AMMI Canada — CACMID Annual Conference  
May 3–6, 2017 • Toronto, Ontario

### ORAL PRESENTATIONS

<table>
<thead>
<tr>
<th>Thursday, May 4, 2017</th>
<th>Friday, May 5, 2017</th>
<th>Saturday, May 6, 2017</th>
</tr>
</thead>
<tbody>
<tr>
<td>Session A</td>
<td>A01.S–A05</td>
<td>Session D</td>
</tr>
<tr>
<td>Session B</td>
<td>B01–B05</td>
<td>Session E</td>
</tr>
<tr>
<td>Session C</td>
<td>C01–C05</td>
<td>Session F</td>
</tr>
<tr>
<td>Session G</td>
<td>G01–G07</td>
<td>Session H</td>
</tr>
<tr>
<td>Session I</td>
<td>I01.S–I07</td>
<td>Session J</td>
</tr>
<tr>
<td>Session K</td>
<td>K01–K05</td>
<td>Session L</td>
</tr>
</tbody>
</table>

### STUDENT POSTER PRESENTATIONS

**Thursday, May 4–Friday May 5, 2017**  
SP01–SP48

### INCUBATOR POSTER PRESENTATIONS

**Thursday, May 4–Friday May 5, 2017**  
IP01–IP12

### POSTER PRESENTATIONS

**Thursday, May 4–Friday May 5, 2017**  
P01–P72

### AUTHOR INDEX
Enteropathogen Detection in Children with Acute Gastroenteritis: A Comparison of Rectal Flocked Swabs and Stool Specimens

B PARSONS1, S Freedman2,3, BE Lee1,4, J Xie2,3, A Nettel-Aguirre1, L Chui1,3, XL Pang1,3, R Zhou1, J Dickinson2,3, O Vanderkooi2,3, S Ali1,3, L Osterreicher1, K Lowerison2,3, P Tar}1

1University of Alberta, Edmonton, AB, 2University of Calgary, Calgary, AB, 3Alberta Health Services, AB, 4Washington University School of Medicine, St. Louis, MO, USA

RESULTS: Submission rate was 75.5% (1147/1519) for stool and 99.7% (1514/1519) for swabs. Positive pathogen yield was 75.9% (871/1147) for stool and 67.6% (1024/1514) for swabs (OR=1.41; 95% CI: 1.29, 1.53). Comparative yield adjusted OR in stool relative to swabs were 1.24 (95% CI: 1.11, 1.38) and 1.76 (95% CI: 1.47, 2.11) in children with and without diarrhea at presentation, respectively. When the entire cohort was considered, the positive pathogen rates were 57.3% and 67.4 for stool specimens and rectal swabs. The overall yield unadjusted OR was 0.65 (95% CI: 0.59, 0.72). Performance varied based on presence of diarrhea and location of specimen collection.

CONCLUSIONS: Compared to paired stool specimens, rectal swabs have a lower diagnostic yield. When the effect of higher rectal swab submission rates is considered, the yield is greater for swabs. When enteropathogen identification is required and stool is unavailable or unlikely to be submitted, rectal swabs should be performed.

Clostridium difficile Colonization in Ontario (COLON): Acute Care Hospital Pilot Feasibility Study: Preliminary Findings

J JOHNSTONE1,3, G Broukhanski1, K Adomako1, E Nadoliny1, KC Katz2, C Vermeiren2, W Ciccotelli3, P Young1, A McGeer4,5, J Bartoszko6, D Chaul, L Rosella1,6, N Daneman1,6, S Weese7, V Allen1,5, G Garber1,5

1Public Health Ontario, Toronto, ON, 2North York General Hospital, Toronto, ON, 3Grand River Hospital, Kitchener, ON, 4Mount Sinai Hospital, Toronto, ON, 5University of Toronto, Toronto, ON, 6Institute for Evaluation Sciences, Toronto, ON, 7University of Guelph, Guelph, ON

OBJECTIVES: Clostridium difficile colonization is an important reservoir for healthcare associated C. difficile infection. The objectives of this pilot study were to: 1. determine the feasibility of testing for C. difficile using antimicrobial resistant organism (ARO) screening rectal swabs obtained from patients as part of routine care and 2. determine the proportion of swabs that tested positive for C. difficile and successfully strain typed.

METHODS: A Routinely collected ARO screening rectal swabs were obtained over a 4-week period from 3 acute care hospital laboratories. The swabs were de-identified and sent to a reference laboratory for C. difficile testing. Isolation of C. difficile culture was performed by direct inoculation of CHROMagar; DNA was extracted by boiling and PCR was set to ribotype and analyze by Modified Multiple-Locus Variable-number tandem-repeat Analysis (MMLVA). Ribotypes were identified using an on-line database; MMLVA profiles were entered into BioNumerics software. NAP was inferred based on
ribotyping results. The study received Research Ethics Board approval.

RESULTS: In total, 2692 ARO screening rectal swabs were routinely collected during the study period; 2085 (77%) were sent to the reference laboratory [hospital 1 649/685 (95%), hospital 2 835/855 (98%), hospital 3 601/1152 (52%)]. Of the 2085 sent for C. difficile testing, 140 (7%) were positive for C. difficile [hospital 1 37/649 (6%), hospital 2 58/835 (7%), hospital 3 45/601 (8%)] and all were strain typed; 84/140 (60%) were toxigenic and 56/140 (40%) were non-toxigenic. NAP1 (15%) and NAP4 (13%) were most common.

CONCLUSION: Use of routinely collected ARO screening rectal swabs for the detection of C. difficile colonization is feasible; sufficient human resources and work flow integration were identified as essential for maximizing proportion of swabs sent to the reference laboratory. C. difficile was present in 7% of patients in this study, representing toxigenic strains (including NAP1 and NAP4) as well as non-toxigenic strains. Next steps include linking these results to a large provincial population database to determine the proportion of community-acquired versus healthcare associated C. difficile colonization, as well as the risk of C. difficile infection according to colonization status (non-colonized, toxigenic strain colonized or non-toxigenic strain colonized).

A03
Identification of Shiga Toxin-Producing Shigella flexneri from Travel and Non-Travel Related Cases in Alberta
L CHUI1,2, K Yuen1, S Zhi1, B Parsons1, S Delannoy3, P Fach3, C Ferrato2, KA Simmonds4

1University of Alberta, Edmonton, AB, 2Provincial Laboratory for Public Health, Edmonton, AB, 3French Agency for Food Environmental and Occupational Health (Anses), Maisons-Alfort, France, 4Alberta Health, Edmonton, AB

INTRODUCTION AND OBJECTIVES: Shigella infections can cause severe disease and the majority of the reported cases are travel related. In the past years, Quebec, France and the USA have identified Shiga-toxin (Stx)-producing Shigella associated with travel to Mexico and the Caribbean, indicating the potential emerging strain of Stx-producing Shigella in these ‘high-risk’ regions. In 2015, the identification of two children in Alberta infected with Stx-producing Shigella flexneri with no travel history led to an investigation into the prevalence of these strains in Alberta and their further characterization.

MATERIALS AND METHODS: A total of 366 Shigella flexneri from 2003 to 2015 were included in this study. All isolates were retrieved from frozen skim milk stocks and cultured onto sheep blood agar plates. DNA was extracted from a single colony by rapid lysis and assayed for the presence of stx1 and stx2 genes by qPCR. All positive stx1/2 genes samples were further subtyped. Production of shiga toxins was confirmed using the QUIKCHEK lateral flow immunoassay. Pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS) were performed to study the relatedness of these isolates. Demographic data of all positive patients were reviewed and collated.

RESULTS: Of the 366 samples tested, there were 26 positive for shiga toxins and they were all identified as stx1a. Fourteen of the patients have travel history to the Dominican Republic, 1 travelled to Turks and Caicos Island and the remaining 11 cases have not travelled outside Canada. The ages range from 2 to 71 years. All the isolates from the two groups of patients have very similar PFGE patterns and were further confirmed by WGS data.

CONCLUSIONS: We found 26 (7.1%) of all Shigella flexneri isolates in Alberta carry the stx1 gene belonging to the subtype of stx1a and 42.3% of these cases have no travel history. This is the first study reporting the local acquisition of Stx-producing Shigella flexneri infection in Canada.

A04
Norovirus Outbreak in Alberta, Canada — Which Strain will Win the Indy Race?
XL PANG1,2, ME Hasing2, YY Qiu2, G Tipples1,2, BE Lee2

1Alberta Health Services, Edmonton, AB, 2University of Alberta, Edmonton, AB

BACKGROUND: Norovirus (NoV) GII genotype 4 (GII.4) variants which emerge every two to three years accounts for 85% of global NoV epidemics. We updated the molecular epidemiology of NoV outbreaks from July 2010 to June 2016 in Alberta.

METHODS: Stool samples submitted for outbreak investigations to Alberta Provincial Laboratory for Public
Health were tested for NoV GI and GII using RT-qPCR. One sample from each NoV outbreak was genotyped using region C primers. The annual cycle for NoV was defined from July of the previous year to June of the following year.

RESULTS: NoV was identified in 65% (741/1141) of the suspected NoV outbreaks. The previously described biennial pattern of NoV outbreaks was not observed from July 2011 to June 2016. There has been a gradual decrease in the annual number of NoV outbreaks since July 2012. NoV GII outbreaks were more common (88.1%) than GI (10.4%) and mixed GI-GII (1.5%). Diverse genotypes were observed for both NoV GI and GII outbreaks. GI.3, 5 and 6 were common among GI outbreaks. While GII.4 remained as the predominant strain among GII outbreaks until the end of 2015, the proportion of GII.4 declined from 85% to 20% in 2016. GII.4 2006b, the predominant strain for 3 annual cycles since July 2006, was mostly displaced by GII.4 New Orleans 2009 in 2010/11; and GII.4 New Orleans 2009 was later overtaken by GII.4 Sydney 2012 in 2012/13 which then declined in numbers in 2015/2016. The first GII.17 outbreak was identified in September 2014 and accounted to 16% of all GII outbreaks in 2015/2016. A new recombinant GII strain (GII.P16_GII.4 Sydney 2012), which emerged in February 2016, has been on the rise, causing 36% of all GII outbreaks during 2015/2016, and might become the predominant strain in 2016/2017.

CONCLUSION: Norovirus GII.4 has ended its predominant role in NoV gastroenteritis outbreaks in Alberta as of winter of 2016. A new recombinant strain (GII.P16_GII.4 Sydney 2012) has emerged while the proportion of GII.17 outbreaks has slowly increased in Alberta. The question remains as to which strain will win this race.

A05
Norovirus Genotypes Analysis of Gastrointestinal Outbreaks in British Columbia from 2012–2016
F TSANG1, D Eisler1, A Li1, L Li1, S Man1, C Tchao1, B Auk1, N Prystajecky1,2

1British Columbia Centre for Disease Control, Public Health Laboratory, Vancouver, BC, 2University of British Columbia, Vancouver, BC

BACKGROUND: Norovirus is the predominant etiological agent for gastrointestinal outbreaks in British Columbia, Canada. Norovirus is spread from person-to-person, fomites or contaminated food commodities. With the availability of norovirus genotypes by sequencing, it helps provide a better picture of the epidemiology, change of predominance genotypes and relatedness of outbreaks.

METHODS: From 2012–2016, each gastrointestinal outbreak that tested positive for norovirus in the BCCDC Public Health Laboratory was sequenced. Sanger sequencing targeting region C capsid of the virus was performed on one representative sample from each outbreak. Sequences were analyzed using an automated workflow and genotypes were assigned by sequence comparisons to the CaliciNet database reference strains.

RESULTS: 634 norovirus positive samples were sequenced. GII.4. New Orleans was the predominant genotype (52%) in gastrointestinal outbreaks tested in 2012, whereas GII.4. Sydney was the predominant genotype in 2013–2015 (66%, 76%, and 62% respectively). In 2016, a significant shift in genotype distribution was observed; GII.4 Sydney decreased to 28% of gastrointestinal outbreaks in 2016. We observed the re-emergence of GII.4G (Yerseke) (27%) and the increasing occurrence of GII.17 (8%), and GII.6b (7%) and GI.6a (7%). No changes in sample submission or positivity rates were observed in 2016.

CONCLUSIONS: Analysis of norovirus genotypes showed shifts in the predominant genotypes over time. 2016 was notably different compared to other years, where there is no one specific genotype predominant in the community. GII.4G (Yerseke), which was initially described in 2006, first re-emerged in 2015 (7%) and increased to 27% in 2016. It was not seen in years 2013–2014. The increase of GI.6a in 2016 was associated predominantly in food related outbreaks. Despite the shift in genotypes, there was no evidence that strain replacement is occurring in British Columbia in 2016.
Thursday, May 4, 2017
11:15–12:30 Session B
Room: Pine

B01
7 versus 14 days of Antibiotic Treatment for Critically Ill Patients with Bloodstream Infection: A Pilot Randomized Clinical Trial

N DANEMAN1, AH Rishu1, R Pinto1, P Aslanian1, SM Bagshaw3, A Carignan4, E Charbonney5, B Coburn5, DJ Cook6, M Detsky7, P Dodek8, R Hall9, A Kumar10, F Lamontagne4, F Lauzier11, JC Marshall12, CM Martin13, L McIntyre9, R Hall19, A Kumar10, F Lamontagne4, F Lauzier11, JC Marshall12, CM Martin13, L McIntyre14, J Muscedere15, S Reynolds8, W Sligl1, HT Stelfox16, E Wilcox5, R Fowler1

1Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 2Université de Montréal, Montréal, QC, 3University of Alberta, Edmonton, AB, 4Université de Sherbrooke, Sherbrooke, QC, 5University Health Network, University of Toronto, Toronto, ON, 6McMaster University, Hamilton, ON, 7Sinai Health System, University of Toronto, Toronto, ON, 8University of British Columbia, Vancouver, BC, 9Dalhousie University, Halifax, NS, 10University of Manitoba, Winnipeg, MB, 11Université de Sherbrooke, Sherbrooke, QC, 12University Health Network, University of Toronto, Toronto, ON, 13University of Western Ontario, London, ON, 14The Ottawa Hospital, Ottawa, ON, 15University of Calgary, Calgary, AB

OBJECTIVES: Shorter duration antibiotic treatment is sufficient for a range of bacterial infections, but has not been adequately studied for bloodstream infections. We sought to test the feasibility of a trial comparing 7 versus 14 days of antibiotics for critically ill patients with bloodstream infections.

METHODS: We conducted a pilot randomized clinical trial (RCT) of 7 versus 14 days of antibiotic treatment among critically ill patients with bloodstream infection, across 11 intensive care units (ICUs). Eligible patients were adults with a positive blood culture yielding pathogenic bacteria identified while in ICU. We excluded patients with severe immunosuppression, foci of infection with an established requirement for prolonged treatment, single cultures with potential contaminants, or cultures yielding Staphylococcus aureus or fungi. The primary feasibility outcomes were recruitment rate and adherence to treatment duration protocol. Secondary clinical outcomes were analyzed without separation by treatment group.

RESULTS: We successfully achieved our target sample size (n=115) and average recruitment rate of 1 (interquartile range [IQR] 0.3-1.5) patient/ICU/month. Adherence to treatment duration (within ± 2 days) was achieved in 89/115 (77%) patients, and differed by underlying source of infection: 27/32 (84%) lung; 18/29 (62%) intra-abdominal; 20/26 (77%) urinary tract; 8/9 (89%) vascular-catheter; 4/4 (100%) skin and soft-tissue; 2/4 (50%) other; and 10/11 (91%) unknown sources of infection. Patients experienced a median (IQR) 14 (8-17) antibiotic-free-days (of the 28 days after blood cultures were sampled). Antibiotic-related adverse events included hepatitis in 1 (1%) patient, C. difficile in 4 (4%), secondary infection with highly-resistant microorganisms in 10 (9%), and no detected allergy or kidney injury.

CONCLUSION: It is feasible to conduct a multicentre RCT to establish whether 7 days of antibiotics is associated with non-inferior 90-day survival compared with 14 days of treatment; the BALANCE RCT is now funded and underway.

B02
Implementation and Mixed Methods Evaluation of an Antimicrobial Stewardship Service with Hospitalist Physicians at a Large Tertiary Care Urban Centre

BR DALTON1, D Sabuda1, J Bonnett1, D Werry1, C Ondro1, PM Libin1, JM Conly1,2

1Alberta Health Services, Calgary Zone, Calgary, AB, 2Cumming School of Medicine, University of Calgary, Calgary, AB

INTRODUCTION: Antimicrobial resistance (AR) is a global health crisis. High intensity use of antimicrobials in hospitals creates an environment that selects for AR organisms. Opportunities to improve antimicrobial prescribing on the hospitalist service at our centre were recognized and following consultation a prospective audit and feedback program (PAAFP) was initiated in May 2015.

METHODS: The antimicrobial stewardship (AS) service involved the assessment of hospitalist patients by infectious diseases trained pharmacists regarding need for antimicrobials, specific agents used, route of administration and duration of therapy. Assessments 5 days/week were supported by an on-call infectious diseases physician (IDP). Suggestions were tracked and an assessment for acceptance was conducted. Use of
antimicrobials was assessed by monthly compilation of days of therapy per 100 patient days (DOT/100PD) using electronic medication administration record and hospitalist census data. An uncontrolled pre/post-implementation evaluation was conducted using interrupted time series analysis (ITS) to assess the statistical significance of the change at 10 months post- versus a 12-month pre-implementation baseline. We also tracked if any unusual outbreaks occurred during this period.

RESULTS: At ten months, post-implementation 678 suggestions involving 445 patients were made. Overall 79.8% (355) of patients tracked had suggestions wholly or partially accepted. The most common type of suggestion was “stop antibiotics” (23%), “change route of antibiotics” (20%) and “narrow spectrum of antibiotic” (17%). Significant changes in use of all antimicrobials (pre- versus post- monthly average decrease = 5.0 DOT/100 PD, slope change -1.35, p= 0.035) and proportion antibiotics given by parenteral route (pre- versus post-; 45.2% vs 44.7%, slope change -0.013, p=0.011) were observed.

DISCUSSION: High suggestion acceptance and a significant reduction in antimicrobial use was observed. The experience from this project will be applied to a medical teaching unit AS service and other AS activities. A pharmacist led, IDP supported, PAAFP for the hospitalist service was successfully adopted and had high levels of acceptance.

B03.S
Antimicrobial Stewardship in Long-term Care: A Retrospective Cohort
C PENNEY1, S Boyd1, A Mansfield1, J Dalton2, J O’Keefe2, P Daley1

1Memorial University of Newfoundland, St. John’s, NL, 2Eastern Health - Regional Health Authority, St. John’s, NL

BACKGROUND: Long term care (LTC) is a setting in which antimicrobial stewardship effort may create significant benefit because prevalence of antibiotic use in LTC is high.

OBJECTIVES: 1. To retrospectively measure antibiotic use in ten LTC facilities during a one-year period. 2. To determine the appropriateness of antimicrobial prescription based on published guidelines. 3. To report the cost associated with inappropriate antibiotic use. 4. To correlate antibiotic selection with susceptibility result for urine cultures.

METHODS: Prescription data between January 2015 to January 2016 was collected from the pharmacy database for LTC facilities located within the regional health authority. 500 prescriptions were randomly selected (proportionally by facility size) for chart review.

RESULTS: Of the 3,148 total antibiotic prescriptions given to 1,313 residents, 800 (25.4%) were quinolones, 570 (18.1%) were cephalosporins, 518 (16.5%) were amnopenicillins, 426 (13.5%) were urinary anti-infectives and 391 (12.4%) were sulfonamides. The remaining 443 (14.1%) were other drug classes. Of the 500 randomly selected prescriptions, 448 charts (89.6%) were available for review (9 prescriptions were for conditions which are not included in published guidelines. 2 prescriptions were not antibiotics. 44 prescriptions were unable to be assessed due to missing information). Mean age of included residents was 82.6 ± 12.1 years. 272 (60.7%) were female with an average activities of daily living score of 19.4 ± 8.4 out of 28. Urinary tract infection was the most common indication (176/448 prescriptions, 39.2%, 29.5% appropriate), followed by lower respiratory tract infection (144/448, 31.0%, 36.1% appropriate) and skin and soft tissue infection (75, 16.7%, 32.2% appropriate). 265/448 (59.2%) of prescriptions did NOT meet the minimum indication criteria based on published guidelines. Total cost of 265 inappropriate prescriptions was $2,055.85. Among urine cultures, 125 prescriptions had susceptibility available, and 80/125 (64.0%) prescriptions matched susceptibility results.

CONCLUSIONS: There is a very high proportion of inappropriate antibiotic prescription in LTC. The highest proportion of inappropriate prescription is for urinary tract infection. Many of these are inappropriate treatment of asymptomatic bacteriuria based on nurse-initiated urine culture testing.

JA SRIGLEY1,2 , L Pelude3 , N Thampi4,5 , J Vayalumkal6,7 , K Amaratunga1 , K Bush1 , JC Collett1 , C Ellis9 , J Embree10 , L Forrester11 , C Frenette12,13 , E Henderson7 , M John9 , BL Johnston15 , JM Langley16,17 , BE Lee18 , M-A Lefebvre19 , C Lemieux20,21 , A McGeer22 , E Noseworthy23,1 , C Quach24,25 , S Richardson21,26 , M Science21,26 , S Smith18,27 , J So22 , K Suh28,29 , G Taylor18,27 , and Canadian Nosocomial Infection Surveillance Program

1BC Children’s & Women’s Hospitals, Vancouver, BC, 2University of British Columbia, Vancouver, BC, 3Public Health Agency of Canada, Ottawa, ON, 4Children’s Hospital of Eastern Ontario, Ottawa, ON, 5University of Ottawa, Ottawa, ON, 6Alberta Children’s Hospital, Department of Pediatrics, Calgary, AB, 7University of Calgary, Calgary, AB, 8Infection Prevention and Control Program, Alberta Health Services, Calgary, AB, 9The Moncton Hospital, Horizon Health Network, Moncton, NB, 10The Children’s Hospital, Winnipeg, MB, 11Vancouver Coastal Health, Vancouver, BC, 12McGill University Health Centre, Montréal, QC, 13McGill University, Montréal, QC, 14London Health Sciences Centre, London, ON, 15Nova Scotia Health Authority, Halifax, NS, 16WK Health Centre, Halifax, NS, 17Dalhousie University, Halifax, NS, 18University of Alberta, Edmonton, AB, 19Montreal Children’s Hospital, McGill University Health Centre, Montréal, QC, 20Infection Prevention and Control, University Health Network, Toronto, ON, 21University of Toronto, Toronto, ON, 22Sinai Health System, Toronto, ON, 23Eastern Health, Health Sciences Centre, St. John’s, NF, 24CHU Sainte-Justine, Sainte-Justine, QC, 25Department of Microbiology, Infectious Diseases & Immunology, Université de Montréal, Montréal, QC, 26Department of Paediatrics, The Hospital for Sick Children, Toronto, ON, 27University of Alberta Hospital, Edmonton, AB, 28Infection Prevention and Control, The Ottawa Hospital, Ottawa, ON, 29Ottawa Hospital Research Institute, Ottawa, ON

OBJECTIVE: To describe the epidemiology of health care-associated central line-associated bloodstream infections (CLABSIs) in Canadian pediatric and neonatal intensive care units (PICUs, NICUs).

METHODS: As of 2015, sixty-two acute care hospitals across Canada participated in the Canadian Nosocomial Infection Surveillance Program (CNISP), a collaboration between the Public Health Agency of Canada and the Association of Medical Microbiology and Infectious Disease Canada. An average of 10 PICUs and 16 NICUs per year contributed CLABSI data from January 1, 2009, to December 31, 2015 using standardized definitions based on the Centers for Disease Control/National Healthcare Safety Network. Data were extracted using laboratory-based surveillance and review of medical records. Rates were calculated and expressed per 1,000 line days.

RESULTS: The rate of CLABSI in PICUs was 2.15 in 2009, which dropped to a nadir of 1.33 in 2011 and increased to 2.06 by 2015 (p = 0.84 for 2015 compared to 2009). The NICU CLABSI rate followed a similar pattern, with a peak of 5.72 in 2009, decreasing to 2.19 by 2012, and increasing to 2.46 in 2015 (p < 0.001 for 2015 compared to 2009). CLABSI rates in NICUs were inversely correlated with birth weight (BW), with an overall rate of 5.70 observed in low BW (≤750 grams) neonates. Neonates with BW >1,500 grams had the greatest decrease in rates in 2015 compared to 2009 (86%). The most common organisms isolated in PICUs as of 2015 were coagulase-negative Staphylococcus (33%), Enterococcus species (14%), and Staphylococcus aureus (10%). In NICUs the most common organisms were coagulase-negative Staphylococcus (41%) and S. aureus (11%), followed by Enterococcus species, E. coli, and Klebsiella species (9% each). In 2015, morality rates (30 days post positive blood culture) were 8% in NICUs and 11% in PICUs.

CONCLUSIONS: Based on CNISP data from 2009-2015, PICU CLABSI rates have not significantly changed but NICU CLABSI rates have dropped more than twofold in the same time period among participating Canadian sites. Renewed efforts on CLABSI prevention, particularly in PICUs, may be warranted.

B05 Quantitative Antimicrobial Usage Surveillance amongst CNISP Hospital Sites across Canada Stratified by Bed Sizes: Pilot Study Results 2009 to 2013

K Abdesselam1 , JM Conly2 , GE Evans3 , KC Katz4 , G Germain5 , P Kibsey6 , A McGeer7 , L Pelude3 , AE Simor8 , K Suh9 , D Thirion10 , K Weiss11 , K Amaratunga1 , D Gravel1 , and Canadian Nosocomial Infection Surveillance Program

1Center for Communicable Diseases and Infection Control, Ottawa, ON, 2Cumming School of Medicine, University of Calgary, Calgary, AB, 3Kingston General Hospital, Queen’s University, Kingston, ON, 4North York General Hospital, North York, ON, 5Health PEI, Charlottetown, PE, 6Vancouver Island Health, Victoria, BC, 7Mount Sinai Hospital, Toronto, ON, 8Sunnybrook Health Sciences, Toronto, ON, 9The Ottawa Hospital, Ottawa, ON, 10Faculty of Pharmacy, University of Montreal, Montreal, QC, 11Jewish General Hospital, Montreal, QC
BACKGROUND: Antimicrobial resistance (AMR) is a serious and growing issue with global ramifications. Antimicrobial utilization (AMU) is of particular importance in understanding the emergence of AMR. The aim of this pilot study was to assess the feasibility and identify the gaps/limitations of surveying AMU inpatients in acute tertiary care hospitals across Canada.

OBJECTIVES: To identify trends and patterns of AMU in acute-care hospitals in Canada.

METHODS: A total of 28 CNISP hospitals (21 adult, 4 mixed and 3 pediatric) across 10 provinces participated in a 5-fiscal year pilot surveillance study. Complete data was obtained on 65 J01 antimicrobials from 23 CNISP hospital pharmacies and analyzed using Defined Daily Doses (DDD) per 1000 hospital days (or patient-days) as per the World Health Organization, for each class of antibacterial (ATC code J01A-X). A descriptive epidemiologic analysis was conducted nationally stratified by bed size, which were categorized as follows: ≤ 200, 201-500, >500.

RESULTS: Overall AMU in sites ≤ 200 beds decreased from 629.57 to 597.3 DDD/1,000 patient-days between 2009-2013. In sites with 201-500 and >500 beds, increases in AMU of 596.6 to 608.3 and 386.4 to 627.6 DDD/1,000 patient-days, respectively, were demonstrated between 2009-2013. The differences of the mean AMU during the 5-fiscal year period, amongst the stratified bed sizes was not significantly different (p=0.99). The top 6 antimicrobials used in the 3 bed size categories were the following: cefazolin, ceftriaxone, ciprofloxacin, metronidazole, Piperacillin/tazobactam and vancomycin.

CONCLUSIONS: These nationally collated findings illustrate the differences in AMU by bed size and suggest a shift has occurred over the 5-year study period. They also emphasize the need for active ongoing surveillance activities on AMU within CNISP to monitor trends and lay the groundwork for further improvements in the AMU surveillance protocol and the establishment of unique Canadian benchmarks for AMU.

Thursday, May 4, 2017
11:15–12:30 Session C
Room: Birchwood Ballroom

C01
Fecal Microbiota Transplantation (FMT) Programs in Southern Ontario — A Descriptive Survey
A. Paterson1, S. Surangiwala1,3,4, S. Hota1,2, SM. Poutanen1,2,3, Microbiota Therapeutics Outcomes Program (MTOP)1,2,3, Southern Ontario Fecal Transplant (SOFT) GROUP1,2,3, McMaster University4

1 Sinai Health System, Toronto, ON, 2 University Health Network, Toronto, ON, 3 University of Toronto, Toronto, ON, 4 McMaster University, Hamilton, ON

BACKGROUND: FMT is an emerging therapy gaining significant traction as a treatment for a variety of illnesses, the most established being Clostridium difficile infection (CDI). Health Canada released a guidance document to provide direction with regards to donor screening criteria. Although FMT is increasingly used, there are no standards for FMT preparation and administration and there has not been a review of FMT methodologies across Canada. This survey describes the state of FMT programs within Southern Ontario.

METHODS: Physician leads of known FMT programs in Southern Ontario (Southern Ontario Fecal Transplant (SOFT) group), representing nine institutions in six cities, were contacted. A web-based survey was administered to evaluate criteria regarding each institution’s FMT program, donor selection and screening criteria, FMT manufacturing protocol, biosafety procedures, patient subgroups receiving the procedure, clinical procedures for FMT administration, and infection control procedures. The survey was comprised of 59 questions and took approximately 20 minutes to complete.

RESULTS: An estimated 1300 FMTs were performed across all institutions, the majority in the past 8 years. All institutions administer FMT to patients with recurrent CDI, but one also uses FMT for initial CDI treatment. 33% also administer FMT to immunocompromised patients with CDI. The majority of institutions use frozen fecal filtrate (either -20°C or -80°C, with or without glycerol) thawed to room temperature as opposed to fresh filtrate. 85% of institutions administer FMT via enema but with significant variation in the amount of stool (20-100g) and the volume of filtrate (50-300mL) used.
in addition to the number of FMTs performed per patient. All organizations generally follow Health Canada recommendations for donor screening, but with variable screening modalities.

CONCLUSIONS: Considerable variability exists in FMT patient selection, manufacturing, storage and administration; further studies are needed to standardize these procedures. Donor screening as recommended by Health Canada is generally followed, but is extensive and is currently addressed using various modalities at multiple sites. To facilitate adhering to Health Canada’s donor stool screening criteria and to reduce screening costs, centralized stool banks to select, screen, and process donor stool would be optimal.

C02 Quality of Assessment and Linkage to Care for Newly Diagnosed Chronic Hepatitis B Patients

LT REMINGTON¹, M Osman², KA Simmonds²,⁴,⁶, C Charlton¹,⁵, K Doucette¹

¹Division of Infectious Diseases, University of Alberta, Edmonton, AB, ²Alberta Health, Edmonton, AB, ³Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, ⁴Department of Community Health Sciences, University of Calgary, Calgary, AB, ⁵Provincial Laboratory for Public Health, Edmonton, AB, ⁶School of Public Health, University of Alberta, Edmonton, AB

Patients with chronic hepatitis B (CHB) infection require lifelong monitoring and assessment to identify those who require treatment or have complications such as hepatocellular carcinoma (HCC). A retrospective study was performed to evaluate the level of care provided to newly diagnosed CHB patients in the province of Alberta. The Alberta Health Communicable Disease Reporting System was used to identify adult CHB cases between January 1st 2008 and December 31st 2012 with follow-up through 2014. 3452 patients were identified with a mean age of 39.22 years (range 18-99). 45.6% of all CHB cases were female; of those, 38.3% were diagnosed during pregnancy. Amongst patients with a known country of origin, 85.9% had immigrated from South East Asia, India, or Africa. The majority (85.7%) of patients were living in large metropolitan centres at the time of diagnosis. Provider identifications from an Alberta billing database showed that only 13% of the 3452 patients were seen by a specialist in viral hepatitis. Mean time from diagnosis to specialist appointment was 318.5 days (median 107). Assessment for appropriate baseline investigations showed that 61.8% of patients had at least one hepatitis B DNA measured in the study period. 54.3% and 55.5% had at least one HBeAg and anti-HBe measured respectively. 82.1% had at least one ALT measured. 47.9% of patients had all parameters available for staging analysis. 59% were in the inactive phase of disease, 4% were immune tolerant, 12% were in the immune clearance phase, and 22% had HBeAg negative CHB. Adequate screening for HCC was defined as yearly abdominal ultrasounds in Asian males ≥40 years of age and Asian women ≥50 years of age. 586 patients met age and ethnicity criteria; of these, 387 (66%) patients were screened by ultrasound within 1 year of diagnosis. However, only 23% of the 387 patients subsequently had appropriate (yearly) HCC interval screening.

Our study shows that, the majority of patients with newly diagnosed CHB in Alberta have not been seen by a viral hepatitis specialist and often have incomplete baseline assessment. HCC screening is poorly adhered to, even in high-risk patients. Interventions to improve the quality of care in those with CHB need to be evaluated.

C03 The Wellness Wheel: A Mobile Outreach Clinic to Address HIV and Hepatitis C in Saskatchewan First Nation Communities

S SKINNER¹,²

¹Regina Qu’Appelle Health Region, Regina, SK, ²University of Saskatchewan, Regina, SK

OBJECTIVES: For the past ten years, Saskatchewan has had the highest rates of HIV and hepatitis C (HCV) in Canada. The burden of these infections is highest among Indigenous peoples, particularly those living on reserve with regional HIV rates 18-times the national average. Racism, stigma, discrimination and previous negative experiences with mainstream healthcare services are major barriers to accessing healthcare services for Indigenous people on-reserve. These issues lead to underutilization of healthcare services and poor health outcomes. To address these barriers, a new healthcare delivery model has been implemented for individuals living on-reserve in Saskatchewan. The primary objective of this delivery model is to improve access to standardised care on-reserve for residents living with HIV, HCV and other chronic diseases.

METHODS: Since 2011, a mobile outreach approach for HIV and HCV care for First Nations people
on-reserve has been undertaken whereby physician, diagnostic (i.e. testing, fibroscan) and clinical care services are provided directly in the community. This model uses a partnership between physicians, local Indigenous leaders and First Nation Inuit Health Branch to develop, implement and review programming. Clinics are operated using shared care, where physicians, nurses and First Nation communities work together to increase service and treatment uptake, with ownership of the programs belonging to the individual communities.

RESULTS: Indigenous community uptake and partnership development have been highly successful. Clinics have expanded from one community site in 2011 to 10 sites directly serving 24 First Nations communities at the end of 2016. Engagement and treatment outcomes for HIV and HCV positive individuals receiving care in their local community have also been excellent with some achieving 90/90/90 targets.

CONCLUSIONS: A new innovative system of health care delivery has led to positive partnerships and treatment outcomes for Indigenous communities affected by HIV and HCV in Saskatchewan. Indigenous health management requires an innovative approach that is community driven to improve outcomes for Indigenous peoples.

**C04.S**

Treatment Outcome in Chronic Hepatitis C Genotype 1 Patients Treated With 8 Weeks vs. 12 Weeks of Ledipasvir/Sofosbuvir based on Viral Load Criteria as Determined using The Abbott RealTime Assay

M REZAEAAVAL1, S Surnner2, S Shafran1,3, K Doucette1,3

1Department of Medicine, University of Alberta, Edmonton, AB, 2Hepatitis Support Program, AB Health Services, Edmonton, AB, 3Division Of Infectious Diseases, University of Alberta, Edmonton, AB

BACKGROUND: Based on post hoc analysis of the ION-3 study and observational data, shortened therapy of 8 rather than 12 weeks of Ledipasvir/Sofosbuvir (LDV/SOF) may be considered for treatment-naive, non-cirrhotic, genotype 1 chronic HCV patients with baseline HCV RNA < 6 million IU/mL. This HCV RNA threshold was established in a trial using the Cobas® TaqMan assay. Recent data highlight interassay variability between this and the Abbott RealTime (ART) assay, used in many clinical laboratories. Based on this, some have suggested a threshold of 2.2 million IU/mL using the ART assay. Our objective was to determine the sustained virologic response at 12 weeks (SVR12) with 8 vs 12 weeks LDV/SOF in those with baseline HCV RNA <6 million IU/mL using the ART assay.

METHODS: A retrospective, single centre cohort study was done including all HCV treatment naive, genotype 1 noncirrhotic patients treated with LDV/SOF Jan/15 to June/16.

RESULTS: Among 212 patients meeting criteria, 69.7% were male, median age was 57 years (IQR 51-62), median BMI 27 (IQR 24-30.6). Genotype was 1a in 71.2%, 1b in 17.9% and other 1 in 10.8%. Fibrosis stage: 26.4% F0/1, 48.1% F2 and 25.5% F3. The median baseline HCV RNA was 826,479 IU/mL with 199 patients (93.9%) < 6 million IU/mL. Of these, 129 (64.8%) received 8 weeks of therapy. SVR12 was similar in those treated with 8 vs 12 weeks [94.5% vs 94.3%; p=0.95]. If 2.2 million IU/mL were used as the threshold to shorten therapy, only 75% of patients would have been eligible. Private vs public medication insurance was associated with 12 weeks of therapy, despite meeting viral load criteria for 8 weeks (p=0.03).

