phenotype in *S. agalactiae* can be explained by the presence of the *hnu* or *lsa* gene families. However, these resistance determinants do not fully explain the CR/ES phenotype detected in *S. aureus* and *S. pneumoniae*. Additional work is required to better understand the mechanism behind this infrequent resistance phenotype.

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PROSPECTIVE EVALUATION OF BIOMÉRIEUX'S CHROMID CARBA-SMART (C-S) AGAR BI-PLATE USED WITH BIOMÉRIEUX'S RAPIDEC CARBA-NP (RC) ASSAY FOR RAPID PHENOTYPIC DETECTION OF CARBAPENEMASE-PRODUCING ORGANISMS (CPO) FROM SURVEILLANCE ESWABS (SS)

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OBJECTIVES: CPO screening agars are typically poorly specific (Sp) and can lack sensitivity (Sn) for various CPO. The C-S bi-plate places OXA agar (Sn/Sp for class D CPO) side-by-side CARB agar (Sn for class A+B but not class D CPO) to improve overall chromID Sn. Similar to CARB, RC is Sn for class A+B but not class D CPO. This study compared CPO detection from SS by the Oxoid ESBL/meropenem disc screen algorithm to the combined abilities of RC used directly from chromogenic colonies on C-S knowing that RC-negative (neg) isolates, especially those grown on OXA agar, will require PCR to rule out CPO.

METHODS: Consecutive rectal +/- nasal SS (56 with known CPO/non-CPO content) were plated by WASP (30µL) to 3 agars: Oxoid ESBL and 2 distinct lots of C-S, with 4 lots used over the study period. Oxidase-neg isolates from ESBL went to meropenem disc using the cutoff of <25mm (Sn 100%, Sp 85%), while from C-S, burgundy [*E. coli* (EC)] or teal [usually *K. pneumoniae* (KP) or *E. cloacae* (ECL) etc.] colonies went directly to RC (1/ species/SS - duplicates referred). By 2h, distinct changes in RC from red to orange or yellow were taken as CPO+, with RC-neg confirmed by PCR (Cepheid CARBA-R or NML).

RESULTS: A total of 33 (3.6%) from 928 SS grew CPO from both ESBL and C-S agars. Results from 1836 CARB/1832 OXA plated, respectively, were: no growth [1500 (81.7%)/1688 (92.1%)]; no significant growth [246 (13.4%)/149 (8.1%); 18/19 *E. faecium* (EFE; dark blue), 40/76 *S. haemolyticus*, 166/49 *P. aeruginosa*, 22/5 *S. maltophilia* (no colour)]; potentially significant (PS) growth from 40 SS [100 (5.5%)/24 (1.3%): 75/10 EC, 88/14 KP, 5/0 ECL]. Of the 100/24 PS, 45/9 unique isolates were tested by RC. From CARB, 31/45 were RC+ (14/15 EC-NDM, 9/9 KP-NDM, 5/5 ECL-NMC, 2/2 KP-VIM, 1/1 ea. EC-NDM/VIM, KP-NDM/VIM, KP-NDM/VIM/OXA48, and ECL/NDM+VIM+OXA48), 5/45 RC-false-neg (FN); 3/3 KP-OXA48, 1/1 EC-OXA48, 1/15 EC-NDM) and 6/45 were RC-true-neg (TN; 4 KP, 1 EC, 1 teal EFE). As anticipated from prior studies, 8/9 CPO from OXA were FN by RC (5 KP-OXA48, 3 EC-OXA48, 1 KP-OXA48/NDM/VIM), while 1 EC was RC-TN.

CONCLUSIONS: While C-S appears equivalent to ESBL in detecting CPO from SS, laboratories considering implementing this otherwise useful combination need to take into account the RC limitation of its inability to detect all OXA48 and occasionally EC-NDM.

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PROSPECTIVE EVALUATION OF BIO-RAD'S BCARBA (BC) ASSAY TESTED FROM VARIOUS AGARS FOR RAPID PHENOTYPIC DETECTION OF DIVERSE CARBAPENEMASE-PRODUCING ORGANISMS (CPO)

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OBJECTIVES: Phenotypic testing of potential CPO prior to PCR reduces costs and improves sensitivity (Sn), as no current molecular assay detects all genotypes. The BC test is based on hydrolysis of a proprietary carbapenem that undergoes a colour-change within 30min exposure to a CPO. Retrospective studies found BC superior to pH indicator-based assays that have proven unreliable in detecting class D CPO. This study assessed BC's utility and accuracy for testing query CPO in a large clinical/research laboratory from in-use agars.