CONCLUSION: In our cohort, using the ART assay, 94 % of HCV treatment naive, genotype 1 noncirrhotic patients were eligible for 8 weeks of LDV/SOF using a threshold of <6 million IU/mL. The SVR12 in those meeting viral load criteria and treated for 8 vs 12 weeks did not differ, suggesting this is safe and more cost effective than a proposed ART assay specific threshold of 2.2 million IU/mL.

**C05**

Creating Capacity for HIV Care in Rural and Remote Communities of Saskatchewan

G Shumilak1, B WUDEL2, E Stevens1, K Ng1, A Mah1, K Stewart2, S Sanche1, K Kasper3, M Hull1, N Press1

1University of British Columbia, Vancouver, BC, 2University of Saskatchewan, Saskatoon, SK, 3University of Manitoba, Winnipeg, MB

OBJECTIVES: Saskatchewan continues to experience an outbreak of HIV infection that is disproportionately impacting rural and remote communities. Lack of access to HIV care providers, limited HIV awareness, stigma,
and isolated geography are significant barriers to implementing routine HIV testing programs, early initiation of cART, and retaining individuals in care. Decentralizing HIV care by enabling family physicians in rural and remote communities to engage in routine HIV testing and longitudinal care of persons living with HIV has been identified as a potential strategy to help end the outbreak.

METHODS: A focused educational seminar targeting family physicians and allied healthcare providers was developed. The seminar contained 12 hours of material and employed both didactic and interactive teaching techniques. Material focused on the 4 domains of HIV Pathophysiology, HIV Transmission and Diagnostics, Principles of Antiretroviral Use, and Longitudinal Care of Persons Living with HIV. Paired-samples t-test was conducted to compare participant knowledge scores prior to the seminar and following completion.

RESULTS: The seminar was delivered to 61 healthcare providers at 4 sites. 37 participants consented to the study. Knowledge scores significantly improved in all 4 domains. There was significant improvement when comparing overall scores prior to the seminar (M=28.5%, SD=16.1%) and following completion (M=88.9%, SD=11.6%); t(36)= 17.9, p<0.01. Comfort in providing HIV-related care significantly improved when comparing scores prior to the seminar (M=2.0, SD=1.4) and following completion (M=7.4, SD=1.5); t(36)= 18.3, p<0.01. The level of optimism regarding the state of the HIV outbreak minimally improved when comparing scores prior to the seminar (M=4.0, SD=1.9) and following completion (M=5.3, SD=2.1); t(36)= 3.9, p<0.01.

CONCLUSION: Focused educational seminars targeting family physicians and allied healthcare providers are an effective intervention to increase the knowledge, comfort, and capacity to provide HIV care to persons living with HIV in rural and remote communities.

Friday, May 5, 2017
11:15-12:30 Session D
Room: Willow

D01
Human seroprevalence of Borrelia miyamotoi in Manitoba, Canada: 2011-2014
K KADKHODA1,2, C Dumouchel3, J Brancato3, A Gretchen3, P Krause3

1 Cadham Provincial Public Health Laboratory, Winnipeg, MB, 2 Department of Medical Microbiology and Infectious Diseases and Department of Immunology, University of Manitoba, Winnipeg, MB, 3 Yale School of Public Health, New Haven, CT, USA

INTRODUCTION & OBJECTIVE: Hard tick-borne relapsing fever caused by Borrelia miyamotoi has been reported in Europe, Japan, and the north-eastern United States. Despite the fact that Manitoba has established black-legged tick populations but no studies done in Manitoba to determine the seroprevalence of B. miyamotoi in this province. To the best of our knowledge, similar studies have not been done in other Canadian provinces. We sought to investigate the presence of B. miyamotoi in humans retrospectively in Manitoba.

METHODS: 250 residual sera were originally collected for the purposes of Lyme disease diagnosis and sent to Cadham Provincial Laboratory from 2011 to 2014 were anonymized and stored. The sera were stratified based on their Lyme serology results into four groups: C6 peptide ELISA negative, C6 peptide ELISA high positive Lyme immunoblot IgM/IgG negative, Lyme immunoblot IgM+/IgG-, and Lyme immunoblot IgG+ (confirmed). The screening and confirmatory test for B. miyamotoi serology was done using in-house developed GlpQ-based ELISA and western blot at School of Public Health, Yale University.

RESULTS: 24/250 (9.6%) sera tested confirmed positive for B. miyamotoi IgG. The positivity among the above-mentioned four groups was: 12/123 (9.75%), 1/30 (3.3%), 0/43 (0%), 11/54 (20.37%). Subjects who were B. miyamotoi sero-positive were predominantly male (54%) and were younger (32 years) on average than those who were sero-negative (44 years). Subjects who were sero-positive for B. burgdorferi were significantly more likely to be B. miyamotoi sero-positive than those who were B. burgdorferi sero-negative (the first 3 groups) (20.3%
vs. 6.6%, respectively, \( P= 0.0093, [\text{OR} 3.6, 95\% \text{ CI}: 1.5 \text{ to } 8.5]\).

**CONCLUSION:** This is the first report on the presence *B. miyamotoi* among humans in Canada. Similar studies in other jurisdictions should raise awareness among clinicians and, also pave the way to make this emerging tick-borne infectious agent notifiable in Canada.

**D02**

**Evaluation of the ZEUS ELISA™ *Borrelia* VlsE1/pepC10 IgG/IgM Enzyme Immunoassay (EIA) for Serological Detection of Lyme Disease**

TF Hatchette1,2, J LeBlanc1, C Jackson1, C Roberts1, K Bernat3, C Loomer3, A Dibernardo3, LR Lindsay3  
1Nova Scotia Health Authority, Halifax, NS, 2Dalhousie University, Halifax, NS, 3National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB

**BACKGROUND:** Currently, the serological diagnosis of *Borrelia burgdorferi* infection in Canada is based on the two-step algorithm recommended by the National Microbiology Laboratory (NML) and the Centers for Disease Control (CDC) consisting of an enzyme immunoassay (EIA) followed by IgM and/or IgG immunoblots (IB).

**OBJECTIVE:** This study evaluated the performance of the ZEUS ELISA™ *Borrelia* VlsE1/pepC10 IgG/IgM Enzyme Immunoassay (EIA) compared to the whole cell (WC) lysate EIA (ZEUS ELISA *Borrelia burgdorferi* IgG/IgM) and the C6 EIA (Immunetics™) in the two-step algorithm for serological diagnosis of *B. burgdorferi* infection.

**METHODS:** Ninety residual sera from the QEII laboratory previously submitted for Lyme disease serology (including both IB positive and negative specimens) and 60 specimens from healthy controls were tested by each of the three EIAs. Specimens that were positive or equivocal in the EIAs were sent to the NML for IB testing and scored according to the CDC criteria. In addition, the NML has defined “borderline” categories for sera where 4 of 10 significant bands on the IgG are reactive, and either a weakly reactive fifth band or the VlsE band is present, while for the IgM only the p25 band is reactive.

**RESULTS:** Overall 66/90 (49 positive; 11 negative) results were concordant between all three EIAs. Eleven specimens were positive only by the WC EIA. The VlsE1/pepC10 EIA identified 11 specimens that were not detected by the C6 EIA (WIB - = 5; IgM IB +/ IgG IB - = 3; IgG IB + = 3). In our specificity panel, 10% of specimens (6/60) were positive on the VlsE1/pepC10 EIA while all were negative on IgG IB; 2 were “borderline” by IgM IB.

**CONCLUSIONS:** The ZEUS ELISA *Borrelia* VlsE1/pepC10 IgG/IgM EIA identified 11 specimens that were not detected using the C6 EIA; and these samples generated positive \((n=4)\) or borderline \((n=3)\) results on the IgG immunoblots which may indicate that it is more sensitive than the C6 EIA. Without clinical information, it is not possible to determine if positive EIA results in the specimens with negative immunoblots were due to detection of early serologic response in acute localized infection or false positive EIA results. The specificity of the VlsE1/pepC10 EIA was 90% and this supports the need to continue supplemental testing with immunoblots.

**D03**

**Specimens Yielding False-Reactive Results on the Abbott Architect HIV Ag/Ab Combo Assay Leading to Misdiagnosis and Negative Patient Impact**

P Lacap1, K Kadkhoda2, J Gill3, D Caswell4, PN Levett4, S Lavoie1, K Kadivar1, P Sandstrom1, J Kim1  
1Public Health Agency of Canada, Winnipeg, MB, 2Cadham Provincial Health Laboratory, Winnipeg, MB, 3Alberta Health Services, Calgary, AB, 4Saskatchewan Disease Control Laboratory, Regina, SK

**OBJECTIVES:** Fourth (4th) generation immunoassays, which are now able to detect HIV-1 p24 antigen, have reduced the window period, bringing it closer to HIV-1 nucleic acid tests (NAT). Here we present results on reference specimens which initially tested repeatedly-reactive on the Abbott Architect HIV Ag/Ab Combo assay and were ultimately confirmed as HIV-negative.

**METHODS:** Sample criteria included: (a) specimens from provincial public health laboratories that were reactive on the Architect and (b) diagnosed HIV-negative by the NLHRS via its serology and/or PCR testing algorithm. These specimens were then tested on an alternative 4th generation Combo test (Siemens ADVIA Centaur HIV Ag/Ab Combo Assay). A select number
of samples were further examined using heterophilic blocking tubes (antibody and antigen).

**RESULTS:** The majority of specimens submitted as reactive on the Architect tested negative on the NLHRS serology and/or PCR algorithms. S/Co values on an alternative 4th gen EIA (Siemens) were below 1.0, consistent with values from HIV-negative specimens. After treating a subset of samples with heterophilic blocking agents, we saw a reduction or elimination of a signal when tested again on the Architect.

**CONCLUSIONS:** According to the new CLSI M-53 algorithm, a sample is first tested on a 4th generation HIV combo immunoassay. This test should have very high sensitivity and high specificity to ensure that truly positive specimens are not missed and truly negative specimens are not further tested. Here we demonstrate that specimens may generate false reactive values when tested on the Architect platform. The cause of this cross reactivity is under investigation.

**D04**

**The Diagnostic Yield of Nucleic Acid Testing for Acute HIV Infection Is Reduced by Fourth Generation EIA Screening**

N CHAHIL1, D Cook1, K Chu1, A Mak1, A Jassem1,2, M Krajden1,2

1British Columbia Centre for Disease Control Public Health Laboratory, Vancouver, BC, 2Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC

**OBJECTIVES:** Detection of pre- and early seroconversion acute HIV infection (AHI) is important to reduce onward transmission. We compared the yield of AHI diagnosis during 15 month periods prior and after a switch to 4th generation (gen) EIA screening from 3rd gen EIA.

**METHODS:** Sera submitted to the BCCDC Public Health Laboratory were screened for HIV antibodies by 3rd gen EIA (Siemens ADVIA Centaur® HIV 1/O/2) from Feb 2014 to May 2015 and for HIV p24 antigen as well as HIV antibody by 4th gen EIA (Siemens ADVIA Centaur® HIV Combo) from Jun 2015 to Aug 2016. For individuals at high risk of HIV infection, pooled nucleic acid testing (NAT) typically in pools of 24 samples (Roche COBAS® Amplicore/ COBAS® TaqMan HIV-1 Test v.2) was performed during both periods on EIA non-reactive samples. Individual HIV NAT testing was also performed on samples with weak EIA signals and seronegative prenatal women. Rates of pre-seroconversion AHI (EIA non-reactive and NAT positive), early seroconversion AHI (EIA reactive, Western blot negative or indeterminate, NAT positive) and established HIV infection (EIA reactive, Western blot positive) were compared between the two periods.

**RESULTS:** A total of 403,092 and 478,693 specimens were screened by EIA during the two periods, respectively. A total of 499 and 553 pooled NAT were performed (representing ~3% of samples). Overall, 544 (by 3rd gen EIA screening) and 560 (by 4th gen EIA screening) HIV infections were diagnosed for a positivity rate of 1.3% and 1.2%, respectively. Of the HIV infections diagnosed, 19 (3.5%) cases of pre-seroconversion AHI were detected during the 3rd gen EIA screening period vs. 6 (1.1%; p<0.01) during the 4rd gen EIA screening period. Using pooled NAT specifically, 10 (1.8%) vs. 5 (0.9%; p=0.2) cases of pre-seroconversion AHI were detected, respectively. For early seroconversion AHI, 32 (5.9%) vs. 55 (9.8%; p=0.02) cases were detected between the time periods, while 493 (90.6%) vs. 499 (89.1%; p=0.4) established HIV infections were detected.

**CONCLUSIONS:** The change from 3rd gen EIA to 4th gen EIA screening for diagnosis of HIV infection significantly decreased the number of pre-seroconversion AHI cases detected by NAT, while early seroconversion AHI detection by NAT increased. A reduction in the number of pre-seroconversion AHI cases detected by pooled NAT was also observed following implementation of 4th gen EIA screening but the finding was not significant. The cost-effectiveness of HIV NAT for diagnosis of AHI in screen-negative individuals is likely to be reduced when using 4th gen EIA as the primary HIV screening test.

**D05**

**The Use of Antibody Avidity Based on Multiplex Microsphere Immunoassay to Differentiate Between Acute and Past Zika and/or Dengue Infections**

A FURUYA1, P Shi2,3,4, S Wong1

1Wadsworth Center, Albany, NY, USA, 2Department of Biochemistry & Molecular Biology, University of Texas Medical Branch, Galveston, TX, USA, 3Department of Pharmacology & Toxicology, University of Texas Medical Branch, Galveston, TX, USA, 4Sealy Center for Structural Biology & Molecular Biophysics, University of Texas Medical Branch, Galveston, TX, USA
Zika virus disease is caused by a virus belonging to the Flaviviridae therefore it is related to dengue, yellow fever, West Nile and Japanese encephalitis viruses. Infection with Zika virus triggers the production of highly cross-reactive antibodies among flaviviruses, making it difficult to diagnose. Although Zika virus infection causes mild disease with symptoms ranging from fever, headache, and joint pain, it is asymptomatic in 80% of cases. However, of major concern is the explosive epidemic of microcephaly in newborns and Guillain–Barré syndrome in adults. For this reason, accurate diagnostic tests are needed to distinguish Zika virus from other flaviviruses. Our lab recently developed a multiplex microsphere immunoassay (MIA) that discriminates dengue from Zika virus by capturing antibodies against viral envelope as well as the virus-specific non-structural proteins from a small amount of patient sera. By modifying this test, we have developed an avidity assay that distinguishes between acute, more recent (intermediate) and past Zika and/or dengue infections. Patient serum samples consisting of seroconversion panels, single (Zika or dengue) and dual (Zika and dengue) infection panels were used. All samples were tested for the presence of anti-Zika and/or anti-dengue antibodies and an avidity index was calculated. Panels that exhibited low avidity indices (<40%) were designated acute, panels with medium avidity indices (40-60%) were designated intermediate, whereas panels with high avidity indices (>60%) were designated past infections. The data presented here reveals that it is possible to distinguish between acute, intermediate and past infections as well as determine which infection (Zika or dengue) occurred first based on the calculation of avidity indices.

Friday, May 5, 2017
11:15-12:30 Session E
Room: Pine

E01.S
Hospital-Acquired Methicillin-resistant Staphylococcus aureus Infections in Canada are an Expensive Problem Worth Preventing
DA Waldner1, KA Simmonds2,3,4, EM Kirwin1, AM Joffe1,5, M Varughese1, S Smith1

1University of Alberta, Department of Medicine, Edmonton, AB, 2University of Alberta, School of Public Health, Edmonton, AB, 3Alberta Health, Edmonton, AB, 4University of Calgary, Department of Community Health Sciences, Calgary, AB, 5Alberta Health Services, Edmonton, AB

OBJECTIVES: Approximately 1 in 280 hospitalized patients in Canada dies from a hospital-acquired infection (HAI). Methicillin-resistant Staphylococcus aureus (MRSA) is a well-known cause of HAI and has been extensively studied both in Canada and internationally. However, there remains a paucity of Canadian literature addressing the economic burden associated with hospital-acquired MRSA (HA-MRSA) infections. The objective of this study was to determine the cost of treating HA-MRSA infections in Canadian hospitals.

METHODS: Provincial health record costing data were used to calculate the total healthcare costs for patients admitted to medicine and intensive care units at two tertiary care centers from 2011-2015, who were diagnosed with HA-MRSA infection or colonization. HA-MRSA was defined as a MRSA case occurring ≥48 hours after hospital admission without evidence of an incubating infection at time of admission. Costs attributable to MRSA infection were estimated by case-matching patients, based on clinical mixed groupers, to controls whose admissions were not complicated by MRSA.

RESULTS: 87 patients with HA-MRSA infection and 292 patients with MRSA colonization, with adequate costing data, were identified. The mean length of stay for patients with HA-MRSA infection and MRSA colonization was 15.1 and 11.8 days longer than case-matched controls, respectively. The mean total cost attributable to HA-MRSA infection was estimated at $38,227.55 per patient.

CONCLUSION: The Canadian Nosocomial Infection Surveillance Program estimates the current incidence of HA-MRSA infection in Canadian hospitals is 1,157 cases per year. We estimate that the total cost associated with treating HA-MRSA infections in Canadian hospitals is currently $44,229,275 per year. Interventions aimed at prevention of transmission are a key cost saving measure for the healthcare system.
E02.S  
Prospective Audit and Feedback of Carbapenem Use at a Tertiary Care Hospital in Edmonton AB

B Savaryn1,2, SR Fryters2, AU Chandran1,2

1Royal Alexandra Hospital, Edmonton, AB, 2University of Alberta, Edmonton, AB

BACKGROUND: Prospective audit and feedback (PAF) is a core strategy in an effective antimicrobial stewardship program. PAF is often applied to broad-spectrum antibiotics such as piperacillin-tazobactam and the carbapenems. The primary objective of this study was to evaluate carbapenem prescribing practices at a tertiary care hospital.

METHODS: A hospital-wide carbapenem PAF was performed for a two-week period in the fall of 2016 at the Royal Alexandra Hospital (RAH) in Edmonton, AB. Using the pharmacy software (VAX), new carbapenem prescriptions were identified during the study period. Concordance with Alberta Health Services (AHS) guidelines was determined for each prescription. Written recommendations were provided using a standardized PAF form for each case.

RESULTS: There were 16 carbapenem prescriptions in total during the study period. Four were excluded because they received 0-1 doses. Of the remaining 12 patients, imipenem was administered in 41.7% cases (5/12), meropenem in 33.3% (4/12), and ertapenem in 25% (3/12). Four cases (33.3%) were discordant with AHS guidelines for carbapenem use. Recommendations to alter any aspect of therapy were made in 50.0% (6/12) of cases. The most common recommendation was to narrow therapy. The attending physician accepted the recommendations 83.3% (5/6) of the time. Carbapenems were most frequently prescribed by general internal medicine (GIM) and critical care (ICU) – three each. GIM prescribed inappropriately in 66.7% (2/3) of the time. Cost savings due to change in antibiotics amounted to $1,643.72 over the study period (~$42,737 annually).

CONCLUSIONS: PAF improved carbapenem prescribing practices at RAH during the study period, and also reduced costs related to antibiotic therapy. Repeat, or ongoing carbapenem PAF, to evaluate the retention of improved prescribing, should be considered.

E03  
ESBL Bacteremia Treatment: Carbapenem vs. De-escalated Therapy

M Holm1, A Brooks1,2, N Irfan1, D Mertz1,2,3, M Duffet1

1Hamilton Health Sciences, Hamilton, ON, 2Department of Medicine, McMaster University, Hamilton, ON, 3Michael G. DeGroote Institute for Infectious Diseases Research (IIDR), Hamilton, ON

BACKGROUND: Managing infections caused by Extended Spectrum Beta Lactamase (ESBL) producing organisms is challenging. Empiric treatment generally includes carbapenem therapy. Some clinicians then de-escalate to targeted therapy based on sensitivity results, while others continue carbapenem because of concern that in vitro susceptibility may not consistently predict clinical efficacy.

PURPOSE: Our objective was to compare treatment outcomes (mortality and ESBL reoccurrence) in hospitalized patients with bacteremia caused by ESBL producing E. coli or K. pneumonia treated with carbapenem or de-escalated therapy.

METHODS: This was a retrospective cohort study of adult patients with ESBL bacteremia between January 2011 and April 2016 at the Juravinski and Hamilton General Hospital. We defined treatment failure as death or reoccurrence within 30 days of completion of antimicrobial therapy. We included patients with at least 1 positive culture for ESBL producing E. coli or K. pneumonia and excluded those that died or were discharged within 48 hours of targeted therapy, received an aminoglycoside for targeted treatment or had a carbapenem resistant organism.

RESULTS: We included 112 patients. The median age was 74.5 (IQR 62-82 years) and 45% were female. E. coli and K. pneumonia occurred in 93 (83%) and 19 (17%) patients respectively. Twenty patients (18%) received de-escalated therapy after a median 3 days (IQR 2-7 days). Fifteen patients (75%) received a fluoroquinolone, 5 patients (25%) received co-trimoxazole. Treatment failure were similar (carbapenem versus de-escalated, 34 (37%) versus 5 (25%) patients, p=0.31), mortality occurring in 15 (16.3%) versus 3 (15%) patients (p=0.89) and re-occurrence occurring in 19 (20.7%) versus 2 (10%) of patients (p=0.27). In the de-escalated group, the average duration therapy was shorter (13.4 versus 16.6 days, p=0.06).
CONCLUSIONS: This study suggests that de-escalation of carbapenem therapy led to comparable treatment outcomes and could be considered for patients when appropriate.

E04
Impact of a Choosing Wisely Campaign on Laboratory Utilization of Respiratory Virus Testing in a Paediatric Tertiary Hospital
A Petrich1,2, D Savlov1,2, O Ostrow1,2, J Friedman1,2, S Richardson1,2
1The Hospital for Sick Children, Toronto, ON, 2University of Toronto, Toronto, ON

BACKGROUND: In an effort to introduce improved but more costly respiratory virus testing and to reduce the number of unnecessary nps samples taken, the microbiology laboratory at SickKids Hospital, Toronto, ON participated with a multidisciplinary team on a hospital-wide Choosing Wisely Campaign in 2016.

OBJECTIVES: To stop DFA testing for respiratory viruses and replace with a rapid influenza A/B amplification assay (Alere i) and multiplex PCR (NXTAG™ Respiratory Pathogen Panel, Luminex Corp.) and to launch a hospital-wide Choosing Wisely campaign to decrease the number of unnecessary nps samples.

METHODS: A multidisciplinary team of experts including Microbiology, Paediatric Medicine, Emergency and Infectious Diseases reviewed published guidelines and generated a pathway listing indications for viral respiratory testing. An education program was developed and the electronic order set was modified to force selection of an appropriate indication when ordering. Multiplex PCR (15 viruses) offered daily was considered the routine test for inpatients. A rapid influenza A/B nucleic amplification assay targeted to Emergency was introduced. This assay provided results within 1 hour directing timely use of antiviral therapy and appropriate management of patients. The rapid influenza A/B could only be ordered for inpatients with Microbiologist approval. The main outcome measure was the total number of respiratory virus tests performed hospital-wide and with Emergency and Paediatric Medicine analyzed separately taking into account patient volumes.

RESULTS: Total respiratory virus testing in 2016 decreased by 38.8% and 17.4% compared to 2014 and 2015 respectively. When patient volumes were taken into account respiratory virus testing rates decreased by 38.5% and 32.4% in the ED and Paediatric Medicine respectively, compared with 2014. Testing rates reduced by 14.3% and 28.2% from 2015 rates.

CONCLUSION: A hospital-wide Choosing Wisely campaign to decrease unnecessary respiratory viral testing was successful reducing the total number of tests ordered. Further data analysis to review the clinical impact of improved testing is ongoing.

E05
A Novel Approach to Communication of Antimicrobial Utilization and Resistance Data in British Columbia: Interactive Web-based Dashboards
M McCabe1, L Dale2, M Striha3, DM Patrick1,2
1BC Centre for Disease Control, Vancouver, BC, 2University of British Columbia, Vancouver, BC, 3Simon Fraser University, Burnaby, BC

BACKGROUND: Communication of provincial antimicrobial prescribing and resistance trends to prescribers and the public is an essential component of antimicrobial stewardship. In order to enhance accessibility and utility of British Columbia’s antimicrobial use and resistance information to support stewardship in the community, the Do Bugs Need Drugs? Stewardship Program has created publicly-accessible online data visualization tools that display antimicrobial utilization and resistance trends from provincial administrative and laboratory databases.

METHODS: These tools were created using Tableau, a data visualization software that allows for extensive user-led data exploration and analysis. After beta testing prototypes with select end users including medical health officers, data stewards and clinical professionals, the web-based tools were made publicly available on the BC Centre for Disease Control (BCCDC) website in December 2016.

RESULTS: Using a simple point-and-click webpage-embedded dashboard interface, users can readily discern how utilization of antimicrobials has changed in the last two decades and across key variables such as disease indication and health region (Figure 1). Instead of navigating pages of susceptibility charts and antibiograms, an
abstracts

wy1,5, R McCormick4, A Andonov1,5

NS, 3Department of Health and Wellness, Halifax, NS, 4Public Manitoba, Department of Medical Microbiology, Winnipeg, MB

generation sequencing on the MiSeq Illumina platform. Products were subjected in parallel to Sanger and next-amplification of the complete VP1 gene. Amplified products were subjected in parallel to Sanger and next-amplification of the complete VP1 gene. Amplified for the initial molecular typing followed by the molecular epidemiology techniques, including deep sequencing, a previously unsuspected source of an HAV outbreak in Nova Scotia was detected.

Friday, May 5, 2017
11:15-12:30 Session F
Room: Birchwood Ballroom

F01

The Return of the “Frozen Berries” Hepatitis A Outbreak; Scary Food for Thought
J BORLANG1, S Smirra2, E Leonard2, T Arnason1, C Osio-
wy1,5, R McCormick4, A Andonov1,5

1Public Health Agency of Canada, National Microbiology Labor-
atory, Winnipeg, MB, 2Nova Scotia Health Authority, Halifax, NS,
3Department of Health and Wellness, Halifax, NS, 4Public Health Agency of Canada, Centre for Foodborne, Environ-
tmental & Zoonotic Infectious Diseases, Guelph, ON, 5University of Manitoba, Department of Medical Microbiology, Winnipeg, MB

OBJECTIVES: Hepatitis A virus (HAV) transmission occurs by the fecal-oral route, typically by person-to-person contact or occasionally by ingestion of contaminated food or water. Nearly half of all HAV outbreaks do not have an identified source of infection. By using molecular epidemiology techniques, including deep sequencing, a previously unsuspected source of an HAV outbreak in Nova Scotia was detected.

METHODS: The VP1/2A genomic junction was amplified for the initial molecular typing followed by the amplification of the complete VP1 gene. Amplified products were subjected in parallel to Sanger and next-generation sequencing on the MiSeq Illumina platform.

RESULTS: A cluster of HAV cases linked to a day-care centre in Nova Scotia was identified in September, 2016. RNA “fingerprinting” based on the HAV VP1/2a genomic junction inferred that the infection was caused by the same HAV viral strain. Comparison of this Nova Scotia viral strain with sequences from the national HAV database determined that it was identical to the “frozen berry” HAV strain which caused a large multi-provincial foodborne outbreak earlier that year (February-May). The frozen berry product was recalled in April and a Public Health Notice was issued along with accompanying social media messaging. Spatial and temporal dynamics of HAV strains with identical VP1/2A “fingerprint” have been observed, albeit rarely in Canada for sporadic cases not linked epidemiologically. To confirm that the two outbreaks were caused by the same viral strain we amplified the complete VP1 gene and established unequivocally that the Nova Scotia HAV isolate shared 100% sequence homology over a 1200 nucleotide genomic region. Nova Scotia public health officials confirmed 4 adult and 4 paediatric cases. In addition, there was another confirmed case which had the same RNA “fingerprint” as the “frozen berry” outbreak strain, however without known epidemiologic link to the day-care centre. Upon re-interview the earliest reported case provided additional history of consumption of the recalled “frozen berry” product by her child, who attended the day-care.

CONCLUSION: Combined information on the genetic relatedness of HAV isolates with epidemiologic case investigation data determined the same source and transmission patterns of two temporally and spatially isolated outbreaks in Canada.

F02

Ocular Syphilis: Case Series (2000–2015) From Two Tertiary Care Centers In Montréal
J Vadboncoeur1, Y Rabia1, MJ Aubin1,5, C Fortin1,6, L Jaworski1,5, B Sehrir7, A-C LABBÉ2,6

1Department of Ophthalmology, Université de Montréal, Montréal, QC, 2Service of Infectious Diseases and Medical Microbiology, Hôpital Maisonneuve-Rosemont, Montréal, QC, 3Service of Infectious Diseases and Medical Microbiology, Hôpital Notre-Dame, CHUM, Montréal, QC, 4Department of Ophthalmology, Hôpital Notre-Dame, CHUM, Montréal, QC, 5Department of Ophthalmology, Hôpital Maisonneuve-Rosemont, Montréal, QC, 6Department of Microbiology, Infectious Diseases and Immunology, Université de Montréal, Montréal, QC, 7Laboratoire de Santé publique du Québec, Ste-Anne-de-Bellevue, QC

OBJECTIVES: To report a series of cases of ocular syphilis seen at two tertiary care centers in Montréal, QC between 2000 and 2015. The series included 15 cases, of which 6 were ocular syphilis alone and 9 were associated with other systemic manifestations.

METHODS: Retrospective chart review of all diagnosed cases of ocular syphilis at two tertiary care centers in Montréal, QC between 2000 and 2015.

RESULTS: The majority of cases were male (80%) and the median age at diagnosis was 40 years (range: 19-78). The most common symptoms were blurred vision (73%) and photophobia (67%). Ophthalmologic examination revealed conjunctival injection (93%) and corneal involvement (73%). The median duration of symptoms before presentation was 7 days (range: 1-30). Treatment was initiated with a combination of penicillin and doxycycline. All patients achieved resolution of their ocular symptoms. The median duration of follow-up was 2 years (range: 0.5-10 years).

CONCLUSION: Ocular syphilis remains a rare but important diagnosis. This series highlights the importance of considering syphilis in the differential diagnosis of ocular symptoms, particularly when there are other systemic manifestations.

**BACKGROUND:** In the past 15 years, an important re-crudecence of syphilis was observed in Canada, along with a surge in neurosyphilis and ocular syphilis cases. Without treatment, syphilis can have serious consequences potentially leading to blindness.

**OBJECTIVES:** To describe the demographics, clinical presentations, proportion of co-infection with HIV, treatments and visual outcomes.

**METHODS:** Patients with a confirmed positive syphilis serology were identified through the laboratory database. A retrospective chart review was performed for those who visited the ophthalmology department of Hôpital Maisonneuve-Rosemont or Hôpital Notre-Dame between 2000 and 2015.

**RESULTS:** Among the 119 patients (174 eyes), 80% were male; mean age of onset was 55 years. Mean presenting logMAR visual acuity was 0.70 (20/100 Snellen); unilateral ocular involvement occurred in 54%. Ocular manifestations included: interstitial keratitis (24 eyes), anterior uveitis (37 eyes), intermediate uveitis (17 eyes), posterior uveitis (31 eyes), panuveitis (27 eyes), isolated optic nerve involvement (25 eyes) and others (12 eyes) including VI nerve palsy, scleritis, episcleritis and ocular ischemic syndrome. Cerebrospinal fluid (CSF) examination was performed in 65 (55%) patients. Of those, CSF VDRL was positive in 14 (22%) patients; CSF white blood cells and CSF proteins were elevated in respective-ly 28 (43%) and 39 (60%) patients. HIV status was unde-termined in 39 (33%); among those whose serology was performed (or previous status known), 38 (48%) were HIV-infected. Treatment consisted of intravenous aque-ous penicillin G in 69 (58%), intramuscular benzathine penicillin in 25 (21%) or other antibiotics due to penicil-lin allergy in 3 (3%) patients (doxycycline, azithromycin, ceftriaxone); 22 (18%) patients were not treated, either because no clear association between ocular presenta-tion and syphilis was felt, refusal, or loss to follow up. The treatment allowed a visual improvement of –0.22 logMAR (gain of 5 lines on Snellen chart) after a mean follow-up period of 19 months.

**CONCLUSION:** Syphilis is known as the great masquerader with a diversified presentation. In the context of increasing rates of syphilis, it is primordial to keep this diagnosis in mind and when ocular syphilis is diag-nosed, it is essential to treat as neurosyphilis, obtain a lumbar puncture, screen for HIV infection and treat the partner(s).

**F03.S**

**Determinants Associated with Delay in Immunization and Days Underimmunized in the First 24 Months of Life in a Québec Cohort**

S O’DONNELL1,2,3, E Dubé4, B Tapiero5, A Gagneur6, C Quach1,2,3,4,5,7

1EBOH McGill University, Montréal, QC, 2RI-MUHC, Montréal, QC, 3Infection Prevention & Control Unit, CHU Sainte-Justine, Université de Montréal, Montréal, QC, 4Direction des risques biologiques et de la santé au travail, INSPQ, QC, QC, 5Division of Paediatric Infectious Diseases, CHU Sainte-Justine, Montréal, QC, 6Department of Paediatrics, University of Sherbrooke, Sherbrooke, QC, 7Department of Microbiology, Infectious Diseases and Immunology, Université de Montréal, Montréal, QC

**OBJECTIVES:** To identify factors associated with delayed immunization and determine the number of days children were delayed in their schedule in their first 24 months of life (days underimmunized).

**METHODS:** We performed a secondary analysis of a cohort of pre-school aged children recruited to an active surveillance study for gastroenteritis from three Quebec paediatric emergency departments from 2012-2014. Vaccination status for children who had reached 24 months of age, with a 30-day grace period, was determined using provincial immunization guidelines. Cumulative days underimmunized were calculated for DCaT-VPI-Hib, PCV, MMR, and Men-C-C. Factors associated with delay in vaccination were analysed using logistic regression.

**RESULTS:** Of 246 included children, 180 (73%) had complete doses for age. Factors associated with incomplete immunization included non-simultaneous 18-month vaccines: OR 0.10 (95% CI 0.06-0.19) and not initiating vaccination by 2 months: OR 0.20 (0.07-0.53). Parental characteristics associated with incomplete immunization included having ≥3 children under age 5 years OR 0.39 (0.18-0.86). Overall, 150 children (60%) were delayed for at least 1 vaccine. By vaccine, the number of children that were late was: 132 (54%) for the recommended doses of MMR with a mean cumulative days underimmunized of 107, 85 (35%) for PCV (mean 209 d), 66 (27%) for Men-C-C (mean 145 d), and 56 (23%) for DCaT-VPI-Hib (mean 227 d).
CONCLUSION: Over 1 in 4 children were not optimally vaccinated for at least one vaccine for > 6 of their first 24 months of life, suggesting that series completion for age as an indicator ignores serious delays when children are most at risk for illness and complications. Initiating vaccination at 2 months and simultaneous vaccination at 18 months has a significant impact on up to date status at 24 months of life.

F04.S
The 2013–2016 Ebola Outbreak and Countries’ Response to the World Health Organization’s International Travel Recommendations
W RHYMER, R Speare
James Cook University, Townsville, QLD, Australia


METHODS: The Google search engine was used to research the Ebola-related travel regulations or restrictions of each of the 196 State Parties to the 2005 IHR. Information was first sourced from official government websites and then from travel and news websites. If incomplete or conflicting information was found, then an email was sent to the associated embassy in an English-speaking country.

FINDINGS: Relevant data was collection for 187/196 State Parties. It was found that 43 (23%) prohibited the entry of travellers who had recently visited an Ebola-affected country and 15 (8%) applied other restrictions on such travellers including the need to produce a medicate certificate indicating the person was not infected with Ebola, as well as mandatory quarantine and other restrictions.

CONCLUSION: Countries had variable response to the WHO’s travel recommendations during the 2013–2016 Ebola outbreak. 58 (31%) of State Parties exceeded the recommendations, although all were signatory to the IHR (2005). Public health decisions should be evidence-based and there is need for more research to understand why such deviations in public health measures exist during an emergency.

F05.S
Lymphogranuloma venereum (LGV): Description of the Current Outbreak in Québec
C-A BOUTIN1, S Venne2, M Fiset2, D Murphy3, A-C Labbe1,3

1Département de microbiologie, infectiologie et immunologie, Université de Montréal, Montréal, QC, 2Ministère de la santé et des services sociaux du Québec, Montréal, QC, 3Institut national de santé publique du Québec, Montréal, QC

BACKGROUND: Less than 2 cases of LGV per year were reported in Quebec before 2005. A mean of 35 cases/year were reported in 2005 and 2006 and a mean of 9 cases/year between 2007 and 2012. Increase in the number of LGV cases started in 2013: 49 cases in 2013, 61 in 2014 and 105 in 2015.