METHODS: From 26 Nov-31 Dec 2015, consecutive clinical and research CPO surveillance swabs with *Enterobacteriaceae* (ENT) exhibiting reduced carbapenem susceptibility as determined by meropenem (MEM) disc screen ≤25mm or by Vitek2 MEM MIC ≥0.5mg/L were tested by BC. Colonies for BC were picked from those closest to MEM discs on Oxoid's Mueller-Hinton Plus (MH) or from primary cultures on 5% Sheep Blood (BA), Oxoid Brilliance UTI Clarity (BUTI) or bioMérieux CARBA-SMART (C-S) agars. As per insert, only MacConkey-based agars were avoided. All suspect CPO were tested using ROSCO's KPC+MBL+OXA48 Confirm kit and/or by PCR (Cepheid Xpert CARBA-R or NML).

RESULTS: In total, BC was performed on 144 strains later confirmed as CPO (85) or non-CPO (60). Of the 110 from MH, 65 were BC-neg, 38 were BC+ [14 NDM: 5 *E. coli* (EC), 9 *K. pneumoniae* (KP); 11 OXA48: 5 EC, 5 KP, 1 *K. oxytoca* (KO); 12 VIM: 6 KP, 4 *C. freundii*, 1 EC, 1 KO; 1 IMP KP] and 7 were BC false-neg [FN; 2 GES5 KO, 5 NMCA *E. cloacae* (ECL)]. Of the 24 from BUTI, 13 were BC-neg (7 burgundy EC, 6 teal KP) and 10 were BC+ (10 NDM: 5 EC, 5 KP). Of the 6 from C-S, 1 was BC-neg, 1 BC+ (VIM: teal KP), and 4 BC-FN (4 teal ECL-NMCA). All 5 tested from BA were BC-neg. Overall, 78/85 CPO tested BC+ regardless of medium resulting in a Sn of 91.7% (95%CI: 86.7-96.2%), while for detecting CPO other than NMC/GES, Sn was 100% (95%CI: 94.4-100). As results with the uncommon NMC/GES CPO correlated with retrospective studies, the FN results here were deemed non-media-related. As no BC false+ results were encountered, specificity was 100% (95%CI: 92.8-100).

CONCLUSIONS: The low-complexity BC test is quick and easy to set-up, simple to interpret and provides a cost-effective yet highly Sn/specific means to detect common CPO.

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CEPHEID GENEXPERT CARBA-R RUO AND IVD ASSAY EVALUATION FOR THE CONFIRMATION OF CARBAPENEMASE PRODUCING GRAM NEGATIVE BACILLI ISOLATES

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OBJECTIVES: Rapid detection and confirmation of carbapenemase producing Gram negative bacilli is important for infection prevention and control and patient management. Carbapenem resistance can be detected phenotypically by the medical microbiology laboratory, however, it may take 48h to 72h and cannot differentiate carbapenemase producers from isolates which are resistant by other mechanisms. Genotypic testing for carbapenemase genes is crucial for infection prevention and control decisions. The Cepheid GeneXpert Carba-R research use only (RUO) assay (KPC, NDM, VIM, OXA-48, IMP-1) and the updated Carba-R IVD assay (same genes with expanded OXA-181/232 coverage) were evaluated for rapid culture confirmation of carbapenem resistant isolates.

METHODS: Retrospective and prospective carbapenem resistant Gram negative *Enterobacteriaceae* and non-fermenters with known or presumed carbapenemase, AmpC, or ESBL genes were tested either individually or in combinations. Isolates were diluted in saline to 0.5 McFarland and approximately 50 μ L added to the sample reagent buffer and processed in the test cartridge. Results from each cartridge type were compared to multiplex qPCR results (assay targeting KPC, NDM, VIM, OXA-48, IMP, and common ESBL genes) from the provincial reference laboratory.

RESULTS: The RUO assay detected 100% (89 isolates) of the KPC-, NDM-, and VIM-harboring isolates, 66% of the IMP-harboring isolates, and 4% of the OXA-48-like isolates. None of the AmpC, ESBL, GES, OXA-23/51, or SME isolates tested positive. The IVD assay (53 isolates) detected 100% of the KPC-, NDM-, OXA-48-like and VIM-harboring isolates and 66% of the IMP-harboring isolates.