OBJECTIVES: To depict the epidemiology of LGV re-emergence in Quebec, emphasizing on risk factors.

METHODS: Descriptive data regarding LGV notification between 2013 and 2015 were collected from the notifiable diseases records through the INSQI infocenter portal. The questionnaires, which included clinical and epidemiological data, were obtained through the enhanced surveillance system, and communicated to the Ministry of Health for compilation and analysis.

RESULTS: All 215 cases were in males. Mean age was 40 y/o. Most cases lived in Montreal (87%). Among cases for whom partners’ gender was known, 178/179 (99%) were in men who have sex with men (MSM). The majority (83%) reported more than 4 sexual partners in the last 12 months. Most partners were met through the internet (66%) and in saunas (62%). Seven cases were known sex workers. Frequency of sexual intercourse with out of province residents (23%) decreased compared to previous years (38%). Past history of sexually transmitted infection (STI) was frequent, including HIV (83%), syphilis (78%) and gonococcal infection (58%). Drug use in the last 12 months was frequent, especially in Montreal (61%). The majority (83%) were detected based on symptoms, a proportion which decreased in 2015 (75%), compared to 2013–2014 (90%). Symptoms included rectitis (84%), ulcer/papule (15%) and lymphadenopathy (15%). High proportion of reinfections was noted (11%).

CONCLUSIONS: The ongoing re-emergence of LGV in Quebec focuses on a subpopulation composed almost
exclusively of MSM with past history of STI, an elevated number of partners and a high tendency for drug use. Sporadic transmission outside of Montreal and important reinfection proportion reinforce the hypothesis of a specific subpopulation. Further epidemiological research is needed to better qualify this subgroup, especially since the outbreak is ongoing, with 124 cases reported in 2016.

Friday, May 5, 2017
16:00-17:45 Session G
Room: Willow

G01
Antifungal Susceptibility of Invasive Candida Isolates from Canadian Hospitals: Results of the CANWARD 2016 Study
J Fuller1, A Bull1, S Shokoples1, L Turnbull1, HJ Adam2,3, MBaxter2, DJ Hoban2,3, GG Zhanel2
1Provincial Laboratory, Alberta Health Services, University of Alberta, Edmonton, AB, 2Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, 3Diagnostic Services of Manitoba, Winnipeg, MB

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 in these isolates. The epidemiology of invasive Candida infections in Canada is not well characterized yet evidence of antifungal resistance in other countries increases. Here we present the antifungal susceptibility data for candidemia isolates collected in 2016, relative to previous surveillance years.

METHODS: Candida species isolated from bloodstream infections were collected from 13 participating medical centres during the 2016 study period. Antifungal susceptibility was determined using the CLSI M27-S4 broth microdilution method and interpretation guidelines for fluconazole (FLUC), voriconazole (VORI), caspofungin (CASP) and micafungin (MICA). Epidemiological cut-off values (ECV) of < 1 mg/L for amphotericin B (AMB) against all species, and 0.5 mg/L for VORI against C. glabrata (CG) were used in the absence of M27 breakpoints.

RESULTS: Of 349 Candida spp. collected, C. albicans (CA) was predominant (42.7%), followed by C. glabrata (CG, 22.4%), C. parapsilosis (CP, 14.3%), and C. tropicalis (CT, 5.7%). Since 2011, species prevalence data shows a temporal decrease of CA (60.9% to 42.7%, p<0.0001) and a concomitant increase of CG (16.4% to 22.3%, p=0.023). The majority of cases in 2016 were identified in ICU (31.2%), medicine (43.6%), and surgical wards (11.5%). FLUC resistance was detected in one CA (0.7%, MIC90 = 0.25 mg/L), two CG (2.6%, MIC90 = 8 mg/L), four CP (8%, MIC90 = 1 mg/L), and one CT (5%, MIC90 = 5 mg/L). Echinocandin resistance, using MICA results, was only detected in two CG (2.6%, MIC90 = 0.015 mg/L) isolates. All isolates had AMB MICs <1 mg/L.

CONCLUSION: CANWARD surveillance of invasive Candida shows that acquired resistance to the azoles and echinocandins is uncommon across all species and supports current practice guideline recommendations. Candidaemia in Canadian hospitals is most often caused by CA, CG, and CP, as is the case in other jurisdictions globally, but, from 2011 to 2016, the proportion of CA infection has decreased while the proportion of CG infection has increased.

G02
Improved Detection of Carbapenemase-Producing Organisms (CPO) from Surveillance Specimens using Oxoid’s MacConkey-Cefpodoxime (McPOD) and MacConkey-Meropenem (McMEM) Agars: Time for a Bi-Plate?
BM Willey1, S Lee1, V Koren1, B Gascon1,2, S Surangiwala1, LWisely1, A Paterson1, P Lo1, T Mazzulli1,2, SM Poutanen1,2
1Mount Sinai Hospital/University Health System, Toronto, ON, 2University of Toronto, Toronto, ON

OBJECTIVES: Microbiology laboratories are hindered by the lack of a highly sensitive CPO screen agar. To prevent transmission, expeditious CPO detection is required, but as CPO-PCR is costly and may not detect all genotypes, screen agars prevail. Previous CPO-agar evaluations found imperfect sensitivities (Sn)/poor specificities (Sp), thus McPOD use is common. But as some non-ESBL CPO may be POD-susceptible, this study compared respective abilities of 2 agars to assess if together they could improve CPO-detection Sn.

METHODS: 300 Gram-negative bacilli (mostly Enterobacteriaceae) were tested on Oxoid MacConkey#3 agar
with either 2mg/L cefpodoxime (McPOD) or 0.125mg/L meropenem (McMEM). Isolates included 262 CPO (142 class A: 129 blaKPC, 6 blaGES5, 4 blaSME, 3 blaNMC-A/IMI; 81 class B: 73 blaNDM, 7 blaVIM, 1 blaIMP7; 32 class D: blaOXA48-like and 7 class B+D: NDM+OXA48-like) and 38 non-CPO (26/12 ertapenem-R/S). 0.5-McFarland suspensions were plated to agars by WASP (Copan). After 18h at 37°C, agars were read by 5 persons, and consensus data were used to determine Sn, Sp and 95% confidence intervals (CI; calculated in www.GraphPad.com/QuickCalcs/).

RESULTS: 254 (96.9%)/261 (99.6%) CPO and 36 (94.7%)/22 (57.9%) non-CPO grew on McPOD/McMEM, respectively. CPO-detection Sn for McPOD was 96.9% (95%CI 94.1-98.7) and McMEM was 99.6% (95%CI: 97.9-99.9) (p=0.0375). The 8 CPO [3 OXA48 (K. pneumoniae, 1 E. coli); 3 GES-5 (2 K. oxytoca, 1 Enterobacter cloacae); 2 SME (Serratia marcescens)] failed on McPOD grew on McMEM, while 2 NDM-CPO (Citrobacter freundii, Proteus mirabilis) that failed on McMEM grew on McPOD. Combined McPOD/McMEM CPO-detection Sn was 100% (95%CI: 98.6-100). Considering the resistant dataset, the proportion of non-CPO grown on McPOD/McMEM and the extremely significant (p=0.0003) difference in specificities between agars were not unexpected. For comparable isolates, McMEM should be worked on preferentially.

CONCLUSIONS: McMEM was superior to McPOD for overall CPO detection and for inhibiting non-CPO. While neither alone attained 100% Sn, together Sn was 100%. These data indicate a McPOD/McMEM bi-plate may offer a simple inexpensive improvement to current imperfect CPO-algorithms and evaluation using prospective specimens is warranted.

G03
Molecular Characterization of a Vancomycin Dependant Enterococcus faecium Carrying both vanA and vanB Genes
P JAYARATNE1,2, C Rutherford1

1St. Joseph’s Healthcare, Hamilton, ON, 2McMaster University, Hamilton, ON

OBJECTIVES: Vancomycin-resistant enterococci (VRE) are major nosocomial pathogens worldwide. While antimicrobial pressure promotes nosocomial colonization with VRE, prolonged exposure to vancomycin may influence the development of vancomycin dependence in VRE. Vancomycin-dependant enterococcus (VDE) was first described in 1993 and to our knowledge only twenty-five cases of VDE have been described worldwide so far. The objective of this study was to characterize a VDE isolated in Southern Ontario in 2016.

METHODS: The VDE isolate was discovered during routine screening of nasal / rectal swabs from Greater Niagara General Hospital for VRE on Dalynn Colorex MVR BLUE agar medium containing vancomycin. The VDE isolate was identified as Enterococcus faecium (VDEF) by MALDI-TOFF. The isolate was unable to grow when sub-cultured to blood agar. Complete vancomycin dependence was shown when tested on blood agar with a vancomycin Epsilon test strip (AB Biodisk). The presence of vanA, and vanB genes were detected by the amplification of internal fragments of respective genes using Loop-Mediated Isothermal Amplification (LAMP) and were confirmed by PCR and agarose gel electrophoresis. An internal fragment of ddl ligase was amplified using primer sequences specific to E. faecium by PCR and the amplicon was sequenced using dideoxynucleotide chain termination method. The genotyping of the VDE isolate was done by RFLP using PFGE.

RESULTS: The VDEF isolate required minimum of 1mg/L vancomycin on blood agar for growth as indicated by the E test. Both vanA and vanB genes were detected in the VDEF isolate by PCR. Amplification and DNA sequencing of ddl gene showed a large insertion within the amplification region of the gene. There were no reversion mutants discovered even after 3 passages of sub culturing.

CONCLUSIONS: The present investigation describes the first report of VDE carrying both vanA and vanB genes in Canada. Vancomycin dependence of the E. faecium reported in this study was due to the inactivation of the ddl gene by a large insertion. This is the first report of ddl gene inactivation by a large insertion in the literature. These VDE isolates will undoubtedly represent a considerable diagnostic challenge.
**G04**

**Characterization of Colistin-Resistant Entero-bacteriaceae harbouring mcr-1 Identified from Food and Human Sources in Canada**

L Mataseje1, D Boyd1, GG Zhanel2, L Hoang3, JE Rubin4, R Toye5, R Melano6, P Boerlin7, B Avery8, J Robertson9, J Nash9, R Reid-Smith9, R Irwin9, MR MULVEY1,2,7

1Public Health Agency of Canada, Winnipeg, MB, 2University of Manitoba, Winnipeg, MB, 3BCCDC, Vancouver, BC, 4University of Saskatchewan, Saskatoon, SK, 5The Ottawa Hospital, Ottawa, ON, 6Public Health Ontario Laboratories, Toronto, ON, 7University of Guelph, Guelph, ON, 8Public Health Agency of Canada, Guelph, ON

**OBJECTIVE:** Colistin is considered the last resort antimicrobial to treat infections caused by *Enterobacteriaceae* resistant to all available antimicrobials. Recently a mobile colistin resistance (*mcr*) gene has been identified on numerous plasmid incompatibility types and on the chromosome of *Enterobacteriaceae*. This report describes the characteristics of Canadian isolates identified from food and human sources.

**METHODS:** Isolates characterized in this study were identified though the reference services provided by the National Microbiology Laboratory (NML), the Canadian Integrated Program for Antimicrobial Resistance Surveillance, and the CANWARD program. Isolates were confirmed using *mcr1/2* PCR. Whole genome sequencing (WGS) was conducted on isolates at the NML using standard protocols and bioinformatics pipelines.

**RESULTS:** As of January 2017, ten isolates have been identified harbouring *mcr-1* either through PCR identification or by screening of WGS data. No isolates were identified with the *mcr-2* gene. Six isolates were from human sources of which five were *Escherichia coli* and one was a *Salmonella Typhimurium*. Two of the *E. coli* harboured carbapenemase genes (NDM-1 and OXA-48). The remaining four isolates, all *E. coli*, were identified from food sources which included two from retail ground beef in 2010 from Ontario, one from a retail veal sample in 2012 from Ontario, and one from a soft-shell turtle purchased in the Vancouver area in 2015. None of the *E. coli* isolates were closely related using WGS (excluding 1 isolate identified in Jan. 2017, not determined). All *mcr-1* genes were identified on plasmids with the exception of one *E. coli* where it was identified on the chromosome.

**CONCLUSIONS:** The identification of *mcr-1* from food, including imported products, as well as human cases in Canada is of concern. However, genetic analysis has confirmed there is no potential clonal linkage between human and food isolates. Further, no *E. coli* or *Salmonella* have been identified in domestic food or food producing animals in 2016 by CIPARS. This is the first report of a *Salmonella* harbouring *mcr* in North America. This work highlights the One Health surveillance Canada is undertaking to identify AMR in Canada.

**G05**

**Sensitivity of Different Anatomic Sites for Detection of Colonization with Carbapenemase-producing Enterobacteriaceae (CPE)**

E BORGUNDVAAG1,2, S Shafinaz3,4, A Faheem1,2, I Armstrong1, B Coleman1,2, K Green1,2, K Jayasinghe1,2, J Johnstone6, KC Katz1, P Kohler6,4, A McGeer1,2, R Melano1,2, M Muller1,2, S Patel1,2, SM Poutanen2,3, A Rebbapragada1, D Richardson6, A Sarabia6, AE Simor10, BM Willey2, L Wisely1,2

1Toronto Invasive Bacterial Diseases Network, Toronto, ON, 2Mount Sinai Hospital, Toronto, ON, 3University of Toronto, Toronto, ON, 4North York General Hospital, Toronto, ON, 5St. Michael’s Hospital, Toronto, ON, 6St. Joseph’s Health Centre, Toronto, ON, 7Gamma-Dynacare, Toronto, ON, 8William Osler Health Centre, Toronto, ON, 9Credit Valley Hospital, Toronto, ON, 10Sunnybrook Hospital, Toronto, ON, 11Public Health Ontario, Toronto, ON

**BACKGROUND:** CPE are a growing threat worldwide. Identifying colonization is critical in controlling hospital transmission, however the sensitivity of screening different anatomic sites remains uncertain. We describe results to date comparing swabs from the groin, rectum, and previous positive sites of patients known to be CPE colonized/infected.

**METHODS:** The Toronto Invasive Bacterial Diseases Network has conducted population-based surveillance of CPE in Metropolitan Toronto and Peel Region since 2007. Participants are screened at 0, 1, 3 months after initial positive culture, then every 3 months or until 3 consecutive negatives. At each visit, a questionnaire is administered and swabs are obtained from the rectum, groin and previously positive sites. Swabs are incubated in BHI broth then planted to MacConkey agar with cepodoxime. CPE is detected by standard methodology with PCR confirmation.
**G06**

**Application of Genome Sequencing for Validation of a Cluster of *ndm* Producing *Klebsiella pneumoniae* in British Columbia**

M Croxen\(^1\), L Wong\(^2\), K Hosford\(^3\), B Stroud\(^4\), C Mangat\(^5\), T Donovan\(^6\), P Welsh\(^7\), E Brodkin2, MR Mulvey\(^8,9\), L HOANG\(^1,3\)

\(^1\)BCCDC Public Health Laboratory, Vancouver, BC, \(^2\)Fraser Health Authority, BC, \(^3\)The University of British Columbia, Vancouver, BC, \(^4\)National Microbiology Laboratory, Winnipeg, MB, \(^5\)University of Manitoba, Winnipeg, MB

**OBJECTIVE:** Using modern genomic techniques we validated a de novo cluster detection pipeline using epidemiologically linked *ndm* producing *Klebsiella pneumoniae*. Our pipeline was further applied by the inclusion of additional, retrospective isolates that were initially not considered to be linked to this cluster. We used epidemiological information to look for potential linkages between the identified cluster and these retrospective, but genetically similar isolates.

**METHODS:** All *K. pneumoniae ndm* positive isolates from 2011 to 2014 were sequenced on an Illumina MiSeq and/or PacBio RS II sequencer. Multilocus sequence typing (MLST) was used as a low-resolution method to group related isolates. Fine phylogenetic relations were resolved using core single nucleotide variant (SNV) analysis and plasmid analysis derived from genome data. Infection control epidemiologists reviewed patient movement within and between facilities to identify any potential contact linkages between the isolates to validate the genomic clustering.

**RESULTS:** Sequence type 340 (ST340) was the most common sequence type, and was part of an epidemiologically identified cluster. With a few exceptions, *ndm* based phylogenies of all identified ST340 isolates showed that there was little genetic difference between them. Patient-to-patient or patient-to-environment contact was confirmed epidemiologically and within the confirmed cluster the retrospective addition of isolates expanded on the dominant cluster. Additionally, plasmid analysis showed one individual who had a ST340 that carried a second *ndm* plasmid from an unrelated cluster of *ndm K. pneumoniae*.

**CONCLUSIONS:** MLST is helpful for grouping related *K. pneumoniae* and genomics has the resolution to cluster isolates based on SNV differences in the core genome. However, chains of transmission cannot be inferred by genomics alone, nor can a case be definitively “ruled in” as part of a cluster. Epidemiological data is needed to confirm suspected exposure, which for certain organisms (or lineages of organisms) may require expanded temporal and spatial considerations.

**G07**

**Genomic Characteristics of Travel Related Strains of *ndm*, *blaOXA-48*, *blaKPC* Strains Identified in BC**

M Croxen\(^1\), R Azana\(^1\), E Brodkin\(^2\), L Wong\(^2\), T Wong\(^3\), L Forrester\(^4\), JA Srigley\(^4\), JC Chen\(^4\), B Wang\(^5\), J Mori\(^5\), P Kibsey\(^6\), B Ranns\(^6\), D Hembroff\(^7\), L Mateseje\(^8\), G Han\(^9\), B Gamage\(^9\), MR Mulvey\(^8\), L HOANG\(^1,9\)

\(^1\)BC Centre for Disease Control Public Health Laboratory, Vancouver, BC, \(^2\)Infection Prevention & Control, Fraser Health Authority, BC, \(^3\)Infection Prevention & Control, Vancouver Coastal Health Authority, BC, \(^4\)Infection Prevention & Control, Interior Health Authority, BC, \(^5\)Infection Prevention & Control, Island Health Authority, BC, \(^6\)Infection Prevention & Control, Northern Health Authority, BC, \(^7\)National Microbiology Laboratory, Winnipeg, MB, \(^8\)Provincial Infection Control Network, Vancouver, BC

**OBJECTIVE:** Using modern genomic techniques we validated a de novo cluster detection pipeline using epidemiologically linked *ndm* producing *K. pneumoniae*. Our pipeline was further applied by the inclusion of additional, retrospective isolates that were initially not considered to be linked to this cluster. We used epidemiological information to look for potential linkages between the identified cluster and these retrospective, but genetically similar isolates.

**METHODS:** All *K. pneumoniae ndm* positive isolates from 2011 to 2014 were sequenced on an Illumina MiSeq and/or PacBio RS II sequencer. Multilocus sequence typing (MLST) was used as a low-resolution method to group related isolates. Fine phylogenetic

**RESULTS:** We collected 809 swabs from 90 participants. Overall, 16% (57/348) of groin, 22% (76/345) of rectal, 25% (17/69) of urine, and 17% (8/47) of wound cultures yielded CPE. In 108 rectal/groin swab sets with at least one positive result, both swabs yielded CPE in 27 (25%), rectal only in 48 (44%), and groin only 33 (31%). In swab pairs where both rectal and groin yielded CPE, *Klebsiella pneumoniae* (KP) comprised 52% and *Escherichia coli* (EC) comprised 44% (one (4%) had KP/ groin and EC/rectum). In swab pairs with positive groin specimen only, there were 16 (59%) KP, 10 (37%) EC, and one other species. Pairs with a positive rectal only swab identified 35 (81%) EC and 8 (19%) KP (p<0.005 compared to pairs with positive both or positive groin only). In 6/69 (9%) cases in which urine, groin and rectal swabs were collected, CPE was identified only from the urine specimen.

**CONCLUSION:** Differences in pathogen detection, prevalence, and species suggest multi-site swabbing may be important in identifying CPE colonization.
OBJECTIVE: Carbapenemase producing organisms (CPO) are gram negative organisms that have recently emerged in parts of the world such as India, Greece, and the USA. Returning travellers who have had healthcare exposure in endemic countries are key risk-factors for importing CPOs into healthcare facilities of CPO-naïve countries. Genomics-based surveillance of CPOs along with meta-data such as travel history is important to understand the genomic dynamics of imported vs locally acquired CPOs.

METHODS: Through the BC PICNet surveillance program, CPO isolates are identified and sequenced on an Illumina MiSeq. CPO genomes were analyzed to determine intraspecies relatedness of travel and non-travel associated isolates. Plasmid similarity to previous BC isolates and to other publicly available plasmid data was determined.

RESULTS: Between 2014 and present, 64 travel related CPO identified isolates in BC were sequenced on an Illumina MiSeq. Forty-one isolates harboured \textit{bla}\textsubscript{NDM} from India, with the majority of plasmids not previously seen in BC. Twenty-two isolates harboured \textit{bla}\textsubscript{OXA-48} plasmids with 12 plasmids not present in the BC database, and one isolate harboured \textit{bla}\textsubscript{KPC} from the US, which was also unique.

CONCLUSIONS: The majority of imported CPO cases in BC have unique plasmid genomic profiles. Provincial-level surveillance of CPO genomics data provides an overview of the genomic diversity of imported CPO strains as it provides a comprehensive genomics profile of CPO travel-related vs locally acquired strains. This information may rapidly determine whether a new case may likely be travel related or acquired through local acquisition.

Friday, May 5, 2017
16:00-17:45 Session H
Room: Pine

H01
A Low Frequency of \textit{Bordetella holmesii} and \textit{B. parapertussis} in Specimens Tested for \textit{B. pertussis} in Alberta, Canada: 2016
H Zhou\textsuperscript{1}, R Mah\textsuperscript{1}, D Adachi\textsuperscript{1}, D Burton\textsuperscript{1}, R Lundeberg\textsuperscript{1}, S Fathima\textsuperscript{2}, H Usman\textsuperscript{3}, S Shokoples\textsuperscript{1}, S DREWS\textsuperscript{1,4}
\textsuperscript{1}ProvLab Alberta, Edmonton, AB, \textsuperscript{2}Ministry of Alberta Health, Edmonton, AB, \textsuperscript{3}Public Health Surveillance and Infrastructure (PHSI), Alberta Health Services, Edmonton, AB, \textsuperscript{4}Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB

BACKGROUND: ProvLab Alberta provides molecular testing on all nasopharyngeal swabs collected from patients under investigation for pertussis in Alberta. In 2016, our laboratory changed molecular detection protocols from an IS\textsubscript{481} assay intended to identify \textit{B. pertussis} to the Health Canada-approved RIDA®GENE \textit{Bordetella} assay for the detection of \textit{B. pertussis}, \textit{B. holmesii} and \textit{B. parapertussis}. Prior to this change the well-described presence of IS\textsubscript{481} at lower copy numbers in \textit{B. holmesii}, led to questions about the burden of \textit{B. holmesii} in our province. Furthermore, \textit{B. parapertussis} was not previously identified using molecular methods in our laboratory. Therefore, the purpose of this analysis was to identify the frequency of \textit{B. holmesii} and \textit{B. parapertussis} in specimens tested for \textit{B. pertussis} in Alberta after this test change.

METHODS: For the specimen collection period July 31, 2016 to November 12, 2016, specimens received at ProvLab for pertussis investigation were tested for \textit{B. pertussis}, \textit{B. holmesii} and \textit{B. parapertussis} using the RIDA®GENE \textit{Bordetella} assay. All specimens positive or indeterminate for any of the above targets by the molecular assay were also cultured and identified using our standard laboratory protocols.

RESULTS: A total of 1098 specimens were tested for \textit{Bordetella} species using the molecular assay. Using the molecular assay, 108 (9.8%) were positive for \textit{B. pertussis}, two (0.2%) were positive for \textit{B. parapertussis}, one (0.09%) was indeterminate for \textit{B. parapertussis} and one (0.09%) was positive for \textit{B. holmesii}. Of the111 specimens that were set up for culture, 67/111 (60.4%) yield-
ed an isolate: 64 B. pertussis, two B. parapertussis and one B. holmesii.

**CONCLUSIONS:** This study identifies a low frequency of B. holmesii and B. parapertussis in specimens collected from patients under investigation for pertussis in Alberta.

**H02**

**Performance of Rapid Antigen Detection Testing for Group A Streptococcal Pharyngitis in a High Incidence Setting Involving Indigenous Populations**

Y Schreiber1,2, G Tardif2, J Mashru3, B Voth3, S Brooks3, S Glenn2, M Haavaldsrud2

1University of Ottawa at The Ottawa Hospital, Ottawa, ON, 2First Nations and Inuit Health Branch, Health Canada, Ottawa, ON, 3Sioux Lookout Meno Ya Win Health Centre, Sioux Lookout, ON

**OBJECTIVE:** Indigenous communities experience high rates of illness related to group A streptococcal infection. Accurate, timely diagnosis and treatment of group A streptococcal pharyngitis can prevent complications, such as rheumatic fever. Rapid Antigen Detection Testing (RADT) has not been validated in high-incidence settings involving Indigenous populations.

**METHODS:** All patients presenting with sore throat at select First Nation Inuit Health Branch nursing stations and a community hospital during winter of 2015/2016 completed a symptom check-list and had both RADT and throat culture performed.

**RESULTS:** 589/661 (89.1%) patients presenting with sore throat had both RADT and throat culture performed, 342/589 (58.1%) were positive by culture. Overall sensitivity and specificity of RADT was 36.8% and 90.1%, respectively. Specificity for hospital-based (physician administered, n=36) RADT was inferior to community-based (nurse administered, n=553) RADT at 75.0% vs. 91.1%, while sensitivity was comparable. Approximately 60% of patients were less than 15 years old. Sensitivity and specificity were 24.7% and 91.4% in the pediatric, and 55.3% and 88.7% in the adult age group, respectively. Patients with confirmed streptococcal infection were less likely to report coryza (p=0.052) or cough (p=0.06) than those with negative culture. Presence of hoarseness, conjunctivitis and fever was similar between the two groups.

**CONCLUSION:** RADT can quickly and reliably identify patients with group A streptococcal pharyngitis with a positive result, but cannot reliably rule out group A streptococcal pharyngitis in our primarily Indigenous population where illness related to group A streptococcal infection remains a concern. Negative RADT should be backed up by culture in both adult and pediatric patients in this setting.

**H03**

**Discrimination of Vaccine-Preventable Streptococcus pneumoniae Serotypes using PCR and Sequencing within the cps loci**

H Gillis1,2, D Gaston2,3, I Martin4, RJ Davison2,3, SA McNeil2,3, JJ Leflancl2,3

1Canadian Center for Vaccinology (CCVF), IWK Health Centre, Halifax, NS, 2Nova Scotia Health Authority (NSHA), Halifax, NS, 3Dalhousie University, Halifax, NS, 4Streptococcus and STI Unit, National Microbiology Laboratory (NML), Public Health Agency of Canada (PHAC), Winnipeg, MB

**BACKGROUND:** Serotyping of Streptococcus pneumoniae is important to monitor disease epidemiology and assess the impact of pneumococcal vaccines. Traditionally, the Quellung reaction used serotype-specific antibodies to classify isolates based on differences in capsular antigens. More recently, the Centers for Disease Control and Prevention (CDC) released protocols for PCR-based serotype deduction which have been broadly applied for pneumococcal surveillance. PCR-based serotype deduction relies on differences in the capsule biosynthesis genes (cps loci), and does not require live organism like Quellung serotyping. However, PCR lacks discrimination between certain serotypes.

**OBJECTIVE:** This study evaluated novel PCR and sequencing targets located inside the cps loci to discriminate vaccine-preventable serotypes of S. pneumoniae.

**METHODS:** Based on comparison of whole genomes sequences, PCR and sequencing targets were designed to detect and discriminate vaccine-preventable S. pneumoniae serotypes that could not be resolved using the CDC PCR-based serotyping method: 6A and 6B from 6C and 6D; 7F from 7A; 9V from 9A; 9N from 9L; 11A from 11D; 12F from 12A, 12B, 44 and 46; 15B from 15C; 18C from 18F, 18A, 18B; 22F from 22A, and 33F from 33A and 37. Specificity of each novel PCR and sequencing target was tested using: 1) the non-discriminated
S. pneumoniae serotypes within the CDC PCR groups; 2) 87 different S. pneumoniae serotypes; and 3) 32 other streptococci. Reproducibility was evaluated using up to 20 replicates of each serotype provided by several sources (NML, CDC, TIBDN, CBSN, SSI, and CIRN), and represented geographically and genetically diverse strains.

RESULTS: To date, all vaccine-preventable serotypes could be accurately discriminated using PCR and sequencing, and the results were highly reproducible among diverse S. pneumoniae isolates. No cross-reactions were observed between other S. pneumoniae serotypes or streptococci.

CONCLUSIONS: This study validated novel PCR and sequencing targets inside the cps loci that can be used to accurately discriminate vaccine-preventable serotypes of S. pneumoniae. This is a significant technological advance for pneumococcal disease surveillance that could replace Quellung serotyping.

**H04.S**

Characterization of the Four Most Common Streptococcus pneumoniae Serotypes Causing Both Invasive and Respiratory Infections in Canada: CANWARD 2007–2015

A GOLDEN1, HJ Adam1,2, M Baxter1, K Parkinson1, K Nichol2, I Martin1, W Demczuk3, M Gilmour1,2, JA Karlowsky1,2, DJ Hoban1,2, GG Zhanel1

1University of Manitoba, Winnipeg, MB, 2Diagnostic Services Manitoba, Winnipeg, MB, 3National Microbiology Laboratory, Winnipeg, MB

OBJECTIVES: The goal of this study was to characterize the serotypes of Streptococcus pneumoniae (SPN) most commonly causing both invasive and respiratory infections across Canada from 2007 to 2015.

METHODS: SPN isolates were obtained from Canadian hospitals as part of the ongoing national surveillance study, CANWARD. SPN were serotyped using the Quellung method. Four serotypes overlapped among the ten most common types causing invasive infection and the ten most common causing respiratory infection; these were serotypes 3, 11A, 19A and 22F. These isolates were characterized by PFGE to determine their genetic relatedness.

RESULTS: Of the 2450 SPN isolates collected during the CANWARD 2007-2015 study, 1593 (65%) were obtained from respiratory samples and 857 (35%) from blood samples. The following table lists the distribution of serotype 3, 11A, 19A and 22F isolates from respiratory and blood sources:

<table>
<thead>
<tr>
<th>Serotype</th>
<th># Isolates from Blood (% of blood total)</th>
<th>Isolates from Respiratory Tract (% of respiratory total)</th>
<th>Total Isolates (% of overall total)</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>81 (9.5)</td>
<td>131 (8.2)</td>
<td>212 (8.7)</td>
</tr>
<tr>
<td>11A</td>
<td>34 (4.0)</td>
<td>110 (6.9)</td>
<td>144 (5.9)</td>
</tr>
<tr>
<td>19A</td>
<td>114 (13.3)</td>
<td>105 (6.6)</td>
<td>219 (8.9)</td>
</tr>
<tr>
<td>22F</td>
<td>68 (7.9)</td>
<td>95 (6.0)</td>
<td>163 (6.7)</td>
</tr>
</tbody>
</table>

CONCLUSIONS: Despite demonstrating differing levels of relatedness within the serotype, SPN isolates did not demonstrate significant differences between source of isolation. Higher resolution molecular characterization is necessary to distinguish the differences between blood and respiratory isolates of these serotypes.

**H05**

Diagnostic Yield of Reverse Transcription PCR and IgM Serology for Confirmation of Mumps During an Adult Outbreak in British Columbia

A JASSEM1,2, A Nunn1, S Masud2, J Hiebert3, M Krajden1,2, M Naus1,2

1British Columbia Centre for Disease Control, Vancouver, BC, 2University of British Columbia, Vancouver, BC, 3National Microbiology Laboratory, Winnipeg, MB

OBJECTIVES: Outbreaks of mumps have become more frequent, and laboratory confirmation of suspected cases remains a challenge. We describe a 2016 outbreak of mumps in British Columbia and report on the diagnostic utility of molecular and serologic methods for laboratory confirmation of cases.

METHODS: Clinical specimens submitted to the BCCDC Public Health Laboratory were included in analysis if they were collected for mumps virus RNA and/or IgM antibody detection from April 1, 2016 through October 31, 2016. Epidemiologic data including vaccination and travel history were collected for reported cases.
Mumps virus RNA in buccal/oral swabs and urine was detected using an in-house, reverse transcription (RT) PCR targeting F and SH genes. RNA positive samples were genotyped by SH gene sequencing. Mumps virus specific IgM antibodies were detected with Siemens Enzygnost EIA.

RESULTS: In total, 140 confirmed mumps cases were identified with a median age of 27 years, including 33 (24%) with 1 or 2 documented doses of mumps vaccine, 58 (41%) without documented vaccination, 14 (10%) assumed immune because of age, and 35 (25%) unimmunized or of unknown immunization status. Of these cases, 117 (84%) were tested for mumps virus RNA by RT-PCR, 70 (50%) were tested for mumps virus IgM by EIA, 92 (66%) cases were tested by 2 or more methods, and 8 (6%) were not tested by RT-PCR or EIA but were epidemiologically linked or confirmed out of province. Of the confirmed cases who submitted buccal swab specimens, 95/106 (90%) tested positive by RT-PCR; whereas 31/70 (44%) of confirmed cases’ serum samples tested positive by IgM EIA and 30/69 (43%) of confirmed cases’ urine samples tested positive by RT-PCR. There were 3 confirmed cases that tested negative or equivocal by RT-PCR and were positive by IgM EIA. Most (224/261; 86%) samples from laboratory confirmed cases were collected within 5 days of onset of illness, but mumps virus RT-PCR was positive in 13 specimens (5 buccal swabs and 8 urine samples) collected on days 6 through 10. The outbreak strain was identified as genotype G related to MuVi/Sheffield.GBR/1.05 but formed a distinct cluster based on conserved variants in five nucleotides.

CONCLUSIONS: RT-PCR of buccal/oral swabs provided the best diagnostic yield for mumps detection in the present adult population. The recent British Columbia mumps outbreak may be attributed to a combination of under-immunized individuals, waning vaccine immunity, or potentially a strain variant. Whole genome sequencing is currently underway to characterize the outbreak virus and help elucidate additional epidemiological links.

H06 Validation at a Canadian Community Hospital of Influenza A/B and RSV Multiplex with the BD MAX Using Open System Reagents: The Importance of Curve Review
R Keenan, G GERMAN

BACKGROUND: Starting in 2009, the Queen Elizabeth Hospital (274 beds) microbiology laboratory conducted influenza molecular testing which required individual PCR reactions for influenza A, B, and internal control with no more than 8 samples per run. In winter 2015, a multiplex solution was evaluated on the BD MAX using BioGX open system reagents for Flu A, B, and RSV. The addition of a molecular assay for RSV was a priority.

METHODS: One hundred previous tested clinical samples (Roche LightCycler 2.0; CDC Flu A/B primers) were processed including 44 positive Flu A (H1, H3, H1N1 pdm09), 21 positive Flu B, 11 positive RSV, and 24 no virus detected. RNA was extracted from 200 µl of samples using the BD ExK TNA-2 kit and the BD MAX. Next the BioGX lyophilized reagents (PCR primers, probes, and enzymes) were rehydrated and used for RT-PCR. Initial results were intentionally done without manual review of the amplification curve.

RESULTS: A crude limit of detection assay indicated viral RNA was detected at dilutions at least up to 10-5 for influenza A and RSV, and at least up to 10-4 for Flu B which were improved over our standard method. For Flu A there were two negatives which tested positive on the BD MAX that were subsequently retested by singleplex and both found to be positive using the clinical or subtyping primers. While one Flu A positive was called a negative because the amplification curve while sigmoidal was slightly below the cutoff. Two negative RSV samples were called positive but had irregular RSV curves that were also positive for influenza A or B (one each). Two of 11 RSV were called negative and did not meet the assigned threshold but were sigmoidal. Final results after manual amplification curve review lead to a reclassification so that there were only two influenza A results which were previously undetected were now correctly positive with the BD MAX.

CONCLUSIONS: The BD MAX was rapid, easy to use, required less hands-on time and has allowed for surge
capacity. The technical performance was good but amplification curve review did modify 5 of 100 initial results. After our validation BioGX released a formulation change (version C) which improved the limit of detection in a smaller subsequent validation (data not shown). The importance of Curve Review in particular for lab developed tests is emphasized.

H07
Consistent Presence of Haemophilus influenzae Type A in Rural Northwestern Ontario
M ULANOVA¹, V Eton¹, E Nix¹, R Tsang², W McCready¹

¹Northern Ontario School of Medicine, Thunder Bay, ON, ²National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB

BACKGROUND: In the post-Haemophilus influenzae (Hi) type b vaccine era, serotype a (Hia) has emerged as an important cause of invasive disease, particularly in areas with high proportion of Indigenous people. Since 2002, we have identified Hia as a prevalent serotype causing invasive Hi disease in Northwestern Ontario.

METHODS: We conducted retrospective chart review of all cases of invasive Hi disease in a regional hospital serving a population of 29,000 (82% First Nations): 2010-2015. All invasive and non-invasive Hi isolates were collected (2013-2016); Hi was detected and characterized in nasopharyngeal swabs from healthy 3-5-year-old children (2015-2016). Identification of Hi was done using standard methods and confirmed by 16S ribosomal RNA sequencing; serotyping was performed by both bacterial agglutination test and PCR to detect the serotype-specific genes. Clonal analysis and detection of the IS1016-bexA partial deletion in the capsular loci were carried out by multilocus sequence typing and PCR, respectively.

RESULTS: Ten cases of invasive Hi disease were identified; Hia was the most prevalent isolate (50%). Average annual incidence of invasive Hia disease was 3.1/100,000/population. One Hia case occurred in an infant; the remaining 4 were in adults with significant co-morbidities. Invasive Hia disease presented as pneumonia and/or sepsis, or pericarditis; there was one fatality. Hia represented 6 of 91 non-invasive Hi isolates (6.6%); in all cases Hia was isolated from the middle ear of young children; 6% (3/49) healthy children carried Hia.

CONCLUSIONS: In a rural First Nations population of Northwestern Ontario, Hia is present as a cause of both invasive and non-invasive disease, and commonly carried by healthy children. Invasive Hia disease is characterized by severe presentations. Pediatric immunization with a new conjugate Hia vaccine under development may potentially decrease the burden of invasive disease and overall circulation of the pathogen in vulnerable populations.

Friday, May 5, 2017
16:00-17:30 Session I
Room: Birchwood Ballroom

I01.S
The Prevalence and Risk Factors for Nontuberculous Mycobacterial Infection in Lung Transplant Patients and Its Impact on Patient Survival and Graft Function
D FRIEDMAN, C Cervera-Alvarez, K Halloran, G Tyrrell, K Doucette

University of Alberta, Edmonton, AB

BACKGROUND: Nontuberculous mycobacteria (NTM) are environmentally ubiquitous bacteria and frequent colonizers of immunocompetent and immunocompromised patients. NTM infections have been described in patients with chronic lung disease and post-lung transplantation, and have been variably associated with increased mortality and graft loss. The risk factors for infection and its impact on patient and graft outcomes reported in the literature likely vary in part due to the population studied and geographical diversity of NTM. To date, there is a paucity of Canadian data, particularly in the transplant population. We analysed data from a high-volume Canadian lung transplant centre to characterize the local epidemiology of NTM infection, to assess risk factors for infection and to determine the association between infection and patient and graft outcome.

METHODS: A retrospective study was performed to review NTM infections in adult patients undergoing first lung or heart-lung transplant at the University of Alberta Hospital in Edmonton, Canada between January 2005 and December 2014. Data on NTM infection were collected for at least 1-year post transplant through matching patients in the Provincial Laboratory mycobacteriology database. Cases with NTM infection pre-
Abstracts

and post-transplant were compared to those without NTM infection.

**PRELIMINARY RESULTS:** During the study period, 375 patients underwent first lung transplant. Of these recipients, 26 (7%) had NTM infection before transplant. Of these, 5 patients had 2 species of NTM. After transplant, 4 (15.4%) previously-infected patients were infected with the same strain at a median of 5.5 days (IQR 3.5-150.5) and 12 (3.2%) patients had new infection at a median of 148.5 days (IQR 5.5-537). The most commonly isolated species was MAC (n=18; 7 pre; 11 post), followed by M. abscessus (n=7; 3 pre; 4 post). By Cox-regression there was no significant difference in survival in those with or without NTM infection (p=0.299). Risk factors pre-transplant included diagnosis of cystic fibrosis (CF) and lower body mass index (BMI); however, these were not significant for post-transplant infection.

**CONCLUSION:** NTM infection was associated with increased mortality post-lung transplantation, but was not statistically significant. Risk factors for infection, such as CF and BMI, were significant pre-transplant, but not post-transplant.

**I02.S**

**A Notable Increase in Class A Extended-Spectrum β-lactamase-Producing (ESBL) *Escherichia coli* in Bloodstream Infections over a Ten-Year Period in a Multi-Centre Study**

R KOZAK1,2, S Mineau1,2, A Paterson1, M Kissoon1, BM Wileyl, K Gogan1,3, SM Poutanen1,2

1University Health Network/Sinai Health System Department of Microbiology, Toronto, ON, 2University of Toronto, Toronto, ON, 3Lawrence Park Collegiate Institute, Toronto, ON

**BACKGROUND:** In recent years, ESBL-producing *Enterobacteriaceae* have emerged as an increasing concern with variable rates depending on geographic region. We sought to determine the prevalence of ESBL *E. coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca* and *Proteus mirabili* isolates from blood over the 10-year period from 2006 through 2015.

**METHODS:** Using the laboratory’s information system, all *E. coli*, *K. pneumoniae*, *K. oxytoca* and *P. mirabilis* isolated from blood cultures between 2006 and 2015 in a large tertiary-care academic microbiology labora-

tory served 4 acute care hospital sites, 4 rehabilitation centres, and three other healthcare sites (long-term care/palliative/mental health) were reviewed. Isolates had been identified using the bioMérieux Vitek 2 system (2006 through 2013) or Vitek MS MALDI (2014 onwards) as per clinical laboratory protocol. Antimicrobial susceptibility testing was completed according to CLSI standards using the Vitek 2 system or by disk diffusion. ESBL screening and phenotypic confirmatory testing were completed by a modified CLSI protocol; for more recent years, where phenotypic confirmatory testing was not performed routinely in the clinical laboratory, isolates were subcultured from -80°C freezers and tested. Chi-squared Test for trends was completed using GraphPad Instat.

**RESULTS:** A total of 59/7 isolates were reviewed. The proportion of *E. coli* that were phenotypically consistent with ESBL producers rose dramatically from 6.4% in 2006 to 14.6% by 2015 (P<0.0001). This trend was observed in both intensive care units and emergency departments. By contrast, the proportion of *K. pneumoniae*, *K. oxytoca* and *P. mirabilis* that were ESBL positive remained relatively constant. Susceptibility rates to ciprofloxacin, TMP-SMX, gentamicin, and tobramycin among ESBL-producing *E. coli* in 2015 were 9.3%, 44.0%, 74.7%, and 60.0%, respectively.

**CONCLUSIONS:** Our findings indicated a significant rise in the proportion of ESBL-producing *E. coli* isolated from blood within our cohort over the last 10 years. Identification of this dramatic rise is important to inform empiric treatment, and further work is underway to identify the presence of ST131 among the isolates, as well as characterize ESBL genotypes.

**I03**

**An Outbreak of *Klebsiella pneumoniae* producing NDM in an Acute Care Hospital: The Importance of Patient Room Sharing in Transmission and Regional Tracing in Containment**

S SMITH1,2, R Wiens2, JN Kanji1,3, J Oda2, L Mataseje4, MR Mulvey4, G Taylor1,2

1University of Alberta, Edmonton, AB 2Alberta Health Services, Edmonton, AB, 3Alberta Provincial Laboratory of Public Health, Edmonton, AB, 4National Microbiology Laboratory, Winnipeg, MB

**BACKGROUND:** In recent years, ESBL-producing *Enterobacteriaceae* have emerged as an increasing concern with variable rates depending on geographic region. We sought to determine the prevalence of ESBL *E. coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca* and *Proteus mirabili* isolates from blood over the 10-year period from 2006 through 2015.

**METHODS:** Using the laboratory’s information system, all *E. coli*, *K. pneumoniae*, *K. oxytoca* and *P. mirabilis* isolated from blood cultures between 2006 and 2015 in a large tertiary-care academic microbiology labora-

tory served 4 acute care hospital sites, 4 rehabilitation centres, and three other healthcare sites (long-term care/palliative/mental health) were reviewed. Isolates had been identified using the bioMérieux Vitek 2 system (2006 through 2013) or Vitek MS MALDI (2014 onwards) as per clinical laboratory protocol. Antimicrobial susceptibility testing was completed according to CLSI standards using the Vitek 2 system or by disk diffusion. ESBL screening and phenotypic confirmatory testing were completed by a modified CLSI protocol; for more recent years, where phenotypic confirmatory testing was not performed routinely in the clinical laboratory, isolates were subcultured from -80°C freezers and tested. Chi-squared Test for trends was completed using GraphPad Instat.

**RESULTS:** A total of 59/7 isolates were reviewed. The proportion of *E. coli* that were phenotypically consistent with ESBL producers rose dramatically from 6.4% in 2006 to 14.6% by 2015 (P<0.0001). This trend was observed in both intensive care units and emergency departments. By contrast, the proportion of *K. pneumoniae*, *K. oxytoca* and *P. mirabilis* that were ESBL positive remained relatively constant. Susceptibility rates to ciprofloxacin, TMP-SMX, gentamicin, and tobramycin among ESBL-producing *E. coli* in 2015 were 9.3%, 44.0%, 74.7%, and 60.0%, respectively.

**CONCLUSIONS:** Our findings indicated a significant rise in the proportion of ESBL-producing *E. coli* isolated from blood within our cohort over the last 10 years. Identification of this dramatic rise is important to inform empiric treatment, and further work is underway to identify the presence of ST131 among the isolates, as well as characterize ESBL genotypes.

**I03**

**An Outbreak of *Klebsiella pneumoniae* producing NDM in an Acute Care Hospital: The Importance of Patient Room Sharing in Transmission and Regional Tracing in Containment**

S SMITH1,2, R Wiens2, JN Kanji1,3, J Oda2, L Mataseje4, MR Mulvey4, G Taylor1,2

1University of Alberta, Edmonton, AB 2Alberta Health Services, Edmonton, AB, 3Alberta Provincial Laboratory of Public Health, Edmonton, AB, 4National Microbiology Laboratory, Winnipeg, MB
OBJECTIVE: To describe an outbreak of *Klebsiella pneumoniae* harbouring NDM (NDM-Kp) in an acute care hospital (University of Alberta Hospital - UAH).

METHODS: Following identification of the NDM-Kp index case, who had been admitted four months earlier, contact tracing occurred. A contact was defined as a patient who had been on the same unit as the index or subsequent case. A list of contacts was provided to regional Long Term Care (LTC) and acute care facilities. When a contact presented to these facilities they underwent screening for NDM-Kp (culture based urine and rectal swab). Screening of contacts from community settings or out of region facilities was not performed. Whole Genome Sequencing (WGS) was performed on NDM-Kp isolates to support the investigation.

RESULTS: In March 2016, a clinical urine specimen in a patient (index case) who had been admitted in Dec 2015 was reported as growing NDM-Kp. The presumptive source was a patient on the same unit but different room in Dec 2015-January 2016 as the index patient who had been found on admission to carry NDM-Kp following hospitalization in Egypt. Testing of contacts of the index and subsequent cases revealed a further 10 cases (a total of 11 UAH-acquired cases). One case had cystitis; all others were urine or rectal colonized. Apart from the index case all others had been UAH roommates of non-isolated NDM-Kp carriers; 8 had been roommates within the same large 4 bed room. Three cases were found when tested in LTC facilities, and 4 were found when admitted to four other regional acute care hospitals. No secondary transmission was found in contact screening at LTC or other acute care facilities. WGS was used to compare single-nucleotide variants (SNV) between isolates and predict transmission pathways.

CONCLUSION: In this outbreak silent transmission occurred over an extended period and after index transmission was entirely associated with hospital room and toilet sharing. In a regional health system patients can be admitted to multiple different health facilities, complicating contact tracing and testing. During extended outbreaks WGS is useful in revealing transmission pathways.
Abstracts

32

Burden of Illness and Outcome of Viral Respiratory Tract Infection in Hospitalized Adults
S SMITH1,2, L Zapernick1, A Crocker1, JN Kanji1,3, G Taylor1,2

1University of Alberta, Edmonton, AB, 2Alberta Health Services, Calgary, AB, 3Alberta Provincial Laboratory of Public Health, Edmonton, AB

OBJECTIVE: To assess the frequency, virology and outcome of patients hospitalized with respiratory virus infection (RVI) over consecutive respiratory virus seasons. Patients and Methods: All patients admitted to the University of Alberta Hospital and Mazankowski Alberta Heart Institute who tested positive for a respiratory virus during two consecutive seasons (2014-2015, 2015-2016) were assessed. Demographic data, type of infecting virus and whether RVI was healthcare acquired was determined. At thirty days following positive test, all patients were routinely reviewed to determine outcome (ICU admission or death in hospital), and if dead whether death was attributed to RVI.

RESULTS: In two seasons, 535 RVI were identified (23.9 per 10,000 patient days). Year to year the RVI rate was similar but peak month and responsible virus varied; 10.7% of cases were healthcare acquired. Influenza viruses accounted for 53.5% of cases (influenza A 44.9%, influenza B 8.6%), with an antiviral treatment rate of 47.6% in these cases. At thirty days after initial assessment, 19.4% of RVI patients required ICU admission. Overall RVI attributable mortality was 5.4%. Non-influenza A RVI accounted for nearly half of all ICU admissions and attributable deaths.

CONCLUSION: A consistent burden of RVI in hospital patients was seen but varied in timing and causative virus. RVI, both influenza and non-influenza result in substantial attributable mortality in hospital patients. Given the high burden of morbidity and mortality in non-influenza RVI, testing and isolation of all ILI patients is warranted.

106
Monitoring Healthcare Worker Colonization with MRSA, VRE and C. difficile on the Bone Marrow Transplant Ward
T Woznow1, T WONG1,3, A Stefanovic1,3, M Croxen1, H Hoang2, R Broady2, R Dixon4, E Bryce1,3

1Medical Microbiology and Infection Control, Vancouver Coastal Health, Vancouver, BC, 2BC Centre for Disease Control Public Health Microbiology and Reference Laboratory, Vancouver, BC, 3University of British Columbia, Vancouver, BC, 4Coalition for Healthcare Acquired Infection Reduction, Vancouver, BC

OBJECTIVES: To determine the feasibility of monitoring ARO trends in healthcare workers (HCW) caring for myeloablative (allogeneic) hematopoietic stem-cell transplant (HCST) patients.

METHODS: A year-long pilot project (October 2015-October 2016) monitored MSSA, MRSA, VRE, and C. difficile colonization in 32 HCW and 9 HSCT patients during the patients’ hospital stay. HCWs had weekly nares, perineum and hand cultures performed; while HSCT patients had weekly Baylor washes, stool and axilla cultures. Staphylococcus aureus and Enterococcus species were cultured on routine media, and identified using MALDI-TOF; MRSA and VRE confirmed with selective media. C. difficile was identified using an in-house PCR capable of detecting the tcdB gene. Patient

for HA-CDI per 10,000 patient days in CNISP hospitals peaked in 2011 (6.71) and have since decreased to 4.43 in 2015. By PFGE, NAP-1 was the predominant strain type nationally, accounting for 37.5% of all isolates, followed by NAP-4 (14.3%) and NAP-11 (5.8%). Regionally, NAP-1 was the predominant strain type in Central (47.3%) and Western (30.1%) Canada, but NAP-4 (24.3%) was the predominant strain type in Eastern Canada. A disproportionate frequency of NAP-1 was identified in patients who died (59.4%), who required a colectomy (52.9%), and in patients admitted to an ICU (61.4%). During the study period, the 30-day all-cause and attributable mortality was 13.3% and 4.4%, respectively. Nationally, significant changes in strain types were observed over the surveillance period, including a decrease in NAP-1 and NAP-2 and increases in NAP-4 and NAP-11. Overall resistance rates were 0.04% to vancomycin, 44.4% to moxifloxacin, 1.5% to rifampin, and 28.5% to clindamycin. Resistance was not observed for metronidazole or tigecycline.

CONCLUSIONS: HA-CDI rates in adults are decreasing across Canada. NAP-1 remains the predominant strain type and is associated with more severe outcomes, but its prevalence is decreasing steadily and varies significantly by region.
charts were retrospectively reviewed for evidence of clinical disease.

RESULTS: Sampling compliance from HCWs was 87% (270/311 opportunities), and 90% (129/144) in patients. All patients who were approached consented. Nine (9/32, 28%) HCWs tested positive for MSSA: 5/9 were persistently colonized. One HCW was transiently colonized with MRSA. No HCWs tested positive for VRE or C. difficile. Two (2/8, 22%) patients tested positive for MSSA; both were acquired during their hospitalization. No patients tested positive for MRSA. Four (4/9, 44%) of patients tested positive for VRE; none were hospital acquired. Chart review revealed no evidence of clinical disease related to MSSA or MRSA. One had VRE bacteremia. Six (6/9, 67%) tested positive for C. difficile in the stool; only 1 of which was acquired in hospital (with compatible clinical symptoms).

CONCLUSIONS: Results from this pilot project found low colonization rates of ARO’s in HCWs, and high compliance for sampling. Compliance was similarly high in HSCT patients. Colonization rates of VRE and C. difficile were high but the low number of patients preclude inference as to the cause. Next steps include whole-genome sequencing of positive cultures to determine relatedness, and planning for a larger study.

Saturday, May 6, 2017
11:15-12:30 Session J
Room: Willow

J01.S Neisseria gonorrhoeae Treatment Failure in Québec, Preliminary Results of an Enhanced Surveillance Program
V BOISSONNEAULT1, S Venne2, C Fortin1,3, B Lefebvre3, A-C Labbé1,3

1Département de microbiologie, infectiologie et immunologie de l’Université de Montréal, Montréal, QC, 2Ministère de la santé et des services sociaux du Québec, Montréal, QC, 3Institut national de santé publique du Québec, Montréal, QC

BACKGROUND: Reported cases of Neisseria gonorrhoeae infections are steadily increasing. Of concern, antibiotic resistant strains have been described worldwide, limiting treatment options. Cases of treatment failure have been observed, and prove to be an emerging public health issue.

METHODS: In November 2014, an enhanced surveillance program was instated by the Ministère de la santé du Québec. When a case of suspected N. gonorrhoeae treatment failure is identified by the local public health department, patient information (including re-exposition history and culture results) is collected. Cases are classified either as probable or suspected.

RESULTS: Between November 2014 and October 2016, 13 cases were analyzed: 9 probable and 4 suspected. The population had a mean age of 29 years old (range 19 to 57), consisted of 69% males, and one transmale patient, the latter being the only known sex worker. Men who have sex with men represented 78% of all male cases. The mean number of sexual partner of the last two months before the initial infection was 2.5. No known exposition outside Québec was reported. Indications for initial testing was presence of symptoms (n=7), screening (n=3), history of sexual contact with an individual with N. gonorrhoeae infection (n=2), and history of sexual contact with presence of symptoms (n=1). Multiple sites infection was seen in 54% of cases. All patients had positive NAAT, while 6 had positive culture results at first visit. Ten patients received an initial combination therapy that included either cefixime or ceftriaxone. More than 2 treatments were required for 2 patients. Failure was observed mostly with pharyngeal (46%) and genital infections (54%). Cases of resistance to ciprofloxacin alone (15%), azithromycin alone (8%), ciprofloxacin and tetracycline (8%) were observed. Decreased susceptibility (MIC 0.25 mg/L) to ceftriaxone or cefixime was found in 2 strains.

CONCLUSION: Although not frequent, treatment failure of N. gonorrhoeae infection is observed in Québec, even when recommended treatments were used. The enhanced surveillance program shows the importance of test of cure, ideally by obtaining cultures from patients with treatment failure.
**J02**

**High Levels of Antimicrobial Susceptibility to Antibiotics No Longer Used for Treatment in *Neisseria gonorrhoeae* Isolates from Saskatchewan (2003-2015)**

JR Dillon¹, PN Levett², GB Horsman², SD Thakur¹

¹University of Saskatchewan, Saskatoon, SK, ²Saskatchewan Disease Control Laboratory, Regina, SK

**OBJECTIVE:** *Neisseria gonorrhoeae* (Ng) can be resistant to all classes of antibiotics used for treatment including macrolides (azithromycin) and third generation cephalosporins, the presently recommended combined therapy. To determine temporal trends in resistance and to ascertain whether no longer recommended antibiotics might still be used, the antimicrobial susceptibility (AMS) of Ng isolates from Saskatchewan was determined.

**METHODS:** AMS for 685 Ng cultured specimens, collected from 2003-2015, was determined using the agar dilution method (CLSI).

**RESULTS:** Below 5% (the % recommended for change in treatment) of Ng isolates collected from 2006-2012 were resistant to penicillin in contrast to >5% in 2003 (6.7%), 2004 (6.8%), 2005 (11.5%), 2013 (27.5%) and 2014 (13.5%). Only 3 PPNG were isolated. Chromosomal tetracycline resistance remained above 5% throughout the study and TRNG isolates fluctuated between 0 and 17% of isolates tested. Ciprofloxacin resistance ranged between 0% and 1.9% of isolates tested up to 2009 but was over 5% thereafter. All isolates were susceptible to spectinomycin. Over 95% of Ng isolates tested were susceptible to azithromycin except in 2010 (27.6% resistant; 8/29) and 2013 (7.2% resistant; 5/69). Reduced susceptibility to cefixime (10 isolates) or ceftriaxone (2 isolates) was rare.

**CONCLUSIONS:** Ng isolates in Saskatchewan were sporadically susceptible to several antibiotics (penicillin, ciprofloxacin) which were no longer recommended nationally.

**J03**

**Delayed Serological Response against *Treponema pallidum* may attribute to Upsurge of Syphilis Cases in MSM Populations**

M Morshed¹,³, M-K Lee¹, S Man¹, Y Simpson¹, Q Wong¹, C Montgomery², S Makaroff³, J Wong², T Gannon², M Tyndal²,³, M Krajden¹,³

¹BCCDC Public Health Laboratory, Vancouver, ²BCCDC Clinical Prevention Services, Vancouver, ³University of British Columbia, Vancouver, BC

**BACKGROUND:** Syphilis infections are rising in MSM populations in North America and globally. Serology is the primary means of syphilis diagnosis; however, antibody responses may take 4 to 6 weeks or more. Detection of syphilis by dark-field microscopy (DF) or direct fluorescence antibody (DFA) is not as sensitive or specific as PCR.

**METHODS:** The British Columbia Centre for Disease Control’s Public Health Laboratory (BCCDC PHL) offers dark-field microscopic exam (n=45), direct fluorescence antibody microscopic examination (n=281), and PCR to facilitate rapid syphilis diagnosis. We therefore assessed the comparative sensitivity and specificity of the various syphilis tests. Over a three-year period (2013-2015) 1,260 samples from 1,111 patients were tested by PCR. PCR testing was also performed on 1,444 archived Gonorrhea and Chlamydia (GC-CT) anal swab samples.

**RESULTS:** Compared to PCR, the sensitivity and specificity dark-field microscopy was 54.55% and 100.0% respectively (n=45) and 58.33% and 100.0% for direct fluorescence antibody microscopic examination (n=281), and PCR to facilitate rapid syphilis diagnosis. We therefore assessed the comparative sensitivity and specificity of the various syphilis tests. Over a three-year period (2013-2015) 1,260 samples from 1,111 patients were tested by PCR. PCR testing was also performed on 1,444 archived Gonorrhea and Chlamydia (GC-CT) anal swab samples.

**CONCLUSIONS:** *T. pallidum* PCR significantly more sensitive than DF and DFA. *T. pallidum* PCR also detected active syphilis missed by standard serology, DF and DFA from genitourinary and anal samples. This likely contributes to onward transmission of syphilis.
**J04**

*Mycoplasma genitalium* Antibiotic Resistance Mediated Mutations in Canadian Women with and Without *Chlamydia trachomatis* Infection

M CHERNESKY1, D JANG1, I Martin2, L Hoang3, P Naidu4, PN Levett5, J Wylie6, A Rebbapragada7, S Ratnam8, M Smieja9, B Weinbaum9, D Getman9

1St. Joseph’s Healthcare/McMaster University, Hamilton, ON, 2National Microbiology Laboratory, Winnipeg, MB, 3BCCDC Public Health Laboratory, Vancouver, BC, 4Provincial Health Laboratory, Edmonton, AB, 5Saskatchewan Disease Control Laboratory, Regina, SK, 6Cadham Provincial Laboratory, Winnipeg, MB, 7Dynacare Medical Laboratory, Brampton, ON, 8Newfoundland & Labrador Public Health Laboratory, St. John’s, NL, 9Hologic Inc., San Diego, CA, USA

**BACKGROUND:** *Mycoplasma genitalium* (MG) infections in women have been associated with cervicitis, pelvic inflammatory disease, urethritis, endometritis, salpingitis, preterm birth and are often detected in women found to be harbouring other pathogens. The objectives were to determine the geographic distribution of MG in Canadian women seeking care for STIs by testing remnant samples from Aptima Combo 2 tests which had detected 396 *Chlamydia trachomatis* (CT) positives and 406 CT-aged matched negatives from BC, AB, SK, MB, ON and QC and to determine the rates of macrolide and fluoroquinolone mediated mutations.

**METHODS:** De-identified samples from women aged 15-58 were tested in an MG 16S rRNA transcription mediated amplification (TMA) research assay on a Tigris instrument. Confirmatory testing was performed and tested for macrolide and fluoroquinolone resistance mediating mutations using MgPa PCR with Jensen primers and Sanger sequencing.

**RESULTS:** The MG detection rate was 9.4% (range SK 20% - QC 3.0%). There were 75 MG infections and 26 (47.3%) had A2058C/G or 2059 C/G/T macrolide resistance mutations at region V of the 23S rRNA and one woman 1.9% (1/53) was also harbouring alterations associated with fluoroquinolone resistance. The MG positivity rate in CT infected women was 13.4% compared to 5.4% in women without CT infection (p<0.001). The distribution of macrolide resistance mutations was similar in patients with and without CT infections. MG positive infections were detected in cervical swabs (CS) (7.7%) and first catch urine FCU (11.4%). Although the eastern Canadian provinces were unable to submit Aptima remnant samples to the survey, raw FCU samples from laboratories in NS (n=66) and NL (n=193) identified 5 (1.9%) positive cases, outside of the study.

**CONCLUSIONS:** MG infection and macrolide resistance mediating mutation rates are substantial in Canadian women. Studies using approved diagnostic tests are needed from all Canadian provinces and territories.

**J05**

Urinary Meatal Swabbing Detects More Men Infected with *Mycoplasma genitalium* and Four Other Sexually Transmitted Infections Than First Catch Urine

D JANG1, I Martin2, M Smieja1, B Weinbaum3, D Getman3, M Chernesky1

1St. Joseph’s Healthcare/McMaster University, Hamilton, ON, 2National Microbiology Laboratory, Winnipeg, MB, 3Hologic Inc., San Diego, CA, USA

**BACKGROUND:** *Mycoplasma genitalium* (MG) can cause acute or recurrent urethritis in men. Other male infections include *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (NG), *Trichomonas vaginalis* (TV) and human papillomavirus (HRHPV). The objective was to compare self-collected urinary meatal swabs (UMS) to first catch urine (FCU) from men (n=356) attending a sexually transmitted infections (STI) clinic.

**METHODS:** Each patient collected an FCU and was instructed to grasp the shaft of his penis, pulling back to open the urinary meatus then placing the tip of a swab into the opening and turning it once. A subset of 101 collected 2 different Aptima swabs (unisex swab and vaginal swab). A transcription mediated amplification (TMA) based research test was used for MG. The other analytes were tested with approved Aptima tests.

**RESULTS:** A total of 23.9% had at least one infection. The detection rates for MG were 15.3% for UMS and 12.6% for FCU (p=0.035). PCR confirmatory testing and sequencing for mutations associated with macrolide resistance were present in 55.9% (19/34) of the MG positive FCU samples that had readable 23S rRNA sequences (9 A2058G, 8 A2059G and single cases of A2059C and A2058T mutations). Percent positive from UMS and FCU were 11.3 vs 9.3 (p=0.04) for CT; 1.4 vs 0.8 (p=1.0) for NG; 7.9 vs 1.7 (p<0.001) for TV; and
5.9 vs 3.4 (p=0.08) for HR HPV. The unisex and vaginal swabs detected MG infections in the same 16 patients. Of the 54 men infected with MG, 12 were also infected with TV, 4 with HPV and 1 with NG.

**CONCLUSIONS:** These predominantly asymptomatic men had a high rate of MG infections with substantial macrolide resistance. The UMS identified more men for all 5 STIs than FCU. Both Aptima swabs performed equally well. Patients found it easy and comfortable to self-collect a UMS.

**Saturday, May 6, 2017**  
**11:15-12:30 Session K**  
**Room: Pine**

**K01**  
**Beta-lactam Allergy Skin Testing (BLAST) at the Point-of-care for Patients with Infectious Diseases: A Pragmatic Multicentre Evaluation**  
JA LEIS1,2, L Palmay1, G Ho2, S Raybardhan1, S Gill2, T Kan3, J Campbell4, S Walker5, JB McCreary1, P Das1, B Minnema1, J, E Powis2, H Ferguson1, B Wong3, E Weber1

1Sunnybrook Health Sciences Centre, Toronto, ON, 2Michael Garron Hospital, Toronto, ON, 3North York General Hospital, Toronto, ON, 4Division of Infectious Diseases, Department of Medicine, University of Toronto, Toronto, ON, 5Centre for Quality Improvement and Patient Safety, University of Toronto, Toronto, ON

**OBJECTIVES:** Allergy assessment including beta-lactam allergy skin testing (BLAST) when appropriate is recommended by Antimicrobial Stewardship guidelines but few studies have systematically evaluated its use among hospitalized patients. We aimed to determine the impact of implementing point-of-care BLAST as an antimicrobial stewardship activity.

**METHODS:** We conducted a pragmatic multicentre evaluation of the use of BLAST at the point-of-care for patients with infectious diseases. Pharmacist-physician teams at three hospitals received training by allergists to offer BLAST for patients receiving non-preferred beta-lactam therapy due to severity of their allergy. Exclusion criteria included patients with history suggestive of prior severe non-IgE reactions, recent documented IgE reaction within prior 3-months, being discharged within 24 hours of assessment, or not providing consent to undergo BLAST. Those with negative BLAST received an oral/intravenous penicillin challenge before being switched to the preferred beta-lactam therapy. The primary outcome was the proportion of patients receiving the preferred beta-lactam therapy. A generalized estimating equation model was created to adjust for the correlation among observations at the same hospital.

**RESULTS:** Of 827 patients with reported beta-lactam allergy over the 15-month study, beta-lactam therapy was preferred among 632 (76%). During baseline, 122/246 (50%) received preferred beta-lactam therapy compared to 312/386 (81%) following availability of BLAST (p<0.0001). Days of penicillin and cephalosporin therapy increased while days of carbapenem and fluoroquinolone decreased significantly compared to baseline. In total, 90/154 (58%) eligible patients underwent BLAST of which 85 (94%) were negative, 4 (4%) were non-diagnostic and 1 (1%) was positive; 84 (93%) were switched to preferred beta-lactam therapy with 1 (1%) who developed a non-severe rash 1-day later.

**CONCLUSIONS:** The use of BLAST at the point-of-care greatly improved use of preferred beta-lactam therapy for patients with reported allergy. Larger longitudinal studies are needed to evaluate the safety of BLAST by Antimicrobial Stewardship programs.

**K02**  
**The Clinical Utility of Urine Turbidity and Smell in the Evaluation of Urinary Tract Infections in Hospitalized Adult Patients: A Prospective Observational Cohort Study**  
G Shumilak1, K Ng1, J Kosar2, C MAREK2, S Stewart1, A Shah1

1University of British Columbia, Vancouver, BC, 2University of Saskatchewan, Saskatoon, SK

**OBJECTIVES:** Turbid and malodorous urine are frequently documented in medical resources and patient education tools as clinical manifestations of urinary tract infection (UTI). These physical characteristics are also common triggers to evaluate for potential UTI despite expert opinion arguing against this practice. Research evaluating the clinical utility of urine turbidity and smell in the evaluation of potential UTI remains limited.

**METHODS:** A prospective observational cohort study at a single tertiary care centre was performed. All hospitalized adult patients evaluated for potential UTI were enrolled over an 8-week period. Urine turbidity and smell were assessed within 24 hours of urine
K03
Utilization of Antibiotics in Long Term Care Facilities in British Columbia, Canada
F Marra1, P Sharma1, M MCCABE2, B Zhao2, D George2, C Mill1, M Chong2, DM Patrick1

1University of British Columbia, Vancouver, BC, 2BC Centre for Disease Control, Vancouver, BC

BACKGROUND: Elsewhere, antibiotic use is reported as highly prevalent in long-term care facilities (LTCF); a resident’s annual exposure to at least one course of antibiotic is approximately 50%-80%. The objective of this study was to understand the nature and extent of antibiotic use in the full population of residents in British Columbia’s (BC) LTCF from 2007 to 2014.

METHODS: Population-based data from BC’s central prescription database (PharmaNet) were analyzed to determine the most commonly utilized antibiotics among BC’s LTCF population and describe changing prescribing trends over time. These data were linked to the Medical Services Plan (MSP) physician billing system to identify the indication associated with an antibiotic prescription based on ICD diagnostic codes. Indications most commonly treated with antibiotics were described and Defined Daily Dose (DDD)/1000 LTC inhabitants/day were calculated and compared over time.

RESULTS: Our database included an average of 15,000 residents per year across BC’s 300+ long-term care facilities. Over 419,000 antibiotic prescriptions were dispensed during the eight-year period. Following a 6.3% reduction in overall utilization since 2007, use remained high in 2014 at 29.4 DDD/1000 LTC inhabitants/day - nearly double the utilization in BC’s general population. Although usage of most antibiotics declined, the use of amoxicillin, doxycycline, and amoxicillin-clavulanate increased by 29.8%, 177.4%, 213.5%, respectively. The most prevalent indication in the linked data was urinary tract infection (6.53 DDD/1000 LTC inhabitants/day), with nitrofurantoin, ciprofloxacin and trimethoprim/sulfamethoxazole being the most commonly prescribed agents. This was followed closely by prescriptions for respiratory infections (5.20 DDD/1000 LTC inhabitants/day), with clarithromycin, cefuroxime and moxifloxacin being the most commonly prescribed.

CONCLUSION: Antibiotic use in British Columbia’s LTCF is high relative to the general population and this could contribute to a reservoir for resistant pathogens. Antimicrobial stewardship in LTCF may prove essential to preserving the value of existing antibiotics.
center, three hospital ERs routinely referred all cases of cellulitis requiring outpatient intravenous antibiotics, to a central ER-staffed cellulitis clinic. In October 2014, the policy was changed to refer all cellulitis patients to an Infectious Diseases (ID) specialist-supervised cellulitis clinic in the same facility. We evaluated the effect of automatic ID consultation on disease recurrence rates, hospitalization, and mortality.

METHODS: A retrospective cohort study of all patients seen by the ER clinic in the last 4 months prior to the change in policy (ER Management Cohort [ERMC]) (n=149) and those seen by ID in the first 3 months of the automatic ID consult policy (ID Management Cohort [IDMC]) (n=136).

RESULTS: 54/136 (40%) patients in the IDMC were given an alternative diagnosis (non-cellulitis), compared to 16/149 (11%) in the ERMC (p<0.0001). Antibiotics were discontinued in 16/136 (12%) following ID consultation. Multiple backward logistic regression demonstrated rates of disease recurrence were lower in the IDMC than the ERMC (Hazard Ratio [HR]: 0.06, CI95%: 0.009-0.33, p=0.003), as were rates of hospitalization (HR: 0.11, CI95%: 0.02-0.62, p=0.01). There was no significant difference in mortality.

CONCLUSIONS: Automatic ID consultation for cellulitis diagnosed in the ER was beneficial in differentiating mimickers from true cellulitis, reducing recurrence rates, and preventing hospital admissions.

K05
Methicillin-resistant Staphylococcus aureus (MRSA) infections in Hospitalized Pediatric Patients in Canada 2008–2015 — Canadian Nosocomial Infection Surveillance Program (CNISP)


1University of Calgary, Calgary, AB, 2Alberta Children’s Hospital, Calgary, AB, 3Public Health Agency of Canada, Ottawa, ON, 4University of Alberta, Edmonton, AB, 5Stollery Children’s Hospital, Edmonton, AB, 6University of Manitoba, Winnipeg, MB, 7Health Sciences Centre, Winnipeg, MB, 8Vancouver Coastal Health, Vancouver, BC, 9McGill University, Montréal, QC, 10McGill University Health Centre, Montréal, QC, 11Hamilton Health Sciences, Hamilton, ON, 12National Microbiology Laboratory, Winnipeg, MB, 13IWK Health Center, Halifax, NS, 14University of Toronto, Toronto, ON, 15North York General Hospital, Toronto, ON, 16Vancouver Island Health Authority, Vancouver, BC, 17Dalhousie University, Halifax, NS, 18Sinai Health System, Toronto, ON, 19Université de Montréal, Montréal, QC, 20Centre hospitalier universitaire Sainte-Justine, Montréal, QC, 21Hospital for Sick Children, Toronto, ON, 22Sunnybrook Health Sciences Centre, Toronto, ON, 23University of Alberta Hospital, Edmonton, AB, 24BC Children’s & Women’s Hospitals, Vancouver, BC, 25University of British Columbia, Vancouver, BC, 26Western Memorial Hospital, Corner Brook, NF, 27University of Ottawa, Ottawa, ON, 28Children’s Hospital of Eastern Ontario, Ottawa, ON

OBJECTIVES: The epidemiology of methicillin-resistant Staphylococcus aureus (MRSA) in children hospitalized in Canada was last summarized in 2007. This study describes the epidemiology of MRSA infections in children admitted to Canadian hospitals participating in the CNISP network since 2008.