CONCLUSIONS: The Carba-R IVD assay can be used as an accurate, rapid (less than one hour), culture confirmation of carbapenem resistant Gram negative bacilli isolates containing the five assay target genes.

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ASSESSING THE IMPACT OF PRE-AUTHORIZATION AND PROSPECTIVE AUDIT AND FEEDBACK OF 6 BROAD SPECTRUM ANTIMICROBIALS ON ANTIMICROBIAL PRESCRIBING AND PATIENT OUTCOME

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OBJECTIVES: Studies demonstrate that Antimicrobial Stewardship Programs (ASP) are effective in decreasing antimicrobial utilization and expenditures, decreasing *C. difficile* (CDI) rates and improving patient outcomes. In two combined 620 bed acute care community hospitals, an ASP was initiated that included pre-authorization and prospective audit and feedback of ertapenem, imipenem, meropenem, linezolid, daptomycin and tigecycline. We evaluated the impact of this intervention on antibiotic utilization, expenditures, guideline-concordant prescribing, and patient outcomes including CDI rates, length of stay, readmission rates, and 30-day mortality.

METHODS: This was a prospective study with comparison to pre-intervention trends. We compared all patients that received one of the restricted antibiotics during the first six-months of our intervention (April to September, 2014), to the same six-month period pre-intervention, obtained through retrospective chart review. Comparisons were performed using the χ^2 or Fisher exact tests for percentages and ANOVA, t-test, or Mann-Whitney U test for continuous variables.

RESULTS: A total of 921 cases of antimicrobial prescribing were analyzed. Patient characteristics, including age, gender and serum creatinine, were similar in both groups. There was a 12.5% reduction in the use of ertapenem. Guideline concordant use of all antimicrobials improved from 55.3% to 89.1% ($p < 0.00001$, χ^2). There was no significant change in length of stay, duration of therapy, 30-day readmission rates and 30-day mortality.

CONCLUSION: An ASP consisting of preauthorization and prospective audit and feedback was associated with significant improvements in guideline concordant use of specific broad-spectrum antimicrobials. Once again, this supports the importance of establishing an ASP in all healthcare centres.

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ANTIBIOTIC DECISION-MAKING: PERCEIVED COMPETENCIES AND NEEDS OF PAEDIATRIC RESIDENTS AT A TERTIARY CENTRE

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INTRODUCTION: Residents play a frontline role in prescribing antibiotics in acute care teaching hospitals. Obtaining information on residents' needs and perceptions related to this critical competency is important for directing training needs.

OBJECTIVES: To determine residents' perception of their needs and competencies in prescribing antibiotics to paediatric patients.

METHODS: Residents across all years of training at a tertiary paediatric centre were invited to complete anonymous questionnaires during an academic half-day session. A descriptive analysis was conducted.

RESULTS: Twenty-three residents (PGY1 [6]; PGY2 [7]; PGY3-4 [10]) completed questionnaires; completion rate=88.4%. Residents felt training in medical school (17/23 [74%]) and in PG year 1 (17 [100% of residents who had completed PGY1]) was insufficient to allow competency although 7 (70%) of PGY3-4's felt that training received up to their training year allowed competency in prescribing for common syndromes. Knowledge deficits were identified in antimicrobial pharmacology (12 [52%]), microbiology of common syndromes (20 [87%]) and current guidelines (22 [96%]). Level of comfort in prescribing was highest in neonatal sepsis (21 [93%]), febrile neutropenia (18 [78%]) and septic shock (14 [61%]) and lowest in treating infections in medically complex cases (6 [26%]) or renal disease (2 [9%]). Factors influencing good empiric antibiotic decisions were knowledge of microbiological aetiology (20 [87%]), experience managing similar syndromes (20 [87%]) and use of hospital antibiogram (14 [62%]). Residents felt more case-based learning (21 [93%]), mentorship by resident champion (17 [74%]), and availability of a good pocket resource (22 [96%]) were ways to improve their competencies.

CONCLUSION: Prescribing competencies were perceived to be best for protocol-driven syndromes like neonatal sepsis and inadequate for medically complex conditions with competency at its best in senior residency. Strategies such as case-based learning, access to pocket resources or apps, resident coaches for junior residents should be explored as ways of improving antibiotic decision-making in trainees.