METHODS: Laboratory-based surveillance was conducted at CNISP hospitals from 2008-2015. Clinical and epidemiologic data were identified using medical records. Standardized definitions were used to characterize MRSA infections as community-associated (CA) or healthcare-associated (HA). Rates were calculated and expressed per 10,000 patient-days. Isolates were characterized by pulsed gel electrophoresis and/or spa typing and assigned into Canadian epidemic strain types.

RESULTS: In total, 1,182 MRSA infections were identified in pediatric patients (age ≤ 18 years). Overall, 782 (66%) were CA, 332 (28%) were HA, and 68 were unknown. The median annual ratio of CA versus HA cases was 2.5 with an unusually high ratio of 6.3 in 2009. The median rate of all MRSA infection was 3.80 per 10,000 patient-days, range: 2.92 (2009) to 4.65 (2015). The highest rates were noted in 2014 (4.62) and 2015 (4.65). The median rate of MRSA bloodstream infections (BSI) was 0.29, range: 0.09 (2010) to 0.7 (2015). The median CA-MRSA rate was 2.61, range: 1.76 (2011) to 3.05 (2012). The median HA-MRSA rate was 1.11, range: 0.19 (2009) to 1.69 in 2015. Higher rates of MRSA BSI, CA-MRSA and HA-MRSA infections were observed in three years: 2012, 2014 and 2015. CMRSA10 remains the dominant strain type (46% 2008-2015); however, the proportion of CMRSA2 has increased from 13% in 2008 to 33% in 2015.
CONCLUSIONS: CA infections are more common than HA infections and the rate of MRSA infections has continued to increase in recent years. No obvious correlation with changes in infection rates and MRSA strains is observed.

Saturday, May 6, 2017
11:15-12:30 Session L
Room: Birchwood Ballroom

LO2.S Test Method Evaluation for a Direct MALDI-TOF MS Identification (ID) Protocol of Organisms from Positive Blood Cultures from the BD Bactec Fx System
C Macdonald1,2, A Fehr1, T Dingle1,3, G Tyrrell1,3, P Naidu1,2

BACKGROUND: Recognizing the positive clinical impact of earlier organism ID due to targeted antibiotic selection in bacteremic patients, the Provincial Laboratory for Public Health (ProvLab) compared two published methods for the direct organism ID by MALDI-TOF MS from positive blood culture vials. Currently, in ProvLab, ID is made by MALDI-TOF MS following inoculation and incubation of appropriate solid media. With direct ID, targeted empiric therapy using local antibiogram data, can be provided >24 hours earlier.

METHODS: Following literature review, two methods were selected for an evaluation study based on available equipment, process time, workflow and costs. The Serum Separator Tube (SST) and Differential Centrifugation (DC) were the two selected methods. In the SST method, blood is clotted and bacteria are separated from culture media using a BD vacutainer SST tube. In the DC method, a series of washes and spins at different speeds are used to isolate bacteria. Both methods pro-

RESULTS: 206 results were concordant between Alifax and routine culture (96.7% agreement). 7 results were discordant 5 of them were false positive on Alifax, and two were false negative. Sensitivity is 94.6%, Specificity is 97.1%, PPV is 87.5% and NPV is 98.8%. Time to detection from the 40 spiked specimens was all within 6 hours except for one isolate of H. influenzae that took 9 hours to grow. All identifications were done directly from Alifax vial broth on Bruker MALDI TOF with no discrepancies. Susceptibilities were done on vials with turbidity of 1 McFarland or higher. Susceptibility results from Alifax showed 5.7% minor error rates for S. aureus, 10% for E. faecium and 5.5% for E. coli. Very major error was detected for one antibiotic for E. coli (5.8%).

CONCLUSION: Use of Alifax for detection of growth from sterile site fluid is a reliable and rapid method of detection. Direct Identification by Bruker MALDI will accelerate time to identification. Direct susceptibility testing will require more evaluation.

L02 Evaluation of Alifax HB&L UROQUATTRO for Rapid Detection of Bacteria from Sterile Site Fluid Specimens
H Almohri, E Nagai
LifeLabs Medical Laboratory Services, Toronto, ON

Rapid detection of any bacterial growth from sterile fluid is essential for guiding appropriate antibiotic therapy. Alifax HB&L UROQUATTRO is a semi-automated system for screening of human biological fluids. Technology is based on light scatter; kinetic detection at 30° and 90° with laser light scattering at 650 nm. This allows for detection of bacteria in as little as 6 hours from the original sample.

OBJECTIVE: To evaluate the use of Alifax for detecting bacterial growth in sterile fluid samples in 6 hours, and for identification and susceptibility testing of growing organisms. Method: A total of 213 clinical and spiked fluid (synovial, bursa, breast, inguinal seroma, abdominal, peritoneal, and pleural), were planted on culture media as per routine protocol. 0.5 mL of fluid from these same samples was directly inoculated into vials and incubated on Alifax for different durations. Results were evaluated at 6 hours and 12 hours. At end of testing duration negative vials were removed and terminal Gram stains were performed. Positive vials were removed when flagged; terminal Gram stain, identification on Bruker MALDI Biotyper and when applicable susceptibility testing on BioMérieux Vitek II were performed. Time to detection was evaluated by repeat testing of ATCC spiked vials for the following 4 organisms for 10 days S. aureus, K. pneumoniae, S. pneumoniae, H. influenzae

RESULTS: 206 results were concordant between Alifax and routine culture (96.7% agreement). 7 results were discordant 5 of them were false positive on Alifax, and two were false negative. Sensitivity is 94.6%, Specificity
provide a bacterial pellet which can then be used for MS MALDI-TOF ID. Using 30 positive blood cultures from recent patient samples, the two methods were compared for percent agreement with ID from solid media culture. Included were cultures from both paediatric and adult patients, and the three blood culture vials in use: Aerobic, Lytic and Peds plus. Isolates included: 19 gram positive, 10 gram negative and 1 yeast.

RESULTS: The SST method was superior to DC for both cost and time required ($2.01 vs $3.49 per culture; 20 minutes vs 120 minutes). For Identification agreement (correct and valid ID >95%), the SST resulted in 26/30 (86.7%) correct IDs compared to 17/30 (56.7%) via DC. The SST method, correctly identified 16/19 gram positives (84.2%), 9/10 gram negatives (90%) and 1 yeast (100%). For culture vials, correct IDs occurred in 10/12 (85.7%) Aerobic, 7/7 (100%) Peds Plus and 7/9 (77.8%) Lytic. S. pneumoniae failed to ID via both methods.

CONCLUSION: The SST method was found to be superior in performance to DC for the detection of bacterial pathogens from bacteremic patients stewardship, measuring the effect of early ID on patient outcome in Gram positive bacteremia in ICU patients, will then be conducted.

L03.S
Eggerthella lenta Blood Stream Infections Are Associated with Increased Mortality Following Empiric Piperacillin-Tazobactam Monotherapy: A Single-Centre Retrospective Cohort Study
A UGARTE-TORRES1, MR Gillrie1, T Griener1,2, D Church1,2
1University of Calgary, Calgary, AB, 2Calgary Laboratory Services, Calgary, AB

BACKGROUND: Eggerthella lenta is an anaerobic gram-positive bacilli, that is an opportunistic pathogen of complicated polymicrobial intra-abdominal infections. Most recently this organism has been recognized as an important cause of anaerobic blood-stream infections (BSI) associated with high mortality. E. lenta has been reported to have high minimal inhibitory concentrations (MICs) to piperacillin-tazobactam (PTZ).

OBJECTIVES: To describe the clinical presentation of E. lenta infections and determine the risk factors associated with 30-day mortality.

METHODS: We conducted a retrospective cohort analysis of invasive E. lenta infections in a single regional healthcare system, identified from a centralized microbiology database. A logistic multivariate analysis for 30-day mortality risk factors was conducted including all variables with a p-value <0.05 on a univariate analysis.

RESULTS: We identified 102 cases of invasive E. lenta infections, 94 (92%) were BSI, and 8 (8%) deep abscesses and ulcers. Polymicrobial infections were found in 46% cases; 72.5% of isolates were from a gastrointestinal source, most commonly from appendicitis (30%), nearly all of which (18/22, 82%) were perforated, followed by unknown source (15%), and skin and soft tissue infections (9.8%), primarily sacral ulcers (7/10, 70%). Two-thirds of participants were males with a median Charlson comorbidity score (CCS) of 3 and 95% of the isolates, regardless of source were found to have a PTZ MIC >8 μg/ml. The 30-day mortality for BSI was 45%. Empiric PTZ monotherapy was associated with 30-day mortality in the multivariate analysis (OR 3.9, CI 1.01-15.4; p=0.04), along with a CCS ≥2 (OR 4.4, CI 1.01-20.02; p=0.05), and ICU stay (OR 8.8, CI 1.7-44.3; p=0.008).

CONCLUSIONS: We described the largest case series to date of 102 infections caused by E. lenta. Empiric antibiotic coverage with PTZ for E. lenta BSI was found to be a risk factor for mortality. Our results highlight the importance of review of PTZ MIC breakpoints in selection of appropriate antibiotic management of anaerobic infections where E. lenta is involved.

L04
Urine Flow Cytometry (UFC), A Rapid Method to Screen and Eliminate Urines from Culturing
A Stefanovic1, C Porter1, A Lim1, M Pudek1,2, R Ranasinghe1, T Wong1,2, J Grant1,2, E Bryce1,2, K Ng1, D ROSCOE1,2
1Department of Pathology and Laboratory Medicine, Vancouver, BC, 2University of British Columbia, Vancouver, BC, 3Provincial Infection Control Network, Vancouver, BC

OBJECTIVES: Limitations exist to current urinalysis methods with urine dipstick being colorimetric and subjective, while microscopy is labor intensive requiring specialized technical skills. Urine flow cytometry (UFC) is an automated macroscopic method that quantifies bacterial (BAC) and WBC counts. We aim to examine if UFC can be a screening tool for urine cultures and set a threshold for BAC and/or WBC counts below which we can predict urine culture negativity.
METHODS: All urine specimens submitted to medical microbiology laboratory at an acute, tertiary care center in Vancouver, BC from July 22, 2015 until Feb 17, 2016 have undergone UFC (Sysmex UF-1000i) analysis along with regular urinalysis and urine culture. Positive urine cultures were defined as growth of ≥10⁴ CFU/ml. Correlation of UFC BAC and WBC counts with urine culture was assessed using Receiver Operating Characteristics (ROC) curves. Performance measures such as sensitivity, specificity, negative predictive values, positive predictive value and false negative rate were calculated at various thresholds.

RESULTS: 15,046 urine specimens submitted were analyzed. Most were from hospitalized inpatients (51.3%), followed by Emergency Department (33.3%) and outpatients (15.3%). Average time to UFC result from receipt in the laboratory was 0.76 (1.0) h. At a set threshold of UFC BAC≥20 or WBC≥5 we achieved 96.0% sensitivity, 39.2% specificity, 47.0% PPV, 94.5% NPV and 4.0% false negative rate. With this established threshold, we would be able to eliminate 26% of urines form undergoing urine culture.

CONCLUSIONS: UFC is a rapid and effective screening method for urine cultures. UFC allows us to eliminate urines not meeting the set threshold from undergoing urine culture with results being available within 1h from receipt in the laboratory.

L05
Long-Term Storage of Fecal Filtrate Samples used for Fecal Microbiota Transplants - Determination of Optimal Duration and Conditions
A Paterson¹, M Kissoon¹, S Surangiwala³,⁴, BM Willey¹,², S Hota¹,², SM Poutanen¹,²,³, Microbiota Therapeutics Outcomes Program (MTOP)¹,²,³
¹Sinai Health System, Toronto, ON, ²University Health Network, Toronto, ON, ³University of Toronto, Toronto, ON, ⁴McMaster University, Hamilton, ON

BACKGROUND: Fecal Microbiota Transplants (FMT) aid in re-establishing the normal bowel flora following dysbiosis linked to Clostridium difficile Infection (CDI) through the re-introduction of microbiota from healthy donor stools. As the demand for FMT increases, there is a concomitant strain on clinicians to have a ready supply of fecal filtrate. A solution is to use frozen FMT filtrate. However, there are little data showing the stability and efficacy of frozen filtrate. Furthermore, there are no established guidelines regarding the optimal conditions for FMT filtrate storage. We performed a semi-quantitative analysis of bacterial growth from filtrate created from freshly donated stools which were stored at -20°C and -80°C with and without 10% glycerol for 7, 9 and 12 months.

METHODS: 4 g of fresh stool (defined as receipt within 3 hours of collection) from anonymous donors (n=2) was homogenized with both 40 mL 0.9N sterile saline and 40 mL 0.9N sterile saline containing 10% glycerol. The resulting filtrate was frozen at -20°C and at -80°C in 1.8 mL aliquots. At baseline and after 7, 9 and 12 months storage, 100 μL of filtrate was plated onto selective anaerobic and aerobic agars and streaked using the automated Isoplator (Vista Technology). Semi-quantitative growth was recorded by two blinded readers using a standardized template and the average growths score was determined. Loss of microbial growth was determined as the difference between bacterial growth at each time point compared to baseline.

RESULTS: At 7, 9, and 12 months, fecal filtrate stored at -20°C without 10% glycerol had the greatest loss of microbial growth compared to baseline (34%, 43%, and 30% loss, respectively) followed by filtrate stored at -20°C with glycerol (12%, 15%, and 28% loss) then filtrate stored at 80°C without glycerol (13%, 14%, and 11% loss). Fecal filtrate stored at -80°C with 10% glycerol had the least loss of microbial growth compared to baseline (1%, 6%, and 5% loss).

CONCLUSIONS: FMT filtrate is associated with optimal bacterial viability if stored at -80°C with 10% glycerol, with no significant reduction in viability after storage for 12 months. Viability is significantly impacted when fecal filtrate are stored at -20°C without cryo-protectant. Impact on long-term storage on 16S microbiome analysis is ongoing.
Postoperative mediastinitis is a potentially life-threatening complication of cardiac surgery. Skin flora are the most common etiologies. Rarely, atypical pathogens cause infections which impose unique clinical and diagnostic challenges. We describe a case of culture negative mediastinitis, pericarditis, and loculated pleural effusion secondary to macrolide resistant *M. hominis* in a patient following emergent sternotomy. A 51-year-old hypertensive, dyslipidemic male underwent urgent coronary artery bypass graft surgery. On post-operative day 4, hemodynamic instability with cardiac tamponade required repeat emergent sternotomy. The patient subsequently became febrile with negative cultures and no response to broad spectrum antibiotics. Computed tomography (CT) of the chest confirmed mediastinitis and left loculated pleural effusion. Exploratory sternotomy and debridement after 6 days of fever revealed grey purulent mediastinitis. The sternal wound demonstrated growth of a “hazy” film after 3 days of incubation. After 7 days of incubation, cultures revealed “fried egg” colony appearance. Blood culture system detected CO₂ production, however gram stain was negative. Blood, sternal wound, and pleural fluid specimens were sent for 16S rRNA polymerase chain reaction (PCR) which confirmed the presence of *Mycoplasma hominis* DNA. Moxifloxacin and doxycycline were added to the regimen and he defervesced. Repeat CT scan revealed moderate left pleural effusion, which required thorascopic decortication. Susceptibility testing revealed sensitivity to doxycycline and clindamycin but resistance to penicillin and erythromycin. The patient had a full recovery and continues to do well, with plans to complete 6 months of doxycycline.

Culture-negative mediastinitis with persistent signs and symptoms of infection despite broad spectrum antibiotics should prompt diagnostic and treatment options to cover atypical pathogens. With grey purulent mediastinitis, consider *M. hominis* infection and diagnosis with 16S rRNA PCR. *M. hominis* is intrinsically resistant to macrolides, thus prolonged therapy with fluoroquinolones and/or doxycycline should be considered.

**SP02**

*Staphylococcus aureus* Interaction with *Pseudomonas aeruginosa* Biofilm Associated with Tobramycin Resistance and Failure of Eradication Therapy in Children with Cystic Fibrosis

T BEAUDOIN¹,², Y Yau¹,², V Waters¹,²

¹Hospital for Sick Children, Toronto, ON, ²University of Toronto, Toronto, ON

**RATIONAL:** Initial *Pseudomonas aeruginosa* pulmonary infection in children with cystic fibrosis (CF) is treated with antibiotics to eradicate the organism and prevent the establishment of chronic infection. However, in certain cases eradication therapy fails and the reasons for this are poorly understood. To date, there has been little consideration of the effects of the pulmonary microbiome on the success of *P. aeruginosa* eradication treatment in CF.

**OBJECTIVE:** This study aims to identify the interaction between two main pathogens in cystic fibrosis (CF) lung infection, *S. aureus* and *P. aeruginosa*, and assess the impact on *P. aeruginosa* biofilm formation and antibiotic resistance in the context of failure of eradication therapy.

**METHODS:** Using a novel slide-chamber method with exoproducsts produced by *S. aureus*, we have studied their impact on the formation of *P. aeruginosa* biofilms and antibiotic resistance to tobramycin.

**RESULTS:** We have identified an interaction between Staphylococcal protein A, produced by *S. aureus*, and Psl exopolysaccharide produced by *P. aeruginosa*, that resulted in aggregation and increased resistance to tobramycin. Strikingly, this interaction occurred only in isolates of *P. aeruginosa* recovered from children with CF who failed to clear *P. aeruginosa* following inhaled tobramycin treatment, providing a potential explanation as to why some patients may fail initial eradication therapy.

**CONCLUSIONS:** Our results suggest that bacterial interactions between *S. aureus* and *P. aeruginosa* are a potential source of antibiotic resistance in *P. aeruginosa*.
and may contribute to the failure of eradication therapy in children with CF.

**SP03**
Knowledge of Hepatitis C and Treatment Willingness Amongst People Who Inject Drugs in an Era of Direct Acting Antivirals

A MAH1, M Hull1,2, K DeBeck3, M-J Milloy1,2, S Dobrer1, E Nosova1, E Wood1,2, T Kerr1,2, K Hayashi1,2

1Department of Medicine, University of British Columbia, Vancouver, BC, 2British Columbia Center for Excellence in HIV/AIDS, University of British Columbia, Vancouver, BC, 3School of Population and Public Health, University of British Columbia, Vancouver, BC, 4Faculty of Health Sciences, Simon Fraser University, Burnaby, BC

**OBJECTIVE:** Knowledge of hepatitis C virus (HCV) is believed to be important in altering risk behaviour, improving engagement in care, and promoting willingness to initiate HCV treatment. We assessed factors associated with HCV knowledge and treatment willingness amongst people who inject drugs (PWID) in an era of direct acting antivirals.

**METHODS:** Data were derived from three prospective cohort studies of PWID in Vancouver, between June 2014 and May 2015. HCV knowledge and treatment willingness were assessed using a Likert scale. Multivariable linear regression identified factors associated with higher HCV knowledge and treatment willingness.

**RESULTS:** Amongst 630 participants, mean scores for HCV knowledge and treatment willingness were 25.41 (standard deviation [SD]: 2.52) out of 30, and 6.83 (SD: 1.83) out of 10, respectively. In multivariable analyses, Caucasian ancestry (adjusted linear regression model estimate [β] 0.50; 95% confidence interval [CI] 0.17, 0.82), employment (β 0.76; 95% CI: 0.38, 1.13), diagnosed mental health disorder (β 0.44; 95% CI: 0.11, 0.78) and previous HCV treatment (β 0.94; 95% CI: 0.46, 1.43) were independently associated with higher knowledge. Downtown Eastside (DTES) neighbourhood (i.e., epicenter of Vancouver’s drug scene) residence was independently associated with lower knowledge (β -0.48; 95% CI: -0.81, -0.15). Greater HCV knowledge (β 0.12; 95% CI: 0.07, 0.17) was independently associated with higher HCV treatment willingness. DTES residence (β -0.31; 95% CI: -0.56, -0.06) and daily crack cocaine smoking (β -0.52; 95% CI: -0.92, -0.13) were independently associated with lower treatment willingness.

**CONCLUSION:** Factors that may reflect greater socioeconomic stability, such as neighborhood residence and employment, were associated with HCV knowledge. Higher HCV knowledge was associated with more HCV treatment willingness. Our findings suggest that providing PWID greater access to HCV education may be an integral component of the HCV cascade of care and that efforts might be best targeted to areas of greater socioeconomic disadvantage.

**SP04**
HIV Infection After Prenatal Screening: An Open Window Leading to Perinatal Infection

R LANG1, S Skinner2, J Ferguson3, T Jadavji5, M Stadnyk4, J Gill1

1Department of Medicine, University of Calgary, Calgary, AB, 2Department of Medicine, University of Saskatchewan, Regina, SK, 3Department of Obstetrics and Gynecology, Regina, SK, 4University of Alberta, Northern Alberta Program, Edmonton, AB, 5Department of Pediatrics, University of Calgary, Calgary, AB

**OBJECTIVES:** In the developed world, vertical transmission of HIV has dramatically decreased with universal HIV screening during pregnancy and the subsequent use of antiretroviral therapy (ART) for those with HIV. However, maternal HIV infection acquired after a prenatal negative screening still leaves a theoretical window of vulnerability for perinatal HIV transmission from mother to child to occur (perinatal MTCT). Through this work, we aimed to characterize five cases of perinatal HIV MTCT occurring despite negative maternal HIV prenatal screening, in order to enhance preventative measures.

**METHODS:** Through a quality assurance program in two Canadian Provinces, five cases where perinatal HIV transmission occurred despite negative prenatal screening were identified between 2005 and 2013. Individual charts were reviewed and standardized data extracted, anonymized and analysed.

**RESULTS:** Two mothers had their negative HIV test performed in the second trimester and three mothers had negative testing on presentation in the third trimester. Maternal risk factors such as intravenous drug use,
high-risk sexual behaviour, hepatitis C co-infection, and belonging to high prevalence minority groups were common. All babies were clinically healthy at delivery with a normal weight suggesting late infection. Three babies were tested following subsequent identification of maternal HIV infection and two babies presented with opportunistic infections leading to their diagnoses.

**DISCUSSION:** The characteristics of these cases suggest that to achieve complete elimination of perinatal MTCT, selective clinical management of highly vulnerable mothers at risk for HIV, coupled with the use of new diagnostic molecular testing or pre-exposure prophylaxis may be required.

**SP06**

How Many Bronchial Alveolar Lavage Specimens Do We Need?

BA ALBARADI1,3, L Jiao1, C Hamielec1,2, C Main1,2

1McMaster University, Hamilton, ON, 2Hamilton Health Sciences, Hamilton, ON, 3King Fahad Specialist Hospital, Dammam, Saudi Arabia

**OBJECTIVES:** Bronchoscopy is a valuable diagnostic tool and has significant clinical impact on the management of pneumonia, especially ventilator-associated pneumonia in Intensive Care Unit patients who fail to respond to standard, guideline-based therapy. The investigation of bronchial alveolar lavage (BAL) specimens usually involves an extensive laboratory work up. The objectives of the study were to investigate the optimal number of specimens for bacteriology, virology, mycology, *Pneumocystis jirovecii* (PJP) and *Legionella pneumophila* testing to optimize the utility of BAL specimens with the aim of minimizing harm to patients and optimizing resource utilization for the laboratory.

**METHODS:** BAL specimens in our laboratory were reviewed retrospectively from 01/03/2015 to 01/06/2016 for bacteriology, from 01/03/2015 -31/05/2015 for virology, from 01/01/2015 to 01/01/2016 for mycology, and from 01/01/2013 to 01/01/2016 for *Legionella pneumophila* and PJP.

**RESULTS:** One thousand sixty-three BAL specimens were ordered for bacterial culture, yielding positive results in 45.5%. Among them, a concordance rate of 97.1% was found between two or more specimens acquired from different lung lobes. The concordance rate of multiple virology samples was 98.6% among patients in whom 2 specimens were collected per procedure, and 100% among those with 3 specimens per procedure. To study whether one specimen is sufficient for the detection of filamentous fungi, we reviewed 43 BAL samples which grew *Aspergillus fumigatus* between Jan 1, 2015 to Jan 1, 2016. A concordance rate of 60% was found between two specimens obtained from different lung lobes. A concordance rate of 100% was found among multiple specimens ordered for *Legionella pneumophila* and PJP with positivity rates of 0.14% and 0.92% respectively.

**CONCLUSION:** We recommend a single specimen per BAL be sent from the most purulent lung segment for bacteriology and viral PCR. Single specimens may also be appropriate for PJP and *Legionella pneumophila*, however further study is needed. Multiple specimens should be submitted for mycology investigations. By eliminating duplicate specimens laboratory utilization can be optimized and patient morbidity may be decreased.

**SP06**

How Frequently Does *Mycoplasma pneumoniae* Cause Infection in Children Admitted to the Paediatric Intensive Care Unit?

H ALFARAIDI, K Luinstra, M Smieja, P Jayaratne, JM Perhica

Department of Paediatrics, McMaster University, Hamilton, ON

**OBJECTIVES:** The primary objective of our study was to determine what proportion of paediatric patients with respiratory compromise requiring paediatric intensive care unit (PICU) admission had *Mycoplasma pneumoniae* (MP) detected in respiratory samples.

**METHODS:** A single centre, retrospective cohort study. Eligible children were all those aged 2 months to 18 years admitted to a tertiary-hospital PICU from September 2015 to October 2016 with an acute respiratory illness who had a nasopharyngeal swab (NPS) collected. NPSs from participants were stored and batch-tested (so test results were not available to treating clinicians) using a lab-developed loop-mediated isothermal amplification (LAMP) assay. Demographic and clinical information, including results of MP testing ordered in the course of clinical care, was obtained by retrospective chart review.

**RESULTS:** There were 227 eligible participants, of whom 118 (52%) were diagnosed with pneumonia, 56
(25%) were diagnosed with pure asthma exacerbation, and 26 (11%) were diagnosed with pure bronchiolitis. The median age was 3.1 years (25-75%ile 1.3 y – 6.0 y). Ten participants (8 among the 118 [6.8%] with pneumonia) had respiratory specimens that were positive for MP. The median age range of the MP-positive children was 7.2 y (25-75%ile 2.0 – 15.5 y, p=0.02 as compared to MP-negative participants). Final diagnoses for MP-positive children included uncomplicated pneumonia (7), complicated pneumonia (1), and bronchiolitis (2). The median length of PICU stay for MP-positive patients was 5.9 days (25-75%ile 2-8 d) which was similar to MP-negative patients. The mean PICU length of stay was longer in MP-positive patients receiving macrolide or fluoroquinolone antibiotics (9.0 vs 2.8 days, p=0.04), presumably reflecting confounding by indication.

CONCLUSIONS: Our results document the low prevalence of MP infection in children admitted to the PICU for respiratory compromise and support the recently published Canadian Paediatric Society guidelines that no longer recommend empirical macrolide therapy as treatment for all cases of severe pneumonia. However, rapid MP testing should be considered for children with respiratory compromise, especially in older age groups. Further testing to determine effectiveness of macrolide or fluoroquinolone treatment in PICU patients with MP infection should be undertaken.

SP07
Genomic Epidemiology and Characterization of CTX-M-15-producing Escherichia coli Isolated from Patients in Canadian Hospitals
AJ Denisuk1, HJ Adam1,2, P Lagacé-Wiens1,2, MR Mulvey1,3, M Baxter1, JA Karlowsky1,2, M Gilmour1,3, DJ Hoban1,2, GG Zhanel1
1University of Manitoba, Winnipeg, MB, 2Diagnostic Services Manitoba, Winnipeg, MB, 3National Microbiology Laboratory, Winnipeg, MB

OBJECTIVE: CTX-M-15 represents the dominant genotype among ESBL-producing Escherichia coli (EC) in Canadian hospitals. This study utilized whole-genome sequencing (WGS) to characterize a large cohort of CTX-M-15-producing EC collected from Canadian hospitals from 2007 to 2014.

METHODS: 7,215 EC were collected from January 2007 to December 2014 as part of the ongoing CANWARD national surveillance study. Antimicrobial susceptibility testing was performed in accordance with CLSI guidelines and putative ESBL-producers were identified by phenotypic and genotypic methods. Of 403 ESBL-producing EC identified during this period, 264 (65.5%) were found to produce CTX-M-15 and were selected to undergo WGS. Following preparation of bacterial DNA, 150-bp paired-end indexed reads were generated on the Illumina MiSeq platform, resulting in an average of 1,529,066 reads and 90-times coverage per genome.

RESULTS: The prevalence of ESBL-EC [2007: 3.4%, 2014: 11.6%] increased significantly during the study period (P<0.001), reaching maximum proportion in 2014. Antimicrobials demonstrating the greatest activity against CTX-M-15-producing EC included colistin, amikacin, ertapenem, and meropenem, while 83.0% of isolates were multidrug-resistant (MDR, resistant to ≥3 antimicrobial classes). Sequence type (ST) 131 and 405 were the dominant STs among CTX-M-15-producing EC, comprising 71.2% and 6.8% of isolates, respectively. CTX-M-15-producing EC were largely clonal based on core single nucleotide variant-based phylogeny, which demonstrated a high degree of similarity among CTX-M-15-producing ST-131 isolates circulating in Canadian hospitals. Furthermore, variants of an MDR CTX-M-15-containing plasmid belonging to the IncFII incompatibility group were identified in 75.8% of isolates. CTX-M-15 is found in common association with multiple other resistance determinants, including the β-lactamase genes blaTEM-1 (37.9%) and blaOXA-1 (67.8%), aac(6’)-Ib-cr (66.7%) conferring reduced susceptibility or resistance to ciprofloxacin, as well as multiple aminoglycoside resistance genes.

CONCLUSIONS: CTX-M-15 is present in two-thirds of ESBL-producing EC in Canadian hospitals. These organisms are largely clonal and carry a high burden of antimicrobial resistance. Genetically, CTX-M-15 is widely distributed on variants of a single IncFII plasmid.
SP08
Rapid, Reagent-Free Bacterial Identification Based on Whole-Organism Fingerprinting by Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy with Subspecies-Level Discriminatory Capability

L Lam1, P Lebel2, M Langella1, H Kim1, S Lévesque3, I Ilugovaz1, J Sedman1, A Ismail1

1McGill University, Ste-Anne-de-Bellevue, QC, 2McGill University Health Centre, Montréal, QC, 3Laboratoire de santé publique du Québec, Ste-Anne-de-Bellevue, QC, 4Health Canada, Longueuil, QC

OBJECTIVE: The objective of our work is to develop new rapid and reagent-free methods for microbial identification based on whole-organism fingerprinting by attenuated total reflectance Fourier transform infrared (ATR-FTIR) spectroscopy coupled with multivariate statistical analysis techniques.

METHODS: ATR-FTIR spectral databases were created by employing two portable ATR-FTIR spectrometers to acquire ATR-FTIR spectra of over 1200 clinical isolates of Enterobacteriaceae, enterococci, and staphylococci. ATR-FTIR spectra were acquired by direct transfer of isolated colonies from agar plates onto the ATR sampling surface of the spectrometer. ATR-FTIR spectral acquisition time was ~1 min per spectrum. Spectral data analysis was performed by hierarchical cluster analysis (HCA) and principal component analysis (PCA) in conjunction with the use of a feature selection algorithm.

RESULTS: HCA of the ATR-FTIR spectra showed clustering of replicate spectra acquired on two instruments, demonstrating the excellent instrument-to-instrument spectral reproducibility required for transferability of spectral databases. Classification of approximately 350 clinical isolates of Enterobacteriaceae at the genus and species levels was achieved by HCA of the ATR-FTIR data with an overall rate of correct classification exceeding 98%, including complete differentiation between E. coli (including verotoxin-positive strains) and Shigella spp. PCA of the ATR-FTIR spectra of enterococcal isolates allowed for differentiation of vancomycin-resistant (VRE) from vancomycin-sensitive (VSE) isolates (100% concordance with PCR testing). Discrimination between MRSA and MSSA bases on differences in their ATR-FTIR spectral profiles resulted in 95% concordance with PCR testing. Expansion of the spectral databases to encompass VRE, VSE, MRSA, and MSSA strains from across Canada is underway.

CONCLUSIONS: The results of this study demonstrate the potential utility of ATR-FTIR spectroscopy as a rapid diagnostic tool in clinical bacteriology. In addition, the capability of ATR-FTIR spectroscopy to discriminate between antibiotic-resistant and susceptible strains in the absence of antibiotic provides a new rapid, inexpensive and reagent-free technique that can contribute to the control of antibiotic-resistant nosocomial pathogens.

SP09
Colorimetric Screening of Antibiotic Resistance Biomarkers Using Nucleic Acid Enzymes and Gold Nanoparticles

M Mohamed, J Kim, K Zagorovsky, W Chan

University of Toronto, Toronto, ON

Extensive and improper use of antibiotics have led to rapid evolution of antibiotic resistance (AR). In particular, there is an emerging trend of multi-drug resistant pathogens, which have acquired resistances to multiple antibiotics. Rapid and accurate determination of bacterial susceptibility to antibiotics is critical to deliver effective treatments against infections and to reduce the risk of AR development and spread. Currently, the two major laboratory techniques for detection of AR are phenotypic culture-based tests and genotypic tests. Although phenotypic culture methods such as agar diffusion, microdilution, or selective chromogenic media are cost-effective, they take 24-72 hours for an accurate diagnosis. On the other hand, genotypic tests that uses polymerase chain reaction (PCR) can directly detect the presence of AR genes, are not affected by testing conditions, and are often used to confirm inconclusive phenotypic test results. However, PCR is expensive, uses complex equipment, and requires highly skilled technicians, precluding its use in resource-limited areas. Here, we developed rapid, sensitive and an instrument free colour-based test that can profile antibiotic resistance within 2 hours. Our assay achieved analytical sensitivity of 10^2 to 10^3 DNA copies/reaction when synthetic DNA targets were used, and 10^2 to 10^3 CFU/ml when detecting antibiotic resistance genes in methicillin resistant Staphylococcus aureus strains. Also, our assay was able to detect multiple antibiotic resistance genes in parallel without any cross-reactivity from three different antibiotic resistant S. aureus
strains at the clinical relevant dose of 10⁵ CFU/ml. Our results perfectly matched to the results of both PCR and agar diffusion methods. Furthermore, our assay can be easily adapted to both centralized and remote testing locations to reduce the unnecessary overuse of antibiotics, and ensure that correct therapies are prescribed.

SP10
Evaluating Patient Interest in Fecal Transplantation for Non-Alcoholic Fatty Liver Disease
J Tat-Ko¹, M Beaton¹, S Parvathy¹,2, L Craven¹, J Burton¹, A Rahman¹, T Joy¹, K Qumosani¹, M Silverman¹,2
¹St. Joseph’s Health Care London, London, ON, 2University of Western Ontario, London, ON

OBJECTIVES: Faecal Microbial Transplantation (FMT) for recurrent Clostridium difficile infections has a patient acceptability rate of over 90%. However, the acceptability of FMT as a potential therapy for the many other diseases with potential associations with the microbiome is currently unknown. The aim of this study was to gauge the acceptability of FMT among patients with non-alcoholic fatty liver disease (NAFLD), a population that may also benefit from this therapy.

METHODS: A questionnaire was administered to patients attending a clinic for NAFLD from June to December 2016.

RESULTS: 150 patients were approached with only 50 patients agreeing to complete the questionnaire. Patients who completed the questionnaire had a mean age of 54 years [Range 18-74, SD 13.8] and a mean BMI of 34 [Range 21-58, SD 7.7]. 60% of patients had post-secondary education and 59% were female. Most patients were of Canadian origin (35/49) and European ethnicity (29/48). Overall 45/50 (90%) of patients agreed that they would consent to FMT if data suggested that it would help with their condition. Patients that had post-secondary education were more likely to accept FMT (P<0.05) but sex and BMI were not significantly correlated with acceptance. Acceptance of the FMT was 42/49 (86%) if the FMT was given by oral capsule, via colonoscopy 27/45 (60%), duodenoscopy 25/46 (54%) or enema 18/46 (39%). 24% (12/50) had treatment concerns, with 9/12 of these (75%) reporting that it was unappealing.

CONCLUSION: FMT was considered as a potentially acceptable therapeutic procedure for the majority of NAFLD patients. However, a subgroup of patients found it unappealing. We suspect that this sentiment was shared by many other patients due to the low completion rate of the questionnaires. The modality of administration may affect acceptability. Further studies in other patient groups would be helpful.

SP11
The Association between Respiratory Pathogens and Exacerbation Severity, Health Care Utilization, Treatment Response and Morbidity in Children with an Asthma Exacerbation: A Systematic Review
J Merckx¹, H Kraicer-Melamed¹, FM Ducharme², C Quach¹,³,⁴
¹Department of Epidemiology, Biostatistics & Occupational Health, McGill University, Montréal, QC, ²Department of Pediatrics, CHU Sainte-Justine, Université de Montréal, Montréal, QC, ³Department of Microbiology, Infectious Diseases and Immunology, Université de Montréal, Montréal, QC, ⁴Infection Control & Prevention Unit, Division of Paediatric Infectious Diseases and Department of Medical Microbiology, CHU Sainte-Justine, Université de Montréal, Montréal, QC

BACKGROUND: Asthma exacerbations constitute a large burden of illness in asthmatic children, with 60-80% triggered by respiratory pathogens. The role of pathogens in the clinical evolution of exacerbations is unknown. We systematically reviewed the association between the presence of pathogens and short-term clinical outcomes in children presenting with an exacerbation.

METHODS: PubMed, Embase, Biosis and the Cochrane Central Register of Controlled Trials were systematically searched and screened in duplicate for full text studies on children with an exacerbation reporting on respiratory pathogen exposure and a clinical outcome: exacerbation severity, healthcare (HC) utilization, treatment response or morbidity. The Risk of Bias In Non-Randomized Studies of Interventions tool was used for quality assessment.

RESULTS: We included 28 observational studies (4253 children) reporting on 112 different comparisons between exposure to any pathogen (n=45), rhinovirus (HRV; n=34), atypical bacteria (n=21), specific virus (n=11) or bacteria (n=1) and outcomes of exacerbation severity (n=26), HC utilization (n=38), response to treatment (n=19) and morbidity (n=29). 92/112
Abstracts

SP12
Evaluation of the β-Lacta Test for Detection of ESBL-Producing Organisms Directly from Positive Blood Cultures Using Smudge Plates

M HASSO1, V Porter2, AE Simor1,2

1Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, 2Department of Microbiology, Sunnybrook Health Science Centre, Toronto, ON

BACKGROUND: The ability to rapidly and accurately detect ESBL-producing organisms from positive blood cultures would have a significant impact on early implementation of appropriate antimicrobial therapy in septic patients, and thereby may also improve patient outcome. This study evaluated the accuracy and feasibility of rapid detection of ESBL-producing Enterobacteriaceae using the β LACTA test (Bio-Rad Laboratories) directly from positive blood culture smudge plates.

METHODS: Smudge plates were prepared from positive blood cultures (processed by the Bactec 9240 system, Becton Dickinson) with Gram negative bacilli by inoculating a bacterial concentrate onto chocolate agar incubated for 2 hrs. Smudge plate growth was used for organism identification by the Vitek MALDI-TOF MS (bioMérieux). If E. coli or Klebsiella species were identified, the smudge plate growth was used for the β LACTA test done in accordance with the manufacturer’s instructions. We also did the test using blood culture bottles that were inoculated with 53 known ESBL-producing organisms that had been stored frozen. Antimicrobial susceptibility testing and confirmation of ESBLs were done in accordance with CLSI guidelines.

RESULTS: Prospectively, 115 Enterobacteriaceae were isolated, 83 E. coli and 32 Klebsiella species. The rates of ESBLs were 18% (15/83) in E. coli and 12.5% (4/32) in Klebsiella species. A total of 22 isolates tested positive with the β Lacta test, including all 19 of the ESBL-producers. The sensitivity and specificity of the β-Lacta test were 100% and 96.9% respectively. One of the false positive isolates, an E. coli, had an AmpC β lactamase, which can be picked up by the test. The sensitivity of the test using the frozen ESBL isolates was also 100%.

CONCLUSION: The β-Lacta test was found to be a simple, inexpensive, and accurate method for the rapid detection of ESBL-producing organisms using smudge plates from positive blood cultures.

SP13
Case Conferences for Infective Endocarditis: A Quality Improvement Study

CTAN1, M Hansen2, G Cohen3, K Boyle4, A Yang1, N Daneman1,5,6, N Adhikari1,7,8

1Sunnybrook Research Institute, Toronto, ON, 2Division of Cardiology, Department of Medicine, Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 3Division of Cardiac Surgery, Department of Surgery, Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 4Division of Neurology, Department of Medicine, Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 5Division of Infectious Diseases, Department of Medicine, Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 6Institute for Clinical Evaluative Sciences, Toronto, ON, 7Division of Critical Care Medicine, Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 8Interdepartmental Division of Critical Care, University of Toronto, Toronto, ON

OBJECTIVES: A multidisciplinary approach has been recommended for the management of infective endocarditis. We aimed to evaluate the impacts of multidisciplinary case conferences on morbidity, mortality and quality of care for patients with this disease.

METHODS: We conducted a quasi-experimental study that included 135 consecutive patients admittance. The non-critical overall risk of bias and were included in the descriptive analysis. The heterogeneity in the published data precluded data aggregation. Using only comparisons with a moderate risk of bias showed an association between HRV and increased exacerbation severity on presentation (non overlapping 95% CI) and between the presence of any pathogen and treatment failure (OR 1.57, 95% CI 1.04-2.37). There was also an association between HRV and morbidity (symptom duration after the index visit) for 2/3 comparisons, but not with HC utilization.

CONCLUSION: The lack of good quality data leads to limited strength of evidence on the association between respiratory pathogens and short-term clinical outcomes. Further research on the role of pathogen-treatment interaction and outcomes is needed, which will inform the need for point-of-care, real-time testing for pathogens in children presenting with an asthma exacerbation.

48
OBJECTIVES: This study aimed to compare the CIM to our current phenotypic method for detecting carbapenemases in *Enterobacteriaceae*.

**METHODS:** Ninety-six archived isolates of the *Enterobacteriaceae* family were selected for CIM evaluation. The gold standard test was the gene type characterized by the Toronto Public Health Ontario Laboratory using a multiplex PCR for KPC, NDM, GES, OXA-48-like, VIM and IMP genes. Our current phenotypic test for carbapenemases is the KPC and MBL Confirm Kit™ (Rosco Diagnostica) with a temocillin 30µg disk. For the CIM, a loopful of the isolate was suspended in 400µl sterile water in a microcentrifuge tube. A 10µg meropenem disk was added and incubated at 35°C for 2h in ambient air. A 0.5 McFarland of *E. coli* ATCC 25922 was streaked onto a Muller Hinton Agar (MHA) plate; the meropenem disk from the microcentrifuge tube was then placed onto this plate and incubated at 35°C overnight. Positive carbapenemase activity was indicated by absence of inhibition around the disk.

**RESULTS:** Thirty-one isolates were KPC positive, 26 were NDM positive and 12 were OXA-48-like positive. Twenty-seven isolates were negative for carbapenemase genes. The sensitivity of CIM was 100%, 100% and 91.7% for KPC, NDM and OXA-48-like carbapenemases, respectively. A 10µl loopful was essential to demonstrate a positive result for OXA-48-like producing organisms. Our current phenotypic method had an overall sensitivity of 100% and specificity of 96%.

**CONCLUSIONS:** CIM is an easy, inexpensive method for detecting KPC and MBL carbapenemases. Its detection of OXA-48-like enzymes is dependent on the inoculum size of the tested organism.

**SP14**

Comparison of the Carbapenem Inactivation Method and ROSCO KPC/MBL Confirm Kit for Detection of Carbapenemase-Producing *Enterobacteriaceae*

N Matic1, R Melano1,2, S Patel1,2, B Tam3, M Bignell3, LM Matukas1,3, M Tadros1,3

1Department of Laboratory Medicine & Pathobiology, University of Toronto, Toronto, ON, 2Public Health Ontario Laboratory, Toronto, ON, 3Department of Microbiology, St. Michael’s Hospital, Toronto, ON

**BACKGROUND:** The emergence and spread of carbapenemase-producing *Enterobacteriaceae* (CPE) is a worldwide health threat. The carbapenem inactivation method (CIM) has been described as an easy method with excellent results for phenotypic detection of carbapenemases.

**OBJECTIVES:** After incorporation of twice weekly serum galactomannan screening into high risk
chemotherapy order sets, the primary objective was to determine if there was a change in broad spectrum antifungal use. Secondary objectives were to assess compliance with galactomannan screening and the incidence of invasive aspergillosis and mortality.

METHODS: This single-centre, retrospective, pre-post intervention cohort study included patients treated in a one year period before and after the introduction of galactomannan screening. We included adults with acute myeloid leukemia undergoing induction or reinduction chemotherapy. We excluded patients who received a stem cell transplant or were receiving prophylaxis or treatment for invasive aspergillosis.

RESULTS: We included 65 patients who received 87 courses of chemotherapy, corresponding to 87 episodes of neutropenia (40 episodes before and 47 after the introduction of screening). The average age was 62 years old and 52% were female. The compliance with pre-emptive screening was 71%. Comparing intervention to control groups, 22 (47%) vs 18 (45%) (p>0.99) of episodes received any broad spectrum antifungal, 12 (26%) vs 5 (13%) (p=0.21) were treated for invasive aspergillosis, and 10 (21%) vs 13 (33%) (p=0.35) received an empiric echinocandin without escalation. Possible aspergillosis rates were 15% in both groups, probable aspergillosis 11% vs 5% (p=0.58), and negative for aspergillosis 17% vs 23% (p=0.73). At 3 months, 6 (23%) vs 8 (20%) of patients in intervention and control groups, respectively, died.

CONCLUSION: In spite of high use of pre-emptive galactomannan screening, we did not find significant differences in outcomes at our centre. A multicentre study would be required to further evaluate the effectiveness of this type of screening strategy.

SP16
Increased Incidence of HIV, Hepatitis C, Invasive Group A Streptococcal Disease and Endocarditis in PWIDs: London-Middlesex, Ontario
L BALL¹, G Hovhannisyan², K Gupta³, S Koivu⁴, T Coleman⁵, A Sherazi¹, D Laczo¹, T Mele¹, M Silverman⁶
¹Schulich School of Medicine & Dentistry, London, ON, ²London-Middlesex Public Health Unit, London, ON, ³Department of Medicine, Division of Infectious Disease, Schulich School of Medicine & Dentistry, Western University, London, ON, ⁴Department of Family Medicine, Schulich School of Medicine & Dentistry, Western University, London, ON, ⁵Department of Medicine, Schulich School of Medicine & Dentistry, Western University, London, ON

OBJECTIVE: To characterize four outbreaks of infectious complications of injection drug use (IDU).

METHODS: Reported incidence of HIV, Hepatitis C (HCV), and invasive Group A Streptococcal Disease (iGAS) in the Middlesex-London (ML) Region of Ontario (population 469,296) using passive surveillance data. We reviewed electronic records from acute care hospitals to identify IDU associated infective endocarditis (IDUaIE).

RESULTS: The crude rate of newly diagnosed HIV cases in ML increased from 5.9 to 12.2/100,000 from 2005 to 2016, while decreasing from 7.4 to 5.0/100,000 provincewide. Persons who inject drugs (PWID) represented 8% of incident HIV diagnoses in the province during 2013-4, while 70% of cases in 2016 were in PWID in ML. The crude rate of new HCV infections increased from 32.5 to 47.4/100,000 from 2005 to 2016, while provincial rates fell to 30.1/100,000. The proportion of PWID-associated iGAS cases associated with PWID increased from 19% in 2010 to 42% in 2016. Hospital admissions for IDUaIE increased from 32.5 to 47.4/100,000 from 2005 to 2016, while provincial rates fell to 30.1/100,000. The proportion of PWID-associated iGAS cases associated with PWID increased from 19% in 2010 to 42% in 2016. Hospital admissions for IDUaIE increased from 29 (6.7/100,000) in 2009 to 81 (17.2/100,000) in 2015. A 4.6 fold increase in the number of inpatient days associated with IDUaIE was observed, with over 1,900 inpatient days in 2015.

CONCLUSION: Four simultaneous infectious outbreaks (HIV, HCV, iGAS, IDUaIE) are occurring in PWID in ML despite large local opiate substitution programs and the second largest needle exchange program in Canada. A public health emergency was
declared on June 16, 2016. We believe that the observed increases cannot be solely attributable to more PWID in ML; rather other factors, such as changes in drugs used, methods and/or frequency of injecting, are likely driving the outbreaks. Studies to clarify these factors are ongoing.

**SP17**

**Severe Multifocal Tuberculosis with Dilated Cardiomyopathy in a Young Patient: Revisiting ‘The Great Mimicker’**

C Hogan¹, LY Kong¹, M Palayew², DC Vinh¹, C Greenaway²

¹McGill University Health Centre, Montréal, QC, ²Jewish General Hospital, Montréal, QC

**BACKGROUND:** Although tuberculosis can affect virtually any organ system, myocardial involvement is extremely rare. Moreover, disseminated skeletal tuberculosis is usually seen in young patients and/or immunosuppressed hosts. The differential diagnosis for a combination of these clinical features is wide and includes mycobacterial disease, endemic fungal mycoses and malignancy including lymphoma.

**CASE:** A previously healthy Filipino 19-year-old male in Canada for the last six years presented in September 2016 with a six-month history of non-healing upper sternal wound and unintentional weight loss. Imaging revealed bilateral pleural effusions, multilevel destructive skeletal lesions (sternum, T1-T2, T11, right ribs) as well as dilated cardiomyopathy with a left ventricular ejection fraction of 5% without pericardial involvement. Both sternal biopsy and thoracentesis fluid were TB PCR positive, and cultures grew pan-sensitive *Mycobacterium tuberculosis*. He was treated with standard quadruple therapy, but developed significant hepatitis with both pyrazinamide and rifampin. Immunologic work-up, including immunoglobulins, enumeration of lymphocytes, and more specialized genetic testing, is underway to investigate possible genetic defects that predispose to severe tuberculosis disease.

**CONCLUSION:** Clinicians should remain aware of tuberculosis as a possible etiology for dilated cardiomyopathy, even in the absence of pericardial involvement. Aggressive anti-tuberculous therapy should be instituted to optimize reversibility, with close of follow-up of liver enzymes and function in the setting of congestive hepatitis from right-sided heart failure. Immunologic work-up should be pursued in cases of severe disseminated disease to try to uncover treatable immune defects.

**SP18**

**Syphilis Re-Infection Amid a Global Resurgence: A Systematic Review and Meta-Analysis**

A Shakeri²,³, B Wong¹,³, A Burchell¹,³, DHS Tan¹,³, A Al-Salman², D Gesink¹, V Allen³, S Aral⁴, C Ziegler⁵, S Mishra¹,³

¹University of Toronto, Toronto, ON, ²Royal College of Surgeons, Dublin, Ireland, ³Public Health Ontario, Toronto, ON, ⁴Centre for Disease Control and Prevention, Atlanta, GA, USA, ⁵St. Michael’s Hospital, Toronto, ON

**INTRODUCTION:** Syphilis has re-emerged across industrialized countries and the rise in cases includes re-infections. We sought to understand sources of temporal and population heterogeneity by estimating syphilis rates and proportions that represent a documented re-infection.

**METHODS:** We performed a systematic review and meta-analysis using a database search of MEDLINE, EMBASE, COCHRANE, SCOPUS, and the grey literature including public health reports and surveillance data for relevant studies reporting the following outcomes: syphilis re-infection rate or proportion of documented syphilis cases that represent a re-infection between January 1, 1980 and May 13, 2016. The population included adults >14 years of age in high-income and upper-middle income countries. We pooled estimates using a DerSimonian and Laird random effects model, and conducted a priori subgroup analyses by time-period, risk-group and HIV status.

**RESULTS:** 74 relevant publications were identified. Re-infection was defined as: a 4-fold rise in rapid plasma reagin (RPR) titre following last RPR after treatment (N=16 studies); failure of RPR decline (N=5 studies); a clinical diagnosis (N=32); or not defined (N=21). The pooled proportion of re-infections among all syphilis cases was 7.8% (I²=63%, 95% CI: 4.3-16.7) from 1980-1990, 9.8% (I²=78%, 95% CI: 6.1-19.7) from 1991-2000, and 21.5% (I²=86%, 95% CI: 15.1-33.2) from 2000-2016. The proportion of re-infections after 2000 among men who have sex with men was 23.7% (I²=77%, 95% CI: 16.4-36.1, N=31), and among persons diagnosed with HIV was 33.7% (I²=68%, 95% CI: 26.8-44.3, N=39). The median re-infection rate among individuals who received follow-up testing was 3.2 per 100 person-years.
Abstracts

CASE 1: A 52-year-old female presented 68 days after lung transplantation after routine imaging showed a mediastinal mass. Biopsy demonstrated *Mycobacterium tuberculosis*. On further review, she revealed exposure to an active case of TB as a child. A tuberculin skin test (TST) performed pre-transplant was negative. She was treated with rifabutin-based quadruple therapy and her immunosuppression dosing was adjusted. At three months of follow-up to date no rejection or drug toxicity has been observed.

CASE 2: A 61-year-old male without epidemiologic risk factors for TB infection presented to hospital 56 days after lung transplantation with weakness and dyspnea. Bronchoalveolar lavage (BAL) demonstrated *M. tuberculosis*. The donor was born in India and pre-transplant chest x-ray showed old granulomatous infection, but historical TST was reportedly negative. The transplant recipient started rifabutin based quadruple therapy and immunosuppression dosing was adjusted. At five months of follow-up to date no rejection or drug toxicity has been observed.

CASE 3: A 23-year-old female presented to hospital 53 days after lung transplantation with fever, dyspnea and cough. BAL confirmed *M. tuberculosis*. The donor was born in Philippines but had a normal pre-transplant CXR and CT. The recipient had no identifiable TB risk factors. She was treated with rifabutin-based quadruple therapy with immunosuppression dose adjustment. She completed TB therapy without rejection or significant drug toxicity.

CONCLUSION: We present two cases of presumed donor-derived TB and one case of reactivation TB that presented shortly after lung transplantation. All patients were treated with rifabutin-based quadruple therapy. With adjustment in immunosuppression no episodes of drug toxicity or rejection have been observed to date.

SP19

**Tuberculosis After Lung Transplantation: Safety and Efficacy of rifabutin Based Treatment in The Setting of Transplant Immunosuppression**

C O’NEIL, K Doucette, R Long, R Cooper

University of Alberta, Edmonton, AB

BACKGROUND: Tuberculosis (TB) is rare but increasingly recognized complication of lung transplantation. Treatment of TB in this setting is challenging due to overlapping drug toxicity, potentially severe drug-drug interactions, and immunosuppression. Rifabutin is known to have a favourable interaction profile as compared to rifampin yet retains its potent bactericidal activity. However, experience in the transplant setting is limited. We present a case series of three patients with active TB presenting shortly after lung transplantation all with favourable treatment outcomes to date with rifabutin-based therapy.

SP20

**What Could Rates of Syphilis Re-Infection Tell Us About Transmission Dynamics of Syphilis Epidemics? Insights from Mathematical Modelling**

J FELDMAN1, S Vivona2, N Moqueet3, S Mishra3

1’Dalhousie University, Halifax, NS, 2’McMaster University, Hamilton, ON, 3’St. Michael’s Hospital, Toronto, ON

BACKGROUND: Rates of syphilis re-infections are increasing – especially among men who have sex with men (MSM) and persons living with HIV. Re-infection rates are sometimes tracked as a marker of the phase of an epidemic, and often reported as the proportion of annual syphilis diagnoses that represent a documented re-infection, and herein referred to as ‘prevalence of repeat infection’. We sought to explore the relationship between the prevalence of repeat infection and the basic reproductive number (R₀) of syphilis epidemics, because the higher the R₀, the more difficult an epidemic is to control.

METHODS: We developed a compartmental, mathematical model of syphilis transmission among MSM. First, we solved a simplified “susceptible->infected->susceptible (SIS)” model represented by a set of coupled ordinary differential equations to derive the relationship...
Mutations in Penicillin Binding Protein 3 are Common Among β-lactam Exposed Pseudomonas aeruginosa from Cystic Fibrosis Patients

S CLARK1,2, Y Zhang3, P Wang4, J Diaz Caballero5, E Tullis6, D Guttman1, D Hwang1,2

1University of Toronto, Toronto, ON, 2Toronto General Hospital Research Institute, Toronto, ON, 3St. Michael’s Hospital, Toronto, ON

BACKGROUND: The opportunistic bacterial pathogen Pseudomonas aeruginosa (Pae) is notoriously recalcitrant to antimicrobials and causes fatal lung infections in individuals with cystic fibrosis (CF). Several β-lactam antibiotics are used clinically as first-line therapies to manage chronic Pae infections. We previously identified associations between novel non-synonymous mutations in the intracellular target of many β-lactams, penicillin binding protein 3 (PBP3, encoded by pbpB), and increased resistance to some β-lactams in sputum-cultured Pae isolates from a CF patient treated aggressively with aztreonam. However, the frequency and significance of pbpB mutation in Pae is not known. We hypothesized that mutation of pbpB is a common adaptation to resist β-lactams in chronic CF infection.

METHODS: We screened a collection of 126 Pae isolates for susceptibility to a panel of β-lactams by agar dilution and sequenced a 700 bp region of pbpB encoding the PBP3 transpeptidase domain. Isolates were selected retrospectively from adults with CF treated with or without any β-lactam during a 3 year period and compared to a subset of environmental Pae strains.

RESULTS: Multiple independent pbpB alleles were common in β-lactam exposed Pae and clustered into discrete groups with varying patterns of susceptibility. Twelve non-synonymous pbpB mutations were found among β-lactam exposed Pae, with some residues mutated in parallel among β-lactam resistant isolates. Environmental and β-lactam naïve Pae were more susceptible to β-lactams and carried synonymous changes in pbpB.

CONCLUSIONS: Our work to-date demonstrates that pbpB mutations are prevalent among Pae from CF patients and may influence susceptibility to some β-lactam antibiotics. Continued efforts will help to better delineate the role of pbpB in β-lactam resistance and determine its utility as a predictor of resistance.

SP22

Testing Assumptions Surrounding Rebounds in Syphilis Epidemics: An Exploratory Modeling Analysis

S VIVONA1,5, N Moqueet2,5, J Feldman3,5, S Mishra5,4

1McMaster University, Hamilton, ON, 2McGill University, Montreal, QC, 3University of King’s College, Halifax, NS, 4University of Toronto, Toronto, ON, 5St. Michael’s Hospital, Toronto, ON

BACKGROUND: Syphilis rebound or resurgence is defined as a sustained increase in syphilis cases following a nadir, and occasionally following interventions. We sought to understand the influence of behavioral (“turnover” in sexual networks) and biological (rate of waning immunity following treatment) conditions under which transmission rebounds following a screen and treat intervention.
**Abstracts**

**METHODS:** We developed a risk-stratified mathematical model of syphilis transmission among men who have sex with men (MSM) to capture the natural history of untreated and treated syphilis and re-infection. We drew on bio-behavioral survey data among MSM in Toronto, Canada and published estimates of biological parameters as model inputs. We calibrated the model to a stable rate of syphilis incidence and new diagnoses based on observed rates in Toronto. We then applied an 'increased screening and treatment' intervention to estimate the probability and timing of syphilis rebounds following the intervention, across a range of parameters that reflected assumptions surrounding (a) ‘turn-over’ within sexual networks; (b) duration of waning immunity; (c) patterns of sexual partnerships (“who has sex with whom”). The intervention represented an increase from 35% annual screening and treatment rates at baseline to 60%.

**RESULTS:** Across 600,000 simulations, the cumulative probability of a rebound at 1, 2, 3, 4 and 5 years after intervention was 0%, 0.04%, 48.6%, 95.4% and 100%, respectively. Assumptions of a shorter duration of immunity as well as the higher rates of turn-over within sexual networks both led to earlier rebounds. Patterns of sexual partnerships were the least influential on the timing or probability of a rebound.

**DISCUSSION:** Our modeling suggests that biological and behavioral factors – many of which remain assumptions – work together to drive syphilis rebounds. More research is needed into quantifying turn-over within sexual networks, and duration of protective immunity following treatment, in order to better predict the potential impact of treatment interventions on syphilis epidemics.

**SP23**

**HIV and Malaria Co-Infection: A Complex Interaction**

LY KONG, T Nguyen, M Libman, C Greenaway

1McGill University Health Centre, Montréal, QC, 2Jewish General Hospital, Montréal, QC

**BACKGROUND:** HIV infection is associated with higher prevalence of clinical malaria episodes, parasite density, and severity of infection. These are modified by age, pregnancy, degree of immunosuppression and prior malaria exposure. Children, pregnant women, and those with advanced immunosuppression have worse clinical outcomes whereas the data in semi-immune adults is conflicting. Malaria infection can cause a transient increase in HIV viral load and decrease in CD4 count, although it is unclear whether this hastens progression of HIV infection to AIDS.

**CASE:** A 55-year-old HIV infected male returned to Canada from visiting family in Cameroon and presented nine days later with altered mental status and fever, with an initial GCS of 10. The patient left Cameroon at age 15 and had not visited a malaria endemic country in 16 years. Initial thin smear revealed *Plasmodium falciparum* infection with 23% parasitemia. Laboratory testing showed anemia (haemoglobin 86g/L), thrombocytopenia (platelet 87 x 10^9/L), hyperbilirubinemia (total bilirubin 47 umol/L), lactic acidosis (lactate 4.7 mmol/L), and acute kidney injury (creatinine 132 umol/L). Artesunate was administered intravenously and the patient underwent partial exchange transfusion with four units of packed red cells. There was dramatic clinical improvement (normalization of mental status and lactate) within 12 hours. There was rapid clearance of parasitemia which was 8% at 24 hours, 0.2% at 48 hours and negative on day 4. The patient was first diagnosed with HIV infection in 2009 but declined therapy. The CD4 count on admission was 17 cells/ul, and the most recent viral load was 594,512 copies/ml (seven months prior to presentation). Upon recovery from his severe malaria infection, the patient is under evaluation and counselling prior to starting treatment for HIV infection.

**CONCLUSION:** The high parasitemia and surprisingly uncomplicated clinical course results from aggressive treatment, but may also reflect a lack of excessive immune activation as a result of advanced HIV infection. Clinicians should be aware of the complex interactions between HIV and malaria, which may lead to unusually high parasitemias and variable severity of illness depending on host factors including prior exposure to malaria and level of immunosuppression.

**SP24**

**Retrospective Review of 103 Prosthetic Joint Infections at A Single Institution in Toronto from 2013-2014**

C KANDEL, D Backstein, A McGeer

University of Toronto, Toronto, ON
BACKGROUND: Prosthetic joint infections (PJIs) are a feared complication of hip and knee arthroplasty and are associated with substantial morbidity and cost through revision operations, prolonged courses of antibiotics and repeat hospitalizations. With an aging population increasing the demand for joint replacements the number of infections will naturally rise. In order to optimize management, the epidemiology of PJIs in Canada must first be characterized. The purpose of this study is to describe the characteristics and management of prosthetic hip and knee joint infections in a single tertiary care hospital in Toronto, Ontario.

METHODS: Patients with PJIs were identified by reviewing all prosthetic hip and knee joint revision procedures at Sinai Health System in Toronto, Ontario from January 1, 2013 until December 31, 2014. Chart reviews were performed to characterize infecting organisms, surgical procedures, antimicrobial therapy and outcomes of each PJI. Success was defined as the absence of recurrent PJI (relapse or re-infection) in the two years following the initial revision operation and chronic suppressive antimicrobial therapy.

RESULTS: 103 PJIs were identified over the two-year period with information available for analysis in 93 (90.3%). The cohort comprises 42 prosthetic hip infections (45.2%) and 51 prosthetic knee infections (54.8%). Staphylococcus aureus was the most frequent cause of infection (23.7%) followed by coagulase-negative staphylococci (21.5%), culture-negative (19.4%), gram-negative bacilli (12.9%), beta-hemolytic streptococci (11.8%), Enterococcus faecalis (6.5%), and polymicrobial infections (8.6%). A two-stage procedure was employed in 67.7%, incision and drainage with liner exchange in 35.5% and one-stage procedure in 7.5%. Success was achieved in 61.3% (hips 59.5% and knees 62.7%).

CONCLUSIONS: New treatment modalities are urgently required to attenuate the morbidity of PJIs. Further study is needed from other institutions over a broader time period to adequately capture the burden of PJIs, and to identify factors associated with treatment success.

SP25
The Prevalence of Antibiotic Use in Bacterial Enteric Illnesses in Canada, 2010-2015

1Department of Population Medicine, University of Guelph, Guelph, ON, 2Centre for Food-borne, Environmental, and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, ON, 3Middlesex London Health Unit, London, ON, 4Alberta Health Services, Calgary, AB, 5Fraser Health Authority, Surrey, BC.

OBJECTIVES: Bacterial enteric illnesses are a significant health concern in Canada and are often treated with antibiotics, despite evidence suggesting they are often unnecessary. The inappropriate use of antibiotics has been identified as causing negative clinical outcomes for patients in addition to fostering the emergence of antibiotic resistant bacteria. The purpose of this study is to gain a more fulsome understanding of the antibiotic prescribing practices for bacterial enteric illnesses in Canada.

METHODS: Data for 2010 to 2015 was collected from three sentinel sites that participate in an enteric illness enhanced passive surveillance system. A standardized questionnaire was administered to all laboratory confirmed cases of enteric illness, which collected information on symptomology, exposure risks, and antibiotic use. A descriptive analysis was conducted on this data to examine the prevalence and types of antibiotics used. This analysis was conducted at the broad bacterial enteric infection level as well as the pathogen specific level.

RESULTS: The descriptive analysis found that 47% of laboratory confirmed cases of bacterial enteric illness received an antibiotic prescription. Fifty-eight percent of Shigella cases received an antibiotic prescription, which was the highest proportion observed amongst the pathogens included. The pathogen with the lowest proportion was verotoxigenic Escherichia coli for which 28% of cases received a prescription. The five most commonly used drugs were ciprofloxacin, azithromycin, metronidazole, erythromycin, and sulfamethoxazole/trimethoprim (TMP/SMX).

CONCLUSION: This study provides evidence that antibiotics are frequently being prescribed by Canadian physicians for the treatment of bacterial enteric infections. This is occurring at a rate that is substantially...
higher than what has previously been recorded in the literature. These findings could be used to inform future antibiotic stewardship program development.

**SP26**

**Timeliness of Diagnosis of HIV in Newfoundland. A Quantitative and Qualitative Study**

S BOYD¹, J Allison¹, C Penney¹, K Burt², P Daley¹

¹Memorial University of Newfoundland, St. John's, NL, ²Eastern Health, St. John's, NL

**OBJECTIVES:** To describe the timeliness of HIV diagnosis in Newfoundland and Labrador (NL) and determine the reasons for delay in HIV diagnosis.

**METHODS:** Demographic and clinical information from individuals diagnosed with HIV in NL between 2006-2016 was anonymously retrospectively reviewed. Patients were invited to participate in semi-structured interviews regarding knowledge about HIV transmission, risk associated with their behavior, testing decision-making, and testing opportunities. Interviews were recorded, transcribed, coded and analyzed for thematic information. The Health Research Ethics Board approved the study.

**RESULTS:** Lab records revealed 58 new HIV diagnoses during the study period. The mean age was 40.6 years, 60/58 (86.2%) lived in urban NL, 53/58 (91.4%) were male, 33/58 (56.9%) were men who have sex with men. 38/58 (65.5%) of positive tests were initiated by a healthcare worker. CD₄ count at diagnosis ranged from 2 to 1408 cells/mm³ with a mean of 387, with 19/58 (32.8%) below 200. 21/58 (36.2%) tested positive for another sexually transmitted infection at diagnosis. 20/58 (34.5%) were asymptomatic at diagnosis, while 8/58 (13.8%) had an AIDS-Indicator condition at diagnosis. For 39/58 (67.2%), the first HIV test was positive, even though 55/58 (94.8%) had had healthcare contact within 5 years prior to diagnosis (mean number of healthcare contacts before diagnosis of 13.7). When comparing early diagnosis (CD₄ >200) with late diagnosis (CD₄ <200) groups, demographic variables were not significantly different. 10/58 (17.2%) agreed to an interview, (mean CD₄ 620 cells/mm³, range 56-1408). Thematic analysis of interviews revealed the major obstacles to testing were fear of knowing their status, social stigma, and lack of access to testing and educational materials.

**CONCLUSIONS:** We defined a large number of missed opportunities for HIV testing among patients who had contact with the healthcare system. This may have been prevented if HIV testing was a routine testing procedure. Education of physicians or change in testing policy may reduce delayed HIV diagnosis. Stigma may be causing delay in diagnosis.

**SP27**

**Stool Specimens that are Toxic for Cell Culture Should be Tested for Clostridium difficile Cytotoxin**

A LANG, L Mushanski, PN Levett

Saskatchewan Disease Control Laboratory, Regina, SK

**OBJECTIVES:** In 2016, 3853 stool specimens were submitted to the Saskatchewan Disease Control Laboratory (SDCL) for viral studies, 1679 for Clostridium difficile cytotoxin (CDT), and 752 for both. Samples cultured for viruses are sometimes toxic for cell culture and are reported to the physician as: “Due to specimen being toxic for cell culture, virus isolation cannot be performed”. This CPE is indistinguishable from that produced by CDT, so toxic viral studies samples were assessed for the presence of CDT.

**METHODS:** Stool samples submitted to SDCL for viral studies that were toxic for cell culture were enrolled from May through December 2016. If there were no associated samples for CDT testing at SDCL, ordering physicians were contacted. If samples previously tested positive or negative, no further testing was carried out. If a previous testing was indeterminate or not carried out, the same sample submitted for viral studies was tested for CDT if the physician agreed.

**RESULTS:** Thirty-nine samples submitted for viral studies at the SDCL were toxic for cell culture. Nineteen of 39 had previous or concurrent CDT testing, 16/39 were tested at the SDCL after consultation with the ordering physician, and 4/39 were lost to follow up. Of those samples that were previously tested, 14/19 were positive and 3/19 were negative for CDT; 2/19 were previously tested but results not divulged. Of the samples tested after consultation 13/16 were positive for CDT. Excluding samples with unknown previous results or those lost to follow up, 27/33 (81.8%) samples that were initially toxic for cell culture were positive for CDT.
CONCLUSIONS: The majority of specimens that were toxic for cell culture were positive for the presence of CDT. The report has been modified to include: “This result may be indicative of C. difficile toxin presence. Consider ordering C. difficile cytotoxin test on this sample if this test has not already been ordered.” This will help guide further testing and patient care.

SP28
Improved Isolation of Salmonella enterica serovar Typhimurium Using the Walk-Away Specimen Processor and FecalSwab System
L GONEAU1, A Mazzulli1, X Trimi1, A Cabrera1, P Lo2, T Mazzulli1,2
1University of Toronto, Toronto, ON, 2University Health Network/Sinai Health System, Toronto, ON

OBJECTIVES: To evaluate the isolation of Salmonella enterica serovar Typhimurium from stool using the automated Walk-Away Specimen Processor (WASP) and novel COPAN FecalSwab™ and selenite media.

METHODS: The ability of the WASP® and Isoplater systems to plant for isolated colonies was compared. Stool specimens were spiked with 10^7, 10^8, or 10^9 CFU/mL S. enterica serovar Typhimurium and inoculated into FecalSwab™ transport media then processed using either planting system. Isolated colonies of pathogen and commensals were enumerated. Pathogen enrichment was assessed by spiking stool with 10^5-10^7 CFU/mL of S. enterica serovar Typhimurium and then directly planting to Hektoen agar, or pre-incubating at 37°C in COPAN selenite broth increased the number of isolated colonies by approximately four-fold (Figure 2; P < 0.001). This step increased the sensitivity of S. enterica serovar Typhimurium colony isolation to initial pathogen inoculum concentrations as low as 10^2 CFU/mL compared with 10^5 CFU/mL for directly plated specimens.

CONCLUSIONS: WASP® automated planting improved colony isolation compared to those planted using the Isoplator, while COPAN selenite broth increased the limit of Salmonella detection in spiked-stool specimens. These features would improve discrimination and isolation of enteric pathogens, increasing the likelihood of establishing the etiology of diarrheal illness due to bacterial pathogens.

SP29
Detection of Viral Antibodies via Dried Oral Swabs
D SPEICHER1,2,3, K Luinstra2, S Castriciano3, M Smieja1,2
1McMaster University, Hamilton, ON, 2St. Joseph’s Healthcare Hamilton, Hamilton, ON, 3Griffith University, Gold Coast, QLD, Australia, 4Copan Italia, Brescia, Italy

OBJECTIVE: Saliva contains viral antibodies and might be used to monitor seropositivity to aid surveillance and vaccination studies. However, endonucleases are problematic. Dried oral swabs could be a non-invasive and simple alternative to blood sample collection. The objective was to produce a modified method which allowed dried oral swabs to aid in detecting viral antibodies.