P66 ABSTRACT WITHDRAWN

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HISTOPLASMA CAPSULATUM VAR. DUBOISII ISOLATED FROM A PATIENT OVER FIVE YEARS POST EXPOSURE

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BACKGROUND: A 76-year-old man presented with a 3-month history of cough, shortness of breath and weight loss. He was born in Portugal and had worked as a miner in Mozambique, Africa 5 years prior to his presentation. He more recently lived in South Dakota. The clinical examination was non-contributory. Chest CT scan showed bilateral infiltrates. Bronchoscopic specimens had no growth in bacterial, mycobacterial and fungal cultures, and were negative for malignancy. Due to ongoing symptoms the patient was taken for VATS-guided lung biopsy. Histopathology showed presence of necrotizing granulomas containing large thick-walled yeast cells.

OBJECTIVE: To identify the pathogen responsible for this patient's presentation.

METHODS: The patient's lung biopsy specimen was worked up using histopathological, microbiological and molecular methods. His urine was tested for *Blastomyces* antigen (BUAg).

RESULTS: The BUAg test was positive and the initial histopathology-based diagnosis was also that of blastomycosis. Initial fungal culture result was no growth. It was later noted, however, that the yeast cells, lacked many features typical of blastomycosis such as the presence of multiple nucleoli and abundant cytoplasmic material. Expert review of the slides gave diagnosis of *Histoplasma capsulatum* var *duboisii* (*H. duboisii*) infection. Remaining biopsy tissue was sent to the reference laboratory and calcofluor white staining demonstrated large lemon-shaped narrow budding yeast cells. Repeat tissue fungal culture had growth and the organism was identified as *H. duboisii*, confirmed by ITS sequencing. A whole body CT scan was negative for any bony or visceral lesions. The patient was initially treated with amphotericin-B and later switched to itraconazole.

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CONCLUSION: African histoplasmosis, caused by *H. duboisii*, is rare outside of Africa. The usual presentation is granulomatous lesions affecting skin, subcutaneous tissue, lymph nodes and bones; isolated pulmonary presentation is very rare. Diagnosing our patient was very challenging. A detailed review of histopathological features and ultimate culture positivity helped to confirm *H. duboisii* infection. Exposure and travel history can also help to distinguish blastomycosis from African histoplasmosis.

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IMPACT OF HOSPITAL-ACQUIRED VIRAL RESPIRATORY TRACT INFECTIONS (HA-VRI) IN CHILDREN ADMITTED TO A TERTIARY CARE HOSPITAL IN MONTREAL, QUEBEC, 2009-2014

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OBJECTIVES: Our objective was to describe the epidemiology of hospital-acquired viral respiratory tract infections (HA-VRI) and their impact in a paediatric population admitted to a tertiary care hospital, The Montreal Children's Hospital (MCH).

METHODS: Symptom-based total hospital surveillance is done at the MCH, using NHSN, CNISP and SPIN definitions. The MCH infection control database was surveyed for all HA-VRI occurring between 2009-2014. HA-VRI were diagnosed from clinical specimens by polymerase chain reaction (PCR) that detected rhinovirus, enterovirus, adenovirus, human metapneumovirus, influenza A and B, respiratory syncytial virus (RSV), coxsackie virus, coronavirus OC43 and 229E, echovirus, and para-influenza virus types 1-4.

RESULTS: 380 cases of HA-VRI were identified. Medical/surgical wards had a higher pooled mean incidence rate compared with neonatal and paediatric intensive care units (3.3 vs. 1.46 and 1.86 per 1000 patient days respectively; $p < 0.001$ and $p = 0.0018$ for medical/surgical wards vs. NICU and PICU respectively). 3.03% ($n = 11/363$) of patients with a HA-VRI required readmission to hospital, for an average length of stay (LOS) of 6.72 days. 5.28% ($n = 15/284$) of patients diagnosed with HA-VRI, not already in the ICU, required ICU admission, for an average ICU LOS of 4.33 days. 33% ($n = 5/15$) of patients admitted to ICU due to HA-VRI required mechanical ventilation (average duration 4.4 days). While RSV caused only 10% of HA-VRI over the study period, it accounted disproportionately for 33% ($n = 5/15$) of ICU admissions. Influenza A and B together accounted for 20% ($n = 3/15$) of patients with HA-VRI requiring ICU admission. Only 5% ($n = 18/359$) of patients were started on antibiotics at HA-VRI symptom onset. 0.8% ($n = 3/363$) of patients died following HA-VRI, on average 10.7 days after HA-VRI symptom onset.

CONCLUSIONS: Incidence rates of HA-VRI were higher than reported *C. difficile* infection rates in the adult population, contributing to morbidity in the paediatric population studied with a non-negligible impact.