METHODS: Study cohort consisted of 50 healthy volunteers (15 males:35 females) with an average age of 43.4 years (range: 18-65 years). From each participant, sera, saliva, and oral swabs (FLOQSwabs, Copan Italia) were collected. Sera and saliva was stored at -80°C. Oral swabs were air dried and stored at room temperature. After extensive optimisation of pre-analytic procedures, seroprevalence for Cytomegalovirus (CMV), Varicella Zoster Virus (VZV), Epstein-Barr virus (EBV), Measles and Mumps IgG antibodies was determined on all sample types via commercial ELISA kits (R-Biopharm and Gold Standard Diagnostics) and processed on the ThunderBolt® Analyzer (Gold Standard Diagnostics).

RESULTS: For all viral antibodies studied, swabs correlated well with saliva. For CMV-IgG, the sensitivity and specificity of swabs compared to serum was 91.7% and 100% respectively. All volunteers were seropositive for VZV-IgG due to vaccination or natural illness. For VZV,
Abstracts

oral swabs were 96.0% sensitive and saliva was 93.9% sensitive; both were 100% specific. For EBV, EBNA-1 IgG, and VCA IgG, sensitivities were 92.1% and 95.5%, respectively; specificities were 100% for both assays. All volunteers were seropositive for Measles-IgG due to vaccination or natural illness. For Measles, oral swabs were 89.1% sensitive and saliva was 93.9% sensitive; specificity could not be determined. Mumps IgG displayed poor sensitivity for oral swabs (75.0%) and saliva (73.8%), but both had 100% specificity.

CONCLUSIONS: Dried oral swabs correlated well for CMV, VZV, EBV, and Measles antibodies with excellent sensitivity and specificity, but had poor sensitivity for detecting antibodies to Mumps. As FLOQSwabs are easy to collect and can be stored at room temperature they are an ideal tool for seroprevalence studies.

SP30
Household Environmental Contamination and Transmission of carbapenemase-producing Enterobacteriaceae

A JAMAL1,3, A Faheem1,2, S Shafinaz1,2, I Armstrong2, E Borgundvaag3, B Coleman1,3, K Green1,3, K Jayasinghe1,3, J Johnstone6, KC Katz4, P Kohler1,3, A McGee1,2, R Melano3, M Muller5, S Patel3, SM Poutanen2,3, A Rebbapragada7, D Richardson1, A Sarabia9, AE Simor1,2, BM Willey2, L Wisely1,2

1Toronto Invasive Bacterial Diseases Network, Toronto, ON, 2Mount Sinai Hospital, Toronto, ON, 3University of Toronto, Toronto, ON, 4North York General Hospital, Toronto, ON, 5St. Michael’s Hospital, Toronto, ON, 6St. Joseph’s Health Centre, Toronto, ON, 7Dynacare, Toronto, ON, 8William Osler Health Centre, Toronto, ON, 9Credit Valley Hospital, Toronto, ON, 10Sunnybrook Hospital, Toronto, ON

BACKGROUND: There is a paucity of data on household transmission of carbapenemase-producing Enterobacteriaceae (CPE). This ongoing study aims to assess the risk of CPE household environmental contamination and transmission.

METHODS: The Toronto Invasive Bacterial Diseases Network has performed population-based surveillance for CPE infection in South-Central Ontario since 2007. Eligible CPE index cases are consented and enrolled in a household transmission sub-study, where household contacts (HHCs) and home environmental surfaces (ESs) are screened for CPE at 0 (baseline), 3, 6, 9, and 12 months.

RESULTS: There were 111 HHCs in 58 households (of which 34 HHCs in 17 households completed follow-up). The median number of HHCs per index case was 1 (IQR 1). A total of 695 and 1366 samples were obtained from HHCs and ESs, respectively. Three (2.7%) HHCs in 3 different households were CPE-positive (1 NDM-producing E. cloacae and 2 NDM-producing E. coli); all CPE-positive samples from HHCs were baseline samples. Each type of ES tested was CPE-positive in at least one household, with 19 (33%) households having one or more CPE-positive ESs. Two households had one or more CPE-positive ESs for over 50% of follow-up visits. Two of the 3 households with CPE-positive HHCs had CPE-positive ESs. The proportion of CPE-positive samples for each ES tested was: bathroom sink drain (3.1%), bathroom sink tap (4.0%), toilet handle (1.7%), toilet drain (6.1%), shower/bath drain (9.5%), kitchen sink tap (1.7%), kitchen sink drain (1.5%), bed (7.4%), sofa chair (5.1%), and telephone (1.1%). Once CPE-positive, only 4 ESs remained CPE-positive when re-tested at a subsequent follow-up visit: a bed, bathroom sink tap, and shower/bath drain in one household, and a bathroom sink tap in a different household. CPE on ESs included NDM-producing K. pneumoniae (17), E. coli (13), and E. cloacae (1), OXA-48-producing K. pneumoniae (3), NDM- & OXA-48-coproducing K. pneumoniae (5), KPC-producing E. coli (2), and VIM-producing E. cloacae (3) and E. horma chei (1).

CONCLUSIONS: CPE can be detected on a variety of ESs in households, but transmission to household contacts is uncommon.

SP31
Candidemia in a Tertiary-Care University Hospital: What Saves Lives?

XS WANG1, MP Cheng1,2, TC Lee1,2

1McGill University, Montréal, QC, 2Division of Infectious Diseases and Department of Medicine, McGill University Health Centre, Montréal, QC

OBJECTIVE: Candida species represent the third most common cause of health-care associated bloodstream infections. The Infectious Disease Society of America (IDSA) have published guidelines for the treatment of these patients; it is unknown if adherence to these guidelines results in improved patient outcomes. The objective of our study was to evaluate the rate of adherence to IDSA guidelines and to determine patient factors associated with improved outcomes.
RESULTS: A total of 81 patients were included in the study. At least one risk factor for invasive candidiasis was present in 67 (83%) patients. 23 (28.4%) patients died within 30 days. Candida albicans was isolated in 58 (72%) patients. The Infectious Disease consult service was involved in 72 (89%) cases. Within 24 hours of culture result, 54 (67%) patients received fluconazole and 23 (28%) received caspofungin; both are first line treatments. Central venous catheters (CVCs) were removed and/or changed in 71% (50/70) of patients who had a CVC at the time of culture. Ophthalmology was consulted for 52 (64%) patients received an echocardiography to assess for vegetation. Treatment lasting 2 weeks or more was given to 39 (48%) patients, and this was associated with 30-day survival (p=0.003, OR 5.0, 95% CI 1.5-19.7).

CONCLUSION: Management of candidemia at the MUHC could be optimized to provide better patient outcomes, for example, by introducing a care bundle.

SP32
Fluconazole Utilization Evaluation, and Review of Invasive Candidiasis in the McMaster University Neonatal Intensive Care Unit (NICU)
S ALGHAMDI, D Mertz, S Khan, M Sung
McMaster University, Hamilton, ON

OBJECTIVES: A retrospective drug utilization evaluation in an NICU to determine appropriateness of treatment. Secondary objectives included determination of the incidence of IC, and type and yield investigations in patients with IC.


RESULTS: Thirty-seven courses of fluconazole were prescribed. The median gestational age of all infants prescribed fluconazole was 25 (IQR 10) and the median age on initiation of fluconazole was 11 days (IQR=21.5). Thirty-two (86.8%) had at least one risk factor for IC. The majority of courses, 17 (45.9%), were for prophylaxis, 12 (32.4%) for treatment of clinical or culture confirmed infection, and 8 (21.6%) for empirical treatment while cultures were pending. Six cases (0.81% from 735 NICU patients during that time periods) developed IC: 3 (37.5%) with candidemia, 1 (12.5%) with CNS infection, 4 (66.6%) with an urinary tract infection, and 1 (12.5%) with a positive peritoneal fluid.

The median length of stay of infants prescribed fluconazole was 118 days (IQR=103). The median duration of therapy (DOT) was 7 days (IQR=7) in non-IC patients, compared to 6.5 days (IQR=2.25) in the IC cases. Fifteen courses (40%) were considered appropriate: 8 for mucocutaneous candida, 6 for culture proven IC, and 3 were empiric initiations with culture negative discontinuation. The main non-appropriate indication was prophylaxis (n=17), but empiric treatment with negative cultures and continued fluconazole also occurred (n=4). ID consultation occurred in all 6 IC patients, and 7 (23%) of non-IC patients. Doses used ranged from 1mg/kg/day (in prophylaxis cases) up to a maximum of 12mg/kg/day. Fluconazole toxicity (ALT > 60) occurred in 1 case (2.7%).

CONCLUSIONS: Although most infants had risk factors for IC, infection is rare. Fluconazole was inappropriately used in the majority of courses, mostly for prophylaxis, or without culture guidance.

SP33
Impact of CMV Infection Post-liver Transplantation According to CMV Serostatus
L MCLAUGHLIN, C Hernandez, K Doucette, D Kabbani, S Fuentes, C Cervera-Alvarez
University of Alberta Hospital, Edmonton, AB

OBJECTIVES: Cytomegalovirus (CMV) is the most common opportunistic pathogen after solid organ transplantation. Previous studies have shown that CMV infection is associated with increased mortality and graft rejection in liver transplant patients. We aimed to further evaluate the clinical outcomes of CMV infection post-liver transplant according to CMV donor and
recipient serostatus, including incidence of CMV infection and time of onset post-transplant.

**METHODS:** We performed a retrospective study evaluating 441 adult liver transplant patients from October 2005 to December 2013 at the University of Alberta Hospital in Edmonton. CMV infection was defined as detection of DNAemia above 250 IU/ml. CMV prophylaxis was initiated according to CMV donor/recipient serostatus: D+/R- received 3 months of anti-viral prophylaxis; D+/R+ underwent a pre-emptive strategy (monitoring for DNAemia and initiation of anti-viral treatment if positive DNAemia was detected); D-/R+ and D-/R- received no scheduled monitoring or prophylaxis.

**RESULTS:** 441 liver transplant patients (294 male; 66.7%) were evaluated. Mean age at transplant was 51 years. The majority of donor livers (85.7%) were from brain death donors. Induction involved basiliximab (60%), daclizumab (34%) or thymoglobulin (8%). According to CMV status, the incidence of CMV infection was: D+/R- 42/78 (54%); D+/R+ 68/143 (48%); D-/R+ 26/156 (18%); D-/R- 2/64 (3%) (p<0.001). Median time to CMV infection was: D+/R- 149 days (IQR 125-184); D+/R+ 33 days (IQR 18-63); D-/R+ 26.5 days (16-35); D-R 255.5 (Range 67-444) (p<0.001). At 2 years post-transplant, mortality was 12% (55/441) and 3% of patients required re-transplant (15/441). Presence of CMV infection did not impact 2-year mortality (10% vs 13% with and without infection respectively, p=0.318).

**Conclusion:** In our study, CMV infection was frequent following liver transplantation and incidence of infection was highest in CMV mismatch (D+/R-) patients. However, presence of CMV infection was not associated with increased mortality at 2 years post transplant.

**SP34**

**Impact of an Antimicrobial Stewardship Program to Reduce Drug-Resistant Bacteremia in Patients with Hematological Malignancies**

Y NATORI

University Health Network, Toronto, ON

**OBJECTIVES:** Infections due to multi-drug resistant (MDR) bacteria are becoming increasingly common in patients with hematological malignancies. Judicious use of antibiotics facilitated by antimicrobial stewardship program (ASP) is recommended, and may thwart the development of MDRs. We assessed the rate of MDR gram negative rods bacteremia during the pre- and post-ASP periods in leukemia patients, following the full implementation of an ASP since Jan 2011.

**METHOD:** Retrospective cohort study from 2007 and 2014. The data was analysed with interrupted time series analysis.

**RESULT:** A total of 1825 number of patients were included in the study, 830 in pre- and 995 in post-ASP intervention periods.

Significant decrease in rate of antibiotic usage over time under ASP program (p=0.011) was noted. The prevalence of MDR isolates declined, but the change was not statistically significant (p=0.72). Also, no statistically significant changes between pre- and post-ASP implementation regarding mortality, readmission and ICU transfer were detected.
CONCLUSION: Our study showed that implementation of an ASP decreased antibiotic consumption in leukemia patients without worsening their outcomes.

SP35
HIV Serology Signal-to-Cutoff Ratio as a Rapid Method to Predict Confirmation of HIV Infection
L Li¹, D Puddicombe¹, S Champagne¹, A Jassem², M Krajden², C Lowe¹, M Payne¹

¹St. Paul’s Hospital, Vancouver, BC, ²BC Centers of Disease Control, Vancouver, BC

OBJECTIVE: To assess the ability of signal-to-cutoff (S/CO) ratio from 4th generation HIV serology to predict subsequent confirmation of HIV infection.

METHODS: Patients from August 2012 to August 2016 with a new positive HIV serology (S/CO ≥1) were included. Serology was performed using the Abbott Architect HIV Ag/Ab Combo assay. S/CO ratios were compared to the results of subsequent confirmatory testing at a reference laboratory, which consisted of: repeat serology testing, HIV-1 RNA NAAT and HIV-1 Western blot. Predictive probabilities (PPs) of a positive confirmatory result were calculated based on a logistic regression model.

RESULTS: 250 patients were included, comprising 84 (34%) HIV negative patients, 136 (54%) chronic infections, and 30 (12%) acute infections. Higher S/CO values were associated with increased odds of confirmed infection (odds ratio 1.18, 95% CI 1.09-1.28, p<0.001). The PP of a confirmed positive result increased with higher S/CO values (figure).

CONCLUSIONS: S/CO values were strongly associated with confirmed HIV infection, with a PP of 100% at a S/CO of 50. These results enable a more informed discussion of S/CO thresholds for reporting preliminary HIV infection prior to a confirmatory result. Patient risk factors and clinical symptoms should also be taken into account but were not available in this study. Earlier diagnosis of HIV, particularly for acute seroconversions, allows earlier initiation of treatment and public health interventions, which can help reduce transmission.

SP36
Carbapenamase Producing Enterobacteriaceae Outbreak in a Large Community Hospital due to Horizontal Dissemination of \( \text{bla}_{\text{kpc}} \) between Different Genera of Enterobacteriaceae
H CANDON¹, L Matukas², S Patel³, R Melano³, N Tijet³, A Eshaghi³, A McGeer⁴,5, J Johnstone²,3,5

¹Mackenzie Health, Richmond Hill, ON, ²St. Joseph’s Health Centre, Toronto, ON, ³Public Health Ontario, Toronto, ON, ⁴Sinai Health System, Toronto, ON, ⁵University of Toronto, Toronto, ON

OBJECTIVE: Carbapenemase-producing Enterobacteriaceae (CPE) due to Klebsiella pneumoniae carbapenemase (KPC) producers are emerging pathogens in Canada. In our hospital we identified a rise in the number of non-travel associated KPC isolates involving various genera. KPC-producers are rare in our hospital thus an investigation was launched, leading to the identification of an outbreak.

METHODS: In this large 380-bed community hospital, all patients colonized or infected with KPC Enterobacteriaceae between January-August 2016 were line listed and investigated. The investigation involved retrospective chart review and environmental testing of plumbing drains in rooms linked to patients positive for KPC isolates (rectal screening swabs and/or clinical samples). To identify plasmids harbouring \( \text{bla}_{\text{kpc}} \), S1 nuclease-PFGE and Southern blot was performed.

RESULTS: Four patients with admissions to our hospital were found to be colonized and/or infected with \( \text{bla}_{\text{kpc}} \)-positive Enterobacteriaceae species: Patient #1 had K. pneumoniae in their sputum, Patient #2 had Citrobacter freundii in a wound, Patient #3 had K. pneumoniae from urine, and Patient #4 had both C. freundii and Escherichia coli from rectal swabs and C. freundii in their sputum. Epidemiological review indicated overlap
in one ICU patient room (Patient #1 and Patient #4); the ICU hand hygiene sink in this room tested positive for KPC-producing C. freundii. S1 nuclease-PFGE and Southern blot analysis revealed similar size KPC-plasmids in all 4 patient isolates and in the hand hygiene sink specimen, suggesting plasmid dissemination.

CONCLUSIONS: This plasmid-mediated cluster of KPC-producing Enterobacteriaceae highlights the importance of considering plasmid-dissemination of carbampenamase resistance genes during outbreak investigations. Moreover, contaminated hospital plumbing continues to emerge as a source for CPE that can be transmitted to patients.

SP37
Fosfomycin Resistant *Escherichia coli* and *Staphylococcus pseudintermedius* Isolated from Canine Urinary Tract Infections
R COURTICE, MAR Priyantha, M Sniatynski, JE Rubin

University of Saskatchewan, Saskatoon, SK

BACKGROUND: *Escherichia coli* and *Staphylococcus pseudintermedius* are the two most common causes of canine urinary tract infections (UTIs). The emergence of resistance to first line antimicrobials, including ESBL and AmpC producing *E. coli* and methicillin-resistant *S. psuedintermedius*, poses challenges for veterinarians treating these infections. Furthermore, as both *E. coli* and *S. psuedintermedius* are potential zoonoses, the emergence of resistance in these organisms is a possible risk to pet owners. Fosfomycin is a peptidoglycan synthesis inhibitor used in the treatment of uncomplicated UTIs in people, and rarely companion animals. The objective of this study was to determine the prevalence of fosfomycin resistance among *E. coli* and *S. psuedintermedius* isolated from canine urine samples submitted to a veterinary diagnostic laboratory in Saskatoon, Saskatchewan.

METHOD: A total of 397 isolates including *E. coli* (n=281) and *S. pseudintermedius* (n=116) from canine urine specimens collected between October, 2013 and June, 2016 were included. Laboratory requisitions were reviewed to ensure that only one isolate/patient was included. Fosfomycin MICs were determined by agar dilution as per CLSI guidelines. Plates containing serial dilutions of fosfomycin from 0.25-64 µg/mL were included, and the MICs were interpreted utilizing EUCAST breakpoints for *E. coli* and *S. aureus*.

RESULTS: The vast majority of isolates were susceptible to fosfomycin. Seven *E. coli* (2.5%) and three *S. pseudintermedius* (2.6%) were resistant. Of the fosfomycin resistant *E. coli*, one also possessed the CMY-2 type β-lactamase. Of the fosfomycin resistant *S. pseudintermedius*, two were also methicillin resistant.

CONCLUSION: The increasing rate of antimicrobial resistance in companion animal pathogens mirrors the emergence of resistance seen in human infectious disease. Our results indicate that fosfomycin resistance is not yet common in canine urinary pathogens, although continued surveillance is required to identify temporal changes in resistance prevalence.

SP38
Clinical and Echocardiographic Predictors of Embolism in Infective Endocarditis
A YANG1, C Tan1, N Daneman1,2, N Adhikari1,2, G Cohen1,2, K Boyle1,2, M Hansen1,2

1University of Toronto, Toronto, ON, 2Sunnybrook Health Sciences Centre, Toronto, ON

OBJECTIVES: Infective endocarditis (IE) is characterized by high morbidity and mortality, often due to catastrophic embolic events. Accurate prediction of embolism could inform clinical decisions such as the timing of surgical intervention. However, existing literature is limited by inclusion of patients with non-modifiable emboli occurring before hospital admission. Our objective was to identify factors associated with new embolism occurring after hospital admission, incorporating results of echocardiography.

METHODS: We performed a retrospective cohort study of consecutive patients with definite or possible infective endocarditis according to Duke criteria admitted to an academic centre (1 October 2013 – 1 July 2016). Clinical and microbiologic characteristics were abstracted from medical records. Echocardiographic characteristics were assessed by two independent echocardiographers, including vegetation location, size, mobility, and extent. The primary outcome was clinical stroke or major arterial embolic complication by 90 days from admission; stroke and emboli occurring before admission were considered in a secondary analysis. We report univariable analyses between echocardiographic variables and the primary outcome, and interpreted p<0.05 as statistically significant.
RESULTS: Among 116 patients with IE, 41 had mitral valve vegetations, 38 had aortic valve vegetations, 63 had native valve involvement, 16 had prosthetic valve involvement, 32 had vegetation size >10mm, and 47 had size <10mm. We did not detect a statistically significant association between any echocardiographic variable and incident embolism. However, these variables were associated with the combined endpoint of embolism occurring before or after hospital admission (mitral vs. aortic valve vegetation [61.0% vs. 31.6%, p<0.0001]; prosthetic vs. native valve vegetation [68.8% vs. 41.3%, p<0.01]; vegetation size >10mm vs. <10mm [53.1% vs. 42.6%, p=0.032]; high vs. low vegetation mobility [51.2% vs. 41.7%, p=0.49]).

CONCLUSIONS: We confirmed the association between conventional echocardiographic variables and embolism in patients with endocarditis; failure to find associations with post-echocardiogram embolism may reflect limited statistical power or the effectiveness of antimicrobial therapy in reducing the risk of embolism.

SP39  
Examining the Effects of Microgravity on the Pathogenicity and Drug Resistance of Candida albicans using a Microfluidics-based Nanosatellite  
University of Toronto, Toronto, ON

Autonomous nanosatellites have created novel opportunities for conducting biological experiments in space without relying on the International Space Station. The microgravity environment in low-Earth orbit has been shown to alter the expression levels of genes involved in pathogenicity, drug resistance, and stress response in the opportunistic fungal pathogen, Candida albicans (CA). Moreover, it is hypothesized that prolonged exposure to microgravity—similar to that of long duration space missions—increases susceptibility to infection from endogenous residents of the human microbiota. Here, our group presents the challenges, initial results, technical design review and the synopsis of the construction-to-launch process of a 3U CubeSat capable of remotely executing microbiology experiments in a microfluidics system. We have developed means of placing CA in passive long-duration storage such that the cells remain dormant during the pre-launch operations. After achieving a stable orbit, growth will be initiated by injecting YPD growth media through the microfluidic pumping system. Our research platform examines gene expression through the use of green fluorescent protein (GFP) as a fusion reporter for 4 candidate virulence factors: MDRI, HSP90, HWP1 and SAP99. These genes play a crucial role in orchestrating drug resistance and hyphal formation within CA, both of which are key virulence mechanisms. After growth initiation, on-board fluorescence sensors will quantify GFP levels as a measure of real-time gene expression. Changes in drug resistance will be measured through optical density measurements of a minimum inhibitory concentration (MIC) assay for fluconazole, a common CA antifungal medication. For the integrity and success of this enterprise, multiple other variables will be monitored and controlled, including temperature, radiation levels, humidity, and pressure. In this presentation, the scientific and engineering aspects of the payload division will be expanded upon, from initial design to launch processes and preliminary results of HERON Nanosatellite Mk. II.

SP40  
Herpes simplex virus Colitis Superinfection in Crohn’s Disease: A Rare Association  
H JAFRI, D Kalina, T Aziz, S Haider  
McMaster University, Hamilton, ON

OBJECTIVE: As the management of Inflammatory Bowel Disease (IBD) continues to be shaped by the introduction of earlier and more toxic immunosuppressive therapies, viral infections have become increasingly common sequelae. These treatments result in loss of immunologic control of chronic viral infection, reactivation of latent infections, and malignancies resulting from oncogenic viruses. Herpes simplex virus (HSV) colitis complicating the course of an IBD flare is a rare phenomenon. Our objective is to raise awareness of this disease entity, as early diagnosis and treatment can impact survival.

METHODS: We present only the 5th published case of HSV colitis in a patient with IBD and review the literature.

RESULTS: A 61-year-old female presented with bloody diarrhea, which was diagnosed as primary presentation of Crohn’s disease via endoscopy. The patient was
treated with intravenous steroids and appropriate antimicrobial therapy, which led to clinical improvement. After fourteen days, the patient became hemodynamically unstable, developed peritonitis, and imaging revealed evidence of bowel perforation at the level of the cecum and splenic flexure. The patient underwent a subtotal colectomy and required admission to the intensive care unit. The post-operative period was complicated by intra-abdominal abscess and Enterobacter cloacae bacteremia. Subsequent pathology of the colon revealed diffuse mucosal inflammation and extensive ulceration that exhibited intra-nuclear inclusions which both morphologically, and immunohistochemically were consistent with HSV-1 and HSV-2. Further examination of the patient revealed oral and abdominal vesicular eruptions, which were positive on a PCR-based assay for HSV-2, suggesting a disseminated HSV infection. The patient was successfully treated with intravenous acyclovir 10 mg/kg q8h for three weeks.

CONCLUSION: Although rare, it is essential to recognize HSV colitis as a clinical entity that may complicate the natural history of Crohn’s Disease. A higher index of suspicion will lead to earlier diagnosis and management, which can lead to improved patient outcomes.

SP41
Following the Path: A Case Report of Gram-positive Rods in Association with Cystic Neutrophilic Granulomatous Mastitis
G PATRIQUIN1, T Burdz2, KA Bernard2,3, P Barnes1, TF Hatchette1

1Dalhousie University, Halifax, NS, 2National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB, 3Department of Medical Microbiology, University of Manitoba, Winnipeg, MB

PRESENTATION: A fifty year old female with a history of a prolactin-secreting pituitary microadenoma developed spontaneous firmness in her right breast. In less than 24 hours, the firmness progressed into a mass which she described as “the size of a small orange,” which prompted mammography and ultrasound. The patient was otherwise asymptomatic.

INVESTIGATIONS: An irregular mass measuring 3.3 x 3.3 x 2.1 cm was visualized by ultrasound, but two weeks later, at the time of planned needle biopsy, the mass could not be redemonstrated on imaging, nor could the lump be palpated. Three days later, the mass was again palpable, and a needle biopsy was inconclusive.

DIAGNOSIS: Surgical resection of the mass revealed a pathological diagnosis of cystic neutrophilic granulomatous mastitis (CNGM). Multiple fat globules featured Gram-positive rods – some in close approximation with neutrophils. The organisms were thought to be mostly consistent with Corynebacterium spp., however subsequent attempts by the National Microbiology Laboratory for molecular identification were unsuccessful.

MANAGEMENT: Given the clinical history and appearance of organisms, we felt that this case was most consistent with an infection due to Corynebacterium spp., most likely C. kroppenstedtii. We recommended a four-week course of doxycycline, as suggested by case reports, for its predicted activity against C. kroppenstedtii, and for its ability to penetrate, and remain active in, lipid-rich tissues. One month post-completion of antibiotics, the patient remained systemically well with no recurrence of the breast mass.

DISCUSSION: Corynebacterium spp. have been associated with CNGM in the literature, however few cases have been described. Here were present a case of CNGM associated with Gram-positive bacilli, with the presumptive etiology of Corynebacterium spp., which has responded to surgical intervention and empiric antibiotics. This case highlights the association of Gram-positive rods with CNGM.

SP42
Raltegravir Induced Alopecia Areata in an HIV Positive Female
A KAPOOR1, S Haider1, M Patel2

1McMaster University, Hamilton, ON, 2Royal College of Surgeons in Ireland, Dublin, Ireland

Integrase inhibitors have become the preferred first-line treatment regimen of HIV-1 infected patients (1,2,3). They have gained favor for being well tolerated, having few drug interactions, and virological and immunological superiority to other classes of antiretroviral drugs. We present only the second reported case of raltegravir induced alopecia areata (4).

CASE: The patient was diagnosed with HIV in Ethiopia in 2003 but started antiretroviral therapy (ART) when
she came to Canada in 2005. She had been on several regimens over the past 11 years but since September 2012 has been on Kivexa (3TC + abacavir) and raltegravir. She maintained good disease control on this regimen and had minimal side effects until March 2015 when she presented with a persistent well-circumscribed patch of hair loss involving the parieto-occipital scalp (Figure 1). She noticed its development acutely after having taken a shower and since that time it increased in size with no areas of regrowth. She was seen immediately after symptom onset by her family doctor and treated with Minoxidil 2.5% for 5 months noting no improvement. At the 5-month mark post symptom initiation she was seen by Dermatology who diagnosed her with alopecia areata and recommended continuation of the topical Minoxidil 2.5%. She then presented to HIV clinic and a decision was made to discontinue her Raltegravir given the temporal relationship and absence of other causes. She was changed to Triumeq (dolutegravir + abacavir + 3TC) and seen in follow up 6 weeks later with significant resolution of her hair loss (Figure 2).

This case illustrates the need for a broad differential to alopecia areata in an HIV positive patient that should always include drugs regardless of class. Further it highlights that although integrase inhibitors have generally been perceived as having few effects patients should still be monitored for potential unanticipated reactions.

CASE 1: A 49-year-old female presented 8 months post-kidney transplantation with an infected intra-abdominal seroma. CT incidentally revealed six hepatic lesions. Two liver biopsies were non-diagnostic and the lesions progressed on imaging. Histopathology of a third liver biopsy indicated characteristic features of AE, confirmed by serology and PCR from hepatic tissue.

CASE 2: A 49-year-old female presented with constitutional and gastrointestinal symptoms. Abdominal CT identified 3 large masses in the right hepatic lobe. Liver biopsy initially suggested visceral larvae migrans. Treatment with albendazole was pursued for 3 months but follow-up imaging was unchanged. Histopathology of a second liver biopsy was consistent with AE, confirmed by serology and tissue PCR.

Both patients have domestic dogs and live on acreages in Alberta, close to areas where coyotes are common. Neither had specific risk exposures when traveling overseas. Local zoonotic epidemiology: Enzootic infection is endemic in Alberta with molecular evidence of the sylvatic presence of a European strain. A sharp increase in detection of hepatic AE had recently been reported in domestic dogs in western Canada.

CONCLUSION: The diagnosis of AE can be challenging. AE should be included in the differential diagnosis of liver mass lesions. The presence of a more virulent parasite strain may lead to the emergence of the disease in humans. A One Health approach is critical to the investigation and surveillance of this infection.

SP43
Alveolar echinococcosis in Alberta: An Emerging Infectious Disease in North America?
S BELGA1, K Doucette1, J Preiksaitis1, A Massolo2, C Klein2, K Kowalewska-Grochowska1, B Sis1, S Houston1

1University of Alberta, Edmonton, AB, 2University of Calgary, Calgary, AB

BACKGROUND: Echinococcus multilocularis (Em) is enzootic in Europe, Asia and North America. When ingested by humans, Em eggs can cause alveolar echinococcosis (AE). Without surgical excision or lifelong antihelminthic suppression, human infections are progressive. They are more common and progress more rapidly in immunocompromised patients. To date, outside of Alaska, only two cases of AE acquired in North America have previously been reported.

CASE 1: A 49-year-old female presented 8 months post-kidney transplantation with an infected intra-abdominal seroma. CT incidentally revealed six hepatic lesions. When reinvestigating her Hepatitis C, tests revealed non-bloody diarrhea. Initial lab work revealed a new
thrombocytopenia. He also had marked renal failure and an elevated CK, ferritin, LD and D-dimer. A bone marrow biopsy revealed HLH. As part of the work up for thrombocytopenia, a rapid HIV antibody based assay was done and was negative. The sample was later routinely tested with a fourth-generation antigen/antibody assay as per local protocol and was strongly positive. The plasma RNA viral load was >10,000,000 IU/mL confirming the diagnosis of an acute HIV infection. The patient was urgently started on antiretroviral therapy and recovered.

CONCLUSION: This case illustrates a diagnostic approach to HLH which is an uncommon but life threatening disease. Following any diagnosis of HLH, rapid identification and treatment of the underlying condition is critical. A negative rapid HIV antibody test can be misleading in the context of early HIV infection and the additional use of fourth generation antigen/antibody test or plasma RNA viral load may be required within the right clinical context for diagnosis.

SP45
Influenza A Virus Replication and Bioaerosol Production in a Ferret Model; Evaluation of Bioaerosol Samplers
C BEKKING1,2, L Yip2, N Doggett1,2, M Finn2, S Mubareka1,2

OBJECTIVE: Our primary objective was to evaluate low and high volume bioaerosol samplers for the recovery of influenza virus RNA in an experimental setting. Our secondary objective was to determine the effects of non-steroidal anti-inflammatory drugs (NSAIDs) on viral shedding and bioaerosol production in a ferret infection model for influenza virus.

METHODS: Ferrets were inoculated intranasally with 10^6 pfu of influenza virus A/California/07/2009 (H1N1) and placed in an environmental chamber maintained at 20°C and 20% relative humidity. Ferrets were injected subcutaneously daily with meloxicam (n=4) or saline (n=4). Animals were anesthetized and nasal washed with 2.0 ml of saline on day 1 post-infection and alternate days thereafter. Nasal titre was determined by plaque assay. Low (Teflon filter and NIOSH cyclone) and high (Andersen 6-stage impactor and Spincon) volume aerosol sampling within the chamber was conducted on alternate days. Viral RNA was extracted and RNA copies were determined using RT-qPCR.

RESULTS: Nasal titres for meloxicam-treated and control ferrets were highest on day 1 (6.85 ± 0.26 log pfu/ml and 6.20 ± 0.22 log pfu/ml, respectively) and declined until termination. No difference in nasal titres was determined between groups. On peak aerosol production days, viral RNA copies per litre air sampled was highest for meloxicam-treated (Teflon=4.54 x 10^3 copies/L air, NIOSH=6.98 x 10^3 copies/L air, Andersen=1.24 x 10^6 copies/L air) compared to untreated ferrets (Teflon=1.82 x 10^2 copies/L air, NIOSH=3.63 x 10^2 copies/L air, Andersen=3.12 x 10^4 copies/L air). Aerosol viral loads were highest from the Anderson impactor and lowest from the Spincon instrument; viable virus was detected from samples recovered from Teflon filter and NIOSH cyclone samplers, both of which also demonstrated ease of use.

CONCLUSION: The Andersen 6-stage impactor recovered more influenza virus RNA compared to other samplers, however Teflon filter and NIOSH cyclone samplers retained virus viability and were more user-friendly. Further investigation is required to understand the relationship between NSAIDs and viral shedding.

SP46
Mechanism of Antibacterial Activity of Carvacrol against Streptococcus pyogenes: Effect on Bacterial Cell Wall/Membrane Disruption and Permeability
NM WIJESUNDARA1, HPV Rupasinghe1,2,3

BACKGROUND: Streptococcus pyogenes causes significant health issue worldwide. Investigation of efficacious anti-streptococcal phytochemicals from herbal medicines has gained a renewed interest due to concerns with antibiotic resistance and some treatment failures. The aim of the present study was to assess anti-bacterial activity of carvacrol against S. pyogenes and its potential mechanism(s).

METHODS: Carvacrol was assessed for the growth inhibition using micro-broth dilution method using two
reference strains and a clinical isolate of S. pyogenes. Bactericidal concentration was identified using agar plating. To evaluate cell wall/membrane leakage, carvacrol treated bacteria supernatants were: measured at 260/280 nm; visualized using agarose gel and assessed for lactose dehydrogenase (LDH) activity. Furthermore, morphological changes were visualized through transmission electron microscopy (TEM).

RESULTS: All the tested strains were susceptible to carvacrol where minimum inhibitory concentration (MIC) and minimum bacterial concentration (MBC) were 125 and 250 μg/mL, respectively. Penicillin G showed significant inhibition with MIC and MBC of 0.008 and 0.016 μg/mL, respectively. Interestingly, time-to-kill was only 5 min for carvacrol at MBC, when compared to 24 hr for Penicillin at MBC. Anti-bacterial effects of carvacrol such as cell wall/membrane disruption, morphological damage and cell density reduction of bacteria were observed at growth phase of treatment at MIC and ½ MIC concentrations. The effect on cytosolic LDH release, and leakage of genomic materials from bacterial were observed with treatment of carvacrol in a dose dependent manner.

CONCLUSION: Carvacrol exhibited growth inhibition and bactericidal properties against S. pyogenes through disruption of bacterial cell wall/membrane and increasing the permeability. Therefore, carvacrol at its inhibitory concentrations could be used for developing a safe and efficacious natural health products for the management of streptococcal pharyngitis. Further investigations are in progress to assess cell wall degraded products using ultra-performances liquid chromatography mass spectrometry and membrane permeability using flow cytometry.

SP47
Epidemiology of Multidrug-Resistant Gram-negative Bacteremia in a Hospital-Based Pediatric Population
R GEIER1,2, S Liu2, S Hughes1, R Rassekh1, J Ting1, A Roberts1, P Tilley1, KT Kang1

1British Columbia Children’s Hospital, Vancouver, BC, 2University of British Columbia, Vancouver, BC

OBJECTIVES: Antimicrobial resistance poses a significant clinical challenge on a global scale. Knowledge of local resistance patterns is crucial for identifying at-risk patients and initiating effective, timely antimicrobial therapy. The aim of this study is to describe the epidemiology and patient characteristics associated with multidrug-resistant Gram-negative bloodstream infections (MDRGN BSIs) in a hospital-based pediatric population.

METHODS: This retrospective descriptive study included patients <19 years old with positive blood cultures for Enterobacteriaceae or non-fermentative Gram-negative bacteria collected between January 1, 2014 and April 26, 2016 at a tertiary pediatric hospital. Blood culture collection and susceptibility testing were performed in accordance with CLSI guidelines. Univariate statistics were performed using Pearson's chi-squared and Fisher’s exact tests.