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A NOVEL MUTATION D404N IN THE CONNECTION SUBDOMAIN OF REVERSE TRANSCRIPTASE OF HIV-1 CRF08_BC SUBTYPE CONFERS CROSS-RESISTANCE TO NNRTIS

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BACKGROUND: Growing evidence suggests that mutations in the connection domain of the HIV-1 reverse transcriptase (RT) can contribute to viral resistance to RT inhibitors. This work is designed to characterize a novel mutation D404N in the connection subdomain of RT of HIV-1 CRF08_BC subtype on drug resistance, viral replication capacity (RC) and RT activity.

METHODS: Mutation D404N alone or together with the other reported mutations were introduced into an HIV-1 CRF08_BC subtype infectious clone by site-directed mutagenesis. The drug susceptibility to nine RT

inhibitors, viral RC and the DNA polymerase activity of viral RT of the constructed virus mutants were investigated. Modelling study using the server SWISS-MODEL was conferred to speculate the possible structure-related drug resistance mechanism of the mutation D404N.

RESULTS: Single mutation D404N and H221Y conferred low-level resistance to nevirapine, efavirenz, rilpivirine and zidovudine. Double mutations Y181C/D404N and Y181C/H221Y significantly reduced susceptibility to NNRTIs. The most pronounced resistance to NNRTIs was observed with the triple mutations Y181C/D404N/H221Y. The virus containing a single mutation D404N displayed approximately 50% of RC compared to the wild type (WT) virus. Modeling study suggested that the D404N mutation might abolish the hydrogen bonds between residue 404 and K30 in p51 or K431 in p66, leading to impaired RT subunit structure and enhanced drug resistance.

CONCLUSION: These results indicate D404N to be a novel NNRTI-associated mutation in the HIV-1 CRF08_BC subtype, which provides valuable information to monitor clinical RTI resistance.

P70 ABSTRACT WITHDRAWN

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VIRAL RESPIRATORY TRACT INFECTIONS (VRTIS) IN THE INTENSIVE CARE UNIT (ICU): CLINICAL DEFINITIONS, FINDINGS AND OUTCOMES

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OBJECTIVES: Most VRTIs are acute, self-limited illnesses. However, adults with multiple conditions requiring ICU support are at greater risk of morbidity and mortality. The objective of this study was to describe the epidemiology, clinical presentation and outcomes of influenza and non-influenza VRTIs in the ICU.

METHODS: The microbiology laboratory database was used to identify all specimens from patients admitted to ICU of Mount Sinai Hospital (10/2011-5/2015) in which a respiratory virus was identified. A retrospective chart review was performed to determine epidemiology, clinical features, application of common definition of influenza-like illness (ILI) and outcomes.

RESULTS: Charts were available for 47/49 cases (24 influenza, and 23 other viruses). 17 cases (3 flu, 14 non-flu) were hospital acquired. The average age of influenza positive patients was 63 vs. 60 years for other viruses. Influenza positive patients were more likely to have underlying cardiac disorders (25.5% vs. 8.5%, $p = 0.01$). The most common reasons for admission were hypotension (22.7% flu vs. 41.7% other) and respiratory disorder (52.5% flu vs. 37.5% other, $p = 0.04$). Influenza positive patients met 1 or more clinical case definitions in 60.8% of cases (vs. 25% other, $p = 0.002$). Specifically, 26% of flu cases met criteria for CDC-ILI, 26% for WHO-ILI, and 57% for ECDC-ILI. Non-influenza cases were more likely to be associated with a change in ventilatory requirements (50% other vs 4.3% flu, $p = 0.004$), the identification of other pathogens (71% other vs 8.7% flu, $p = 0.001$), treatment with antibacterials (75% other vs 30.4% flu, $p = 0.008$), and longer duration of antimicrobial treatment (28 vs 14 days, $p = 0.01$). However, there was no difference in complication rates (70% flu vs. 86% other), discharge status (70% flu vs. 58% other) or 30 day mortality (30% flu vs. 42% other).

CONCLUSION: About one-third of respiratory viral infections identified in the ICU setting are hospital acquired, and these infections carry a significant risk of complications and death. Influenza is more likely to be identified as a single pathogen in the ICU setting. Clinical case definitions of ILI are insufficiently sensitive to diagnose influenza the ICU. Similarly, clinical, laboratory and radiological findings cannot be used to differentiate influenza from illness due to other respiratory viral pathogens.

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