RESULTS: A total of 159 Gram-negative BSIs were identified in the study period, of which 16 were multidrug-resistant (10.06%). Escherichia coli was the most common MDR pathogen, comprising 50% of the MDR episodes. The cumulative incidence of MDRGN BSIs was 0.905 (infectious episodes/1000 hospital admissions) and infection rate was 0.125 (infectious episodes/1000 bed days). Of the MDRGN BSIs, 14 of 16 (87.50%) occurred in patients treated with antibiotics within the last 30 days, and 11 of 16 (68.75%) occurred in patients with an underlying malignancy. The number of BSIs associated with length of stay >21 days was higher in the MDRGN BSI group vs the non-MDRGN BSI group (68.75% vs 44.75%).

CONCLUSION: MDRGN bloodstream infections are not uncommon, particularly in the context of recent antibiotic use and underlying malignancy. They are also associated with longer hospital admissions, highlighting the need for appropriate antimicrobial stewardship in both community and hospital settings.
SP48
Thrombin Cleavage of Plasmodium falciparum Erythrocyte Membrane Protein-1 Inhibits Cytotoadherence
MR Gillrie¹, B Renaux¹, E Russell-Goldman², M Avril³, AJ Brazier³, K Mihara¹, E Di Cera⁴, DA Milner², MD Hollenberg¹, JD Smithh⁴, M Ho⁴
¹University of Calgary, Calgary, AB, ²Harvard Medical School, Boston, Massachusetts, USA, ³Center for Infectious Disease Research, Seattle, Washington, USA, ⁴Saint Louis University School of Medicine, St. Louis, Missouri, USA

Plasmodium falciparum malaria remains one of the deadliest infections worldwide. The pathogenesis of the infection results from the sequestration of infected erythrocytes (IRBC) in vital organs, including the brain, with resulting impairment of blood flow, hypoxia and lactic acidosis. Sequestration occurs through the adhesion of IRBC to host receptors on microvascular endothelium by Plasmodium falciparum erythrocyte membrane protein 1 (PfEMP1), a large family of variant surface antigens each with up to seven extracellular domains that can bind to multiple host receptors. Consequently, anti-adhesive therapies directed at single endothelial adhesion molecules may not be effective. In this study, we demonstrate that the serine protease thrombin, which is pivotal in the activation of the coagulation cascade, cleaved the major parasite adhesin on the surface of IRBC. As a result, adhesion under flow was dramatically reduced and already adherent IRBC were detached. Thrombin cleavage sites were mapped to the DBLδ1 domain and interdomains 1 and 2 in the PfEMP1 of the parasite line IT4var19. Furthermore, we observed an inverse correlation between the presence of thrombin and IRBC in cerebral malaria autopsies of children. We investigated a modified thrombin R67A and thrombin inhibitor hirugen, both of which inhibit the binding of substrates to Exosite I, thereby reducing its pro-inflammatory properties. Both approaches reduced the barrier dysfunction induced by thrombin without affecting its proteolytic activity on PfEMP1, raising the possibility that thrombin cleavage of variant PfEMP1 may be exploited as a broadly inhibitory anti-adhesive therapy.
IP01
The Effect of An Infection Prevention and Control Mobile Application on Patient and Family Knowledge
C TSANG1, C Pearce1, M Lemay2,3, L Kamhuka1, L VanRootselaar1, L Vayalumkal2,3,4

1Bachelor of Health Sciences Student, University of Calgary, Calgary, AB, 2Infection Prevention and Control, Alberta Health Services, Calgary, AB, 3Section of Infectious Diseases, Department of Pediatrics, Alberta Children’s Hospital, Calgary, AB, 4Alberta Children’s Hospital Research Institute, Calgary, AB

BACKGROUND: Sharing infection prevention and control (IPC) knowledge is extremely important in preventing the spread of infections. Education can improve patient IPC knowledge and application. Technology such as mobile devices play an increasing role in the sharing of knowledge. It is important to adapt IPC education strategies to include modern devices used by the general public.

OBJECTIVES: This study evaluated the effectiveness of a multimedia interactive mobile application (app) to increase knowledge in general IPC and hand hygiene (HH) in pediatric patients and their family members.

METHODOLOGY: Patients admitted to inpatient units at the Alberta Children’s Hospital and their family members were invited to participate in the study. Participants were asked to download an IPC education app to their mobile devices. If they could not download the app, they received a verbal education session about basic IPC covering the same details as the app. A researcher administered a questionnaire and monitored participant HH performance prior to and two days after intervention to evaluate change in IPC knowledge and HH performance.

RESULTS: 169 participants took part in the study. The mean questionnaire scores of the participants who received verbal education increased 25.1% (p<0.01) and HH performance score increased 26.1% (p<0.01). The mean questionnaire scores of those who used the mobile app increased 18.8% (p<0.01) and hand hygiene performance scores increased 15.3% (p<0.01). The quiz scores among app users were lower than those who received verbal education session. (p=0.01). However, HH performance was not significantly different between the groups (p=0.9).

CONCLUSIONS: Patient and family centred IPC education was effective via interactive verbal education and a mobile app to increase short term knowledge. Further research is required to determine optimal app design and assess if IPC education through mobile technology can result in sustained increases in IPC knowledge among patients and their families.

IP02
Prevention of Clostridium difficile Infections Through the Detection and Isolation of C. difficile asymptomatic carriers — a three-year follow-up study
Y LONGTIN1,2, P Gervais3,4, J-F Roussy3,4, B Paquet-Bolduc3,4, J Longtin4,5, S Trottier3,4

1Jewish General Hospital, Montréal, QC, 2McGill University, Montréal, QC, 3Quebec Heart and Lung Institute, Québec City, QC, 4Laval University, Québec City, QC, 5Laboratoire de Santé Publique du Québec, Montréal, QC

BACKGROUND: Clostridium difficile infections (CDI) have become the most important healthcare-associated infections in North America, causing more than 30,000 deaths every year. Despite this menace, there have been no major advances in C. difficile prevention over the last 20 years. We have the pleasure of submitting a breakthrough innovation that could help decrease CDI incidence significantly.

METHODS: The Quebec Heart and Lung Institute developed a novel strategy to prevent healthcare-associated infections in North America, causing more than 30,000 deaths every year. Despite this menace, there have been no major advances in C. difficile prevention over the last 20 years. We have the pleasure of submitting a breakthrough innovation that could help decrease CDI incidence significantly.

RESULTS: During the 3 years that followed the implementation of this intervention in November 2013, >16,000 patients were screened for C. difficile. HA-CDI rates decreased significantly, from an average of 6.9 per
10,000 patient-days prior to the intervention, to 3.0 per 10,000 patient-days during 15 months that followed implementation (P<0.001). Poisson regression and ARIMA modelling confirmed that the intervention had a significant impact on HA-CDI rates. By contrast, no significant change in HA-CDI rates were observed among the control groups. More than 3 years following implementation, HA-CDI rates remain 68% lower than the pre-intervention average (average for 2016, 2.2 per 10,000 patient days).

**DISCUSSION:** This innovation is the first of its kind worldwide and is important for several reasons: (1) the intervention is simple to implement; (2) it addresses an urgent need; (3) the magnitude of the effect is sizeable; (4) preliminary cost-effectiveness analysis suggests that the savings in averted CDI is greater that the cost of the intervention. In other words, this intervention is capable of preventing the most important HAI in North America and lead to net cost-savings in the long term.

**IP03 ABSTRACT WITHDRAWN**

**IP04**

**Development of a Model for the Rapid Typing of Group A Streptococcus (GAS) Using Matrix Assisted Laser Desorption Time-of-Flight (MALDI-TOF) and ClinProTools Software**

A CABRERA1, LM Matukas1,2, MP Muller1,2, M Tadros1,2

1Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, 2Microbiology, Department of Laboratory Medicine, St. Michaels Hospital, Toronto, ON, 3Department of Medicine, St Michaels Hospital, Toronto, ON

**BACKGROUND:** Outbreaks of infections due to GAS frequently occur in institutional settings and can be associated with severe disease. Both emm-type based classification and pulse field gel electrophoresis can be used for strain typing, but do not provide same-day results. We explored the potential for MALDI-TOF with the aid of ClinProTools software to rapidly type GAS isolates.

**METHODS:** A total of 42 GAS isolates were evaluated; 29 isolates were from an outbreak (16 emm-type-74 and 13 emm-type-101) and 13 were epidemiologically unrelated (emm-types 1, 2, 12, 31, 73, 87, 89 or untyped). Ethanol-formic acid extraction was used and spectra were acquired with Bruker MALDI Biotyper. A strain classification model was generated using 10 emm-type-74 and 10 emm-type-101 isolates and a ClinProTools-software supported algorithm. The remaining isolates (22) were classified using the developed model as well as visual inspection for the presence/absence of key discriminatory peaks (Fig.1). Each isolate was then assigned into a class: class-1 (emm-type-74), class-2 (emm-type-101) or class-3 (other emm-types).

**RESULTS:** This method was able to classify all tested emm-type-74 isolates into class-1 (6/6 isolates, 100% sensitivity and specificity). Isolates belonging to emm-type-101 were also classified correctly into class-2 (3/3 isolates, 100% sensitivity) but 2 isolates having other emm-types (emm-type 31 and 73) were wrongly classified into this class (2/13 isolates, 89.5% specificity). All other isolates were correctly classified as unrelated into class-3 (11/13 isolates, 84.6% sensitivity and 100% specificity). The overall strain classification agreement was 90.9% (20/22 isolates).

**CONCLUSIONS:** This study suggests that MALDI-TOF and ClinProTools are promising tools for the rapid typing of GAS. This method was most accurate for the classification of emm-type-74 isolates, but was less powerful to discriminate between emm-type-101 from unrelated emm-types. Further studies are required to fully demonstrate the power of MALDI-TOF for strain typing.

**IP05**

**Impact of Automatic Infectious Diseases Consultation for Patients with Staphylococcus aureus Bacteremia**

L DJELIC1,2, N Andany1,2, J Craig2, AE Simor1,2, N Daneman1,2, JA Leis1,2,3

1Division of Infectious Diseases, Sunnybrook Health Sciences Centre, Toronto, ON, 2Division of Infectious Diseases, Department of Medicine, University of Toronto, Toronto, ON, 3Centre for Quality Improvement and Patient Safety, University of Toronto, Toronto, ON

**BACKGROUND:** Multiple observational studies have suggested that patients with Staphylococcus aureus bacteremia (SAB) seen in Infectious Diseases (ID) consultation have improved outcomes but few intervention studies have been performed.

**METHODS:** Automatic laboratory notification as soon as S. aureus was identified in blood cultures between the hours of 8:00 AM – 10:00 PM followed by ID
consultation within 24 hours was introduced in November 2014 at our academic hospital. We performed a 3-year quasi-experimental evaluation comparing baseline (December 2013-October 2014) to intervention (November 2014-September 2016) periods. Patients who died before blood culture positivity, or who were receiving comfort care only, were excluded. The primary outcome was adherence to the following quality of care indicators (QCI) in accordance with published guidelines: early initiation of appropriate therapy (within 24 hours of culture positivity), surveillance blood cultures within 72-hours, echocardiogram, early source control (within 72 hours of culture positivity), and appropriate duration of therapy. Secondary outcomes included transfer to intensive care unit (ICU) and hospital readmission or death within 30 days.

RESULTS: At baseline, ID consultation occurred for 70% (28/40) of patients and increased to 100% (113/113) after automatic notification was implemented (p <.001). QCI improved for surveillance blood cultures (58% vs. 91%), echocardiogram (88% vs. 99%) and appropriate duration of therapy (79% vs. 98%) (all p<0.05) but did not change significantly for early initiation of appropriate therapy (97% vs. 100%) or early source control (86% vs. 92%). Receipt of all five CQIs increased from 45% to 87% (p < 0.0002). Transfer to ICU decreased (38% vs. 16%, p =0.03) but no significant difference was detected in 30-day readmission or death (33% vs. 27%, p=0.54).

CONCLUSIONS: Automatic ID consultation was associated with improved adherence to established CQI for the management of SAB. The lack of significant improvement in patient mortality may be due to the small sample size, and the relatively high rate of baseline ID consultation at our institution.

IP06
Antibiotic Utilization Feedback Reports on General Internal Medicine Service
S RAI1, M Elligsen1, S Walker1, C Peragine1, N Alattas1, N Daneman2,3, JA Leis2,3,4
1Department of Pharmacy, Sunnybrook Health Sciences Centre, Toronto and Lesley Dan Faculty of Pharmacy, University of Toronto, Toronto, ON, 2Division of Infectious Diseases, Sunnybrook Health Sciences Centre, Toronto, ON, 3Division of Infectious Diseases, Department of Medicine, University of Toronto, Toronto, ON, 4Centre for Quality Improvement and Patient Safety, University of Toronto, Toronto, ON

OBJECTIVES: Peer comparison is an increasingly recognized behavioural intervention to improve physician prescribing practices. We sought to measure prescriber-level antibiotic utilization among general internal medicine (GIM) attending physicians to provide peer comparison reports, and assess any impact on physician practices.

METHODS: Antibiotic Days of Therapy (DOT) per 1000 patient days under the care of each GIM physician was calculated using our antimicrobial stewardship database. We included all attending physicians with at least 3-weeks of inpatient service during the study period (January 2nd 2015 to June 27th 2016). Readmission or death within 30-days for patients who received at least one antibiotic was used as a balancing measure. Anonymous, personalized feedback reports were emailed to each GIM physician describing their antibiotic prescribing practices compared to their peers. An electronic survey was conducted 2-months later to assess perceptions regarding feedback and any contemplated changes in practice.

RESULTS: Among 17 GIM physicians, antibiotic prescribing varied from 316 to 569 DOT per 1000 patient days (p<.0002). Despite these differences, there was no significant difference in 30-day readmission or death among their patients who received antibiotics. Of the 10 (63%) physicians that completed the feedback survey, 9 (90%) prescribers found the report represented their practice and 4 (40%) were contemplating changes in practice.

CONCLUSIONS: Provider-level antibiotic utilization at our institution confirmed wide variation in prescribing practices without an obvious difference in patient outcomes. The majority of physicians surveyed felt that antibiotic prescribing feedback reports were useful, but longer term follow up is pending to evaluate the impact of these reports on their subsequent antibiotic prescribing practices.
IP07
Effect of a Comprehensive Model for HIV Care in an Urban Canadian Population with a High Prevalence of Injection Drug Use and Homelessness
K Gupta1, K Cassidy2, S Morris-Rice2, M Silverman1
1Western University, London, ON, 2London Intercommunity Health Center, London, ON

BACKGROUND: In London, Ontario, there are a disproportionate number of people who inject drugs (PWID) compared to similarly sized Canadian communities. An alarming rise in the rate of HIV infection in this already disadvantaged population has been observed and an HIV outbreak was declared by local Public Health in the spring of 2016. HIV care is provided exclusively in an academic hospital and this presents various barriers for PWID. As a result, we see high numbers of patients not initiating and maintaining treatment with combination antiretroviral therapy (cART) and high rates of AIDS.

OBJECTIVES: To engage this population in HIV care using a comprehensive model of HIV care, medication delivery, and intensive case management.

METHODS: In September 2015, a satellite program was created in partnership with an urban community clinic specializing in addiction and homelessness. An academic HIV specialist offers monthly clinics, while on-site nurses offer HIV care and case management. As a strategy to increase compliance with cART, our program began DOT cART paired with daily-dispensed opiate substitution therapy (OST).

RESULTS: Forty-five patients who failed to engage in the academic setting were referred. Forty patients (40/45, 89%) are actively using drugs intravenously. Thirty-eight patients (38/45, 84%) are living in a shelter or marginally housed. Thirteen patients (13/45, 29%) are currently, or have been, exchanging sex for money. Twelve patients (12/45, 27%) had CD4 cell counts <200 cells/mm³ at program entry. As of the end of third quarter of 2016, thirty-five patients (35/45, 78%) are on cART, and 22/35 (63.%) have achieved an undetectable viral load (uVL). DOT with OST was associated with achieving uVL in 71% (10/14, p=0.05).

CONCLUSIONS: Providing HIV care with intensive case management increases engagement in care. Pairing cART with OST has been very effective at establishing virologic suppression in this patient population.

IP08
Designing an Effective Outpatient Antimicrobial Stewardship Program to Reduce Unnecessary Antibiotic Use in Primary Care Using a Mixed-Methods Collaborative Model
W McIsaac1,2, AM Morris1,2, A Senthinathan1,2, Y Nakamachi1,2, M Steinberg1,2, R Moineddin3,6, L Dresser1,2,4, M McIntyre1,2,4, CM Bell1,2,5, J Bloom2,3,6, D Tannenbaum1,3,6
1Sinai Health System, Toronto, ON, 2University Health Network, Toronto, ON, 3Department of Family and Community Medicine, Toronto, ON, 4Leslie Dan Faculty of Pharmacy, Toronto, ON, 5Department of Medicine, Toronto, ON, 6University of Toronto, Toronto, ON

OBJECTIVE: While Antimicrobial Stewardship Programs (ASP) are increasingly common in hospitals, most antibiotics are prescribed in the community where ASPs do not routinely exist. To address this, a collaboration between the Sinai Health System-University Health Network ASP and primary care clinics sought to develop a community-based ASP (CB-ASP). Additional objectives were to assess the feasibility of the program in primary care settings, and evaluate its effectiveness in reducing antibiotic prescriptions.

METHODS: A literature scan identified evidence-based prescribing interventions in primary care for four targeted conditions: acute sinusitis, sore throats (pharyngitis, tonsillitis, URI), acute bronchitis, and acute cystitis. Adults 18 years of age and older were the focus. Consensus between hospital-based ASP experts and community practitioners regarding ASP elements that were important and feasible in these clinics was achieved through iterative discussions. A multi-method evaluation was planned, involving qualitative interviews to assess clinic acceptability and barriers, and a quantitative before-and-after assessment of prescribing.

RESULTS: The CB-ASP program elements were: evidence-based clinical prescribing decision aids, e-learning prescriber training modules in decision aid use and condition-specific communication scripts, promotion of delayed prescribing, patient information aids, clinic work flow modifications and alternate month audit and
OBJECTIVES: We designed and implemented a technological solution, solar-powered oxygen (SPO2) delivery. The objective was to demonstrate safety, feasibility, reliability, replicability, cost-effectiveness, and non-inferiority relative to standard oxygen therapy while developing partnerships for transition-to-scale.

METHODS: SPO2 systems were designed and installed at two hospitals in Jinja and Kambuga, Uganda. The system consisted of solar panels, batteries, an oxygen concentrator, and electrical components and cost approximately $15,000 per unit. A pilot study was undertaken to assess safety and feasibility. Subsequently, a randomized-control trial (RCT) was conducted to test the hypothesis that SPO2 delivery is non-inferior to conventional oxygen delivery using cylinders.

RESULTS: The pilot study (published) demonstrated safety, feasibility, reliability, and replicability of the technology at two resource-limited hospitals in tropical Africa. The RCT demonstrated non-inferiority of SPO2 relative to standard oxygen therapy with cylinders. A cost-effectiveness analysis showed cost per disability-adjusted life year (DALY) averted to be <$30/DALY. Based on these results, planning for transition-to-scale is underway in collaboration with Grand Challenges Canada, the Clinton Health Access Initiative, ELMA Foundation, and the Ministry of Health of Uganda. This transition-to-scale would introduce solar-powered oxygen to 80 sites in Uganda while performing a stepped-wedge cluster-randomized controlled trial to demonstrate mortality benefit of SPO2.

CONCLUSIONS: SPO2 is a reliable, safe, and cost-effective solution to address the lack of oxygen availability in resource-constrained hospitals. If taken to scale, SPO2 could have global impact by reducing deaths from childhood pneumonia.

BACKGROUND: Pneumonia is the leading cause of pediatric mortality globally, causing 0.9 million deaths annually. Supplemental oxygen is essential to managing hypoxemia in severe pneumonia, but access to oxygen in low- and middle-income countries remains limited. Current oxygen delivery methods are unreliable due to issues with supply chain (compressed oxygen cylinders) or electrical power supply (oxygen concentrators).
Abstracts

**IP10**
An Innovative Interaction Design Approach to Enhance Hand Hygiene Compliance and Auditing

J KUPIS¹, H Armen¹, C Pearce², J Kaufman¹, M Bhatnagar¹, JM Conly¹,², G Hallihan¹

¹W21C, University of Calgary, Calgary, AB, ²Infection Prevention & Control, Alberta Health Services, Calgary, AB, ³Emily Carr University, Health Design Lab, Vancouver, BC

**BACKGROUND:** Effective strategies for monitoring and improving hand hygiene compliance (HHC) are critical to reducing nosocomial infections. Remote HHC monitoring technologies may better indicate actual health care worker (HCW) behaviour by removing the Hawthorne effect. Digital technologies enable novel approaches for improving HHC. We sought to implement and evaluate an innovative technology, developed by the Emily Carr University Health Design Lab using principles of interaction design (ID) to remotely monitor and encourage HHC.

**METHODS:** A subset of alcohol-based-rub (ABR) dispensers (n=29) on a four wing 36 bed medical unit were modified to monitor their frequency of use (FoU), and transmit data to local servers over a personal area network. FoU data was collected simultaneously with in-person audits using iScrub Lite (V1.5.1 University of Iowa) for 182 days. For the last 18 days, FoU data was visualized on central displays, providing real-time feedback to unit staff/visitors. This visualization component reflected the ID intervention to enhance HHC. The relationship between audited compliance and FoU data was modelled through simple linear regression. A Student’s t-test was used to compare FoU before and after the intervention.

**RESULTS:** FoU predicted a significant proportion of variance in compliance (R² = .37, β = 7.51, t(125) = 8.54, p < 0.001). The FoU with visualization was higher (M = 7.21, SD = 5.12) than with no visualization (M = 4.79, SD = 4.44), t(46) = 2.01, p = 0.08, with a moderate effect size, d = 0.51. HCW feedback indicated an increase in motivation for HHC and positive reinforcement by the ID.

**CONCLUSIONS:** These data indicate that this system could complement in-person audits for assessing HHC. The visualization element trended towards increased FoU, which was predictive of overall HHC. Data collection and technical developments will continue to improve the innovation. Further development will inform recommendations for scalability and conclusions on effectiveness.

**IP11**
The Pollution Particulate Concentrator (PoPC- Con), an Ambient Pollution Concentrator for the Study of Pathogen-Particulate Interactions

N GROULX¹,², B Urch²,³, C Duchaine⁴, S Mubareka¹,², J Scott²,³

¹Sunnybrook Health Science Center and Research Institute, Toronto, ON, ²University of Toronto, Toronto, ON, ³Dalla Lana School of Public Health, Toronto, ON, ⁴CRIUCPQ, Québec, QC, ⁵Université Laval, Québec, QC

**BACKGROUND:** Severe smog events are associated with the exacerbation of respiratory disease. Despite the significant health burden associated with such events, little is known about how the particulate matter (PM) in air pollution interacts with viruses. In order to improve our understanding of this complex interaction and its implications on human health, new research methods need to be developed.

**OBJECTIVES:** To develop a novel system to characterize interactions between PM and viruses using a particle concentrator capable of concentrating ambient outside PM in an urban setting (PoPCon).

**METHODS:** Phi6 bacteriophage is an enveloped RNA virus used to model influenza virus in biosafety level 1 settings. Phi6 was aerosolized into a 0.43 m³ chamber containing HEPA (High Efficiency Particulate Air) filtered air (control) or unfiltered concentrated ambient fine particles (PM2.5). Virus infectivity was determined by plaque assay. Relative humidity (RH), temperature and ozone were recorded. PM2.5 mass concentration, as well as particle counts and size distribution were also recorded inside the chamber.

**RESULTS:** Concentrated ambient PM2.5 mass concentration ranged from 100 - 405 µg/m³ and was mixed with an artificial aerosol of Phi6 bacteriophage. Preliminary data (n = 5 experiments) reveal that in average, the presence of PM2.5 decreases Phi6 infectivity over time compared to HEPA-filtered air, as the difference in virus inactivation can vary from 12.2% (at t = 0min incubation) to 36.2% (at t = 30min incubation)
CONCLUSIONS: This novel system allows the study of the interactions between aerosolized viruses and high levels of PM2.5 as can occur during smog events. More work is required to understand the precise mechanisms and decipher the contribution of temperature, relative humidity and ozone. This work has implications for the aerosol infectivity and potential transmissibility of human respiratory viruses during air pollution events.

IP12

The Development of an Ambulatory Monitoring System for Infectious Diseases Using Wearable Technology, Bluetooth-Enabled Devices, a Mobile Application, Patient Portal and Electronic Health Record: A Proof Of Concept Study

R Medford1,2, M Yen3

1 Stanford University School of Medicine, Division of Clinical Informatics, Palo Alto, California, USA, 2 Stanford University Center of Innovation in Global Health, Palo Alto, California, USA, 3 Kingston General Hospital, Kingston, ON

OBJECTIVES: The ability to monitor patients in the outpatient setting is a vital component of care in many infectious diseases including skin and soft tissue, respiratory and intraabdominal infections. Initially, patients are followed in clinic with greater frequency and as symptomatology improves, the frequency decreases. Conversely, there is a paucity of data available to the clinician in between these visits and communication between patient and provider may be difficult. To bridge this gap, we are developing an ambulatory monitoring system that is built on Apple Inc’s Health Kit and Care Kit framework, coupled with wearable technology, Bluetooth-enabled devices, a patient-facing mobile application (app) and a clinician-facing dashboard that seamlessly communicates between the patient’s mobile phone and our electronic health record (EHR).

METHODS: A patient-facing mobile app is being created that allows integration of information from a smartwatch (mobility and heart rate) and Bluetooth-enabled devices (scale, blood pressure cuff, pulse oximeter and thermometer). The native app built on the aforementioned framework will allow documentation of medications taken, pain levels and snapshot pictures or video. This data will then be viewable to the patient through the app in real-time. To relay this information to the clinician, we are utilizing our existing patient portal that allows patients to view their EHR. From the patient portal, the data is then available to be viewed via a custom-built physician-facing dashboard. Outlier values and trends are highlighted and can be easily identified and flagged for review by the clinician. Communication between patient and clinician occurs via this platform and recommendations and adjustments of care can be performed as necessary.

RESULTS: We present an innovative approach to help with continuity of care that allows for symptom tracking, vital signs monitoring and analytics with visualizations to help with patient and clinician evaluation of progression of disease.

CONCLUSION: Built upon previous success of our remote glucose home monitoring and congenital heart disease programs, we believe this platform will improve patient care by engaging patients, increasing availability of data to clinicians to make decisions and providing a tool for two-way communication in the ambulatory setting.
RESULTS: All 300 K-SeTs had visible Control bands. KPC K-SeT Test bands were detected in 129/129 (100%) KPC-CPO and in 0/171 (0%) non-KPC isolates (i.e. non-KPC-CPO and non-CPO). This resulted in KPC K-SeT Sn of 100% (95% CI: 97.2-100) and Sp of 100% (95% CI: 97.9-100).

CONCLUSIONS: The KPC K-SeT, the second in a growing list of immuno-chromatographic tests for CPO detection to become available from Coris BioConcept, was extremely easy to use and very simple to interpret. Highly accurate results (100% sensitive/specific for KPC) were available within 15min from primary colonies grown on MacConkey-based agars.

P02
Antimicrobial Susceptibility of Helicobacter pylori Isolates in Manitoba
P LAGACÉ-WIENS1,2, C Turenne1,2, HJ Adam1,2, A Walkty1,2, JA Karlowsky1,2
1Diagnostic Services Manitoba, Winnipeg, MB, 2University of Manitoba, Winnipeg, MB

OBJECTIVE: To determine the antimicrobial susceptibility of Helicobacter pylori isolates recovered from antral biopsies in Manitoba in the 2015 calendar year.

MATERIAL/METHODS: 300 Gram-negative bacilli (mostly Enterobacteriaceae) including 262 CPO [142 class A (129 KPC, 6 GES, 4 SME, 1 NMCA, 2 IMI), 81 class B (73 NDM, 7 VIM, 1 IMP), 32 class D (15 OXA48, 9 OXA181, 6 OXA232, 2 OXA244), 7 class B+D (4 NDM+OXA181, 3 NDM+OXA232) and 38 non-CPO (mixed mechanisms including carbapenem-R porin-mutants) were selected for study. After blinding to prevent bias, isolates were grown on MacConkey agar under ertapenem pressure, and tested by KPC K-SeT as per Coris BioConcept’s package insert. A single colony picked from the agar was emulsified in lysing reagent. This emulsion was then used to inoculate the lateral-flow line assay cartridge. The development of visible lines at test and control positions was documented independently by 5 readers after 15mins at ambient temperature from time of K-SeT inoculation. A Control line had to be detected for a valid test whereas detection of a Test line indicated a KPC-positive result. Consensus data were analysed for Sn/Sp for KPC detection. 95% confidence intervals (95% CI) for all values were calculated using www.graphpad.com.
Abstracts

RESULTS:

<table>
<thead>
<tr>
<th>Organism group</th>
<th>%ID¹</th>
<th>Acc²</th>
<th>%ID</th>
<th>Acc</th>
<th>%ID</th>
<th>Acc</th>
</tr>
</thead>
<tbody>
<tr>
<td>All (n=206)</td>
<td>74.8</td>
<td>100</td>
<td>56.2</td>
<td>98.3</td>
<td>62.9</td>
<td>98.4</td>
</tr>
<tr>
<td>Gram-negative</td>
<td>88.9</td>
<td>100</td>
<td>77.8</td>
<td>100</td>
<td>87.5</td>
<td>100</td>
</tr>
<tr>
<td>Gram positive cocci in clusters (n=47)</td>
<td>74.5</td>
<td>100</td>
<td>68.1</td>
<td>100</td>
<td>86.1</td>
<td>100</td>
</tr>
<tr>
<td>Gram positive cocci in chains (n=39)</td>
<td>59.0</td>
<td>100</td>
<td>20.5</td>
<td>100</td>
<td>46.2</td>
<td>88.9</td>
</tr>
<tr>
<td>Large Gram-positive bacilli (n=19)</td>
<td>89.5</td>
<td>100</td>
<td>68.4</td>
<td>100</td>
<td>77.8</td>
<td>100</td>
</tr>
<tr>
<td>Yeast (n=29)</td>
<td>55.2</td>
<td>100</td>
<td>27.6</td>
<td>100</td>
<td>3.4</td>
<td>100</td>
</tr>
</tbody>
</table>

¹Percentage of blood culture for which identification to species was possible.
²Accuracy of rapid identification to species compared to conventional identification.

CONCLUSION: All methods provide rapid and accurate identification of most blood cultures with Gram-negative bacteria and Gram-positive bacilli. Identification of Gram-positive cocci in chains and clusters is limited by misidentifications within species of closely related streptococci and coagulase-negative staphylococci, respectively.

P03 ABSTRACT WITHDRAWN

P04
Comparison of Three Rapid MALDI-TOF Identification Methods for Positive Blood Cultures
P LAGACÉ-WIENS¹,², HJ Adam¹,², P Pieroni¹, N Konzie¹, K Glor¹, S Kassam¹, W Leduc¹, J Terrick¹, C Espenell¹, JA Karlowsky¹,²

¹Diagnostic Services Manitoba, Winnipeg, MB, ²University of Manitoba, Winnipeg, MB

OBJECTIVE: The accuracy of organism identification using the Bruker Sepsityper™, an in-house extraction method and a smudge plate were compared for the rapid identification of organisms from positive blood cultures.

METHODS: Positive blood cultures were analysed using the commercially available Bruker Sepsityper™ blood culture extraction kit, an in-house saponin-based lysis-centrifugation and solvent extraction method, and an extended direct-transfer identification from a subculture incubated for 4-6 hours (smudge plate). Results were interpreted using Sepsityper™ identification thresholds (1.8 for species and 1.6 for genus) for the Sepsityper™ and saponin methods and the manufacturer-recommended identification thresholds (2.0 for species and 1.7 for genus) for the smudge plates. Positive blood cultures were analysed using the three rapid methods concurrently and compared to conventional subculture and identification using the Bruker MALDI Biotyper™ or alternative identification method (biochemical, sequencing) as needed.

CONCLUSION: Amoxicillin, tetracycline and metronidazole are most active against contemporary H. pylori strains. Levofloxacin and clarithromycin were less active against this collection of isolates.

P04
Comparison of Three Rapid MALDI-TOF Identification Methods for Positive Blood Cultures
P LAGACÉ-WIENS¹,², HJ Adam¹,², P Pieroni¹, N Konzie¹, K Glor¹, S Kassam¹, W Leduc¹, J Terrick¹, C Espenell¹, JA Karlowsky¹,²

¹Diagnostic Services Manitoba, Winnipeg, MB, ²University of Manitoba, Winnipeg, MB

OBJECTIVE: The accuracy of organism identification using the Bruker Sepsityper™, an in-house extraction method and a smudge plate were compared for the rapid identification of organisms from positive blood cultures.

METHODS: Positive blood cultures were analysed using the commercially available Bruker Sepsityper™ blood culture extraction kit, an in-house saponin-based lysis-centrifugation and solvent extraction method, and an extended direct-transfer identification from a subculture incubated for 4-6 hours (smudge plate). Results were interpreted using Sepsityper™ identification thresholds (1.8 for species and 1.6 for genus) for the Sepsityper™ and saponin methods and the manufacturer-recommended identification thresholds (2.0 for species and 1.7 for genus) for the smudge plates. Positive blood cultures were analysed using the three rapid methods concurrently and compared to conventional subculture and identification using the Bruker MALDI Biotyper™ or alternative identification method (biochemical, sequencing) as needed.

CONCLUSION: All methods provide rapid and accurate identification of most blood cultures with Gram-negative bacteria and Gram-positive bacilli. Identification of Gram-positive cocci in chains and clusters is limited by misidentifications within species of closely related streptococci and coagulase-negative staphylococci, respectively.

P05
Comparison of Three Methods of Environmental Sampling for the Recovery of MRSA, VRE and CPO from the Hospital Environment: A Quality Improvement Initiative
L Turnbull², L Chui¹,², G Taylor¹,², P NAIDU¹,²

¹University of Alberta, Edmonton, AB, ²Provincial Laboratory for Public Health, Edmonton, AB

INTRODUCTION: During the last two decades, hospitals throughout the world have experienced a rise in health care associated infections (HAI) along with its financial, individual and societal costs. HAIs contribute significantly to adverse effects in health care. Environmental sampling is an integral part of an Infection Control outbreak investigation in all health care facilities. There have recently been numerous studies addressing the deficiency in knowledge and evidence on methods of environmental sampling.

OBJECTIVES: To determine which of the three methods of environmental sampling is the most sensitive in our hospital environment, cost effective and timely, at producing positive cultures.

METHODS: Stored clinical MRSA, VRE, and CPO isolates (10 GES 5, KPC, INDM), were used to form suspensions of $10^6$ to $10^8$. Pieces of porcelain, stainless steel and plastic were as surrogates for surfaces encountered in patient hospital rooms (sink & toilet, bedrails, remote control). Fifty microlitres of each dilution of each organism was spread onto 2cm X 2cm area on each surface. The surfaces were then cleaned according to our institution’s post-isolation protocol and sampled. One pre-moistened cotton swab was plated directly to the chromogenic plates (current method). The other pre-moistened cotton swab and sterile gauze were incubated in Fastidious Organism Broth (FOB) at 35 ±2°C for 24 hours; the broths were then plated onto chromogenic plates and incubated for a further 24 hours.

OUTCOMES: Of the 162 tests, the gauze/FOB method had the highest rate of recovery (8.6%, 14/162) with the current direct swab method having the lowest recovery rate (1%; 2/162). Based on this study, the laboratory and Infection Control Practitioners have adopted the gauze/FOB method for environmental sampling despite the increased cost.

LIMITATIONS: The study was conducted in a laboratory making the results not directly transposable to the hospital environment; it is postulated that the environmental culture yield would be higher. Positive culture yield.

P06
Antibiotic Prophylaxis in Acute Ischemic and Hemorrhagic Stroke Patients: A Systematic Review and Meta-Analysis
E RENNERT-MAY1, C Zerna1, L Bresee1,2
1University of Calgary, Calgary, AB, 2CADTH, Calgary, AB

OBJECTIVES: Stroke is a major cause of morbidity and mortality. Infections following stroke are associated with increased risk of complications and mortality. We sought to determine if prophylactic antibiotics following acute stroke in hospitalized adult patients aid in preventing infections.

METHODS: We searched Embase (1974-), Medline (1946-), Cochrane Collaboration (1966-), and Pubmed (2015-). We also searched three major Infectious Diseases and Neurology journals in an effort to find unlisted publications, and explored trial registries for ongoing studies. We included randomized controlled trials that considered patients ≥ 18 years of age hospitalized following acute ischemic or hemorrhagic stroke. Screening and data extraction were done independently in duplicate. Meta-analyses were completed to evaluate the primary and secondary outcomes of relative risk (RR) of infection incidence and mortality between treatment and control groups, respectively. Pooled analyses of all included studies were completed. Additionally, separate meta-analyses were performed on studies with 90-day and 180-day follow-up. The impact of heterogeneity, study quality, and bias of included studies was considered in the meta-analyses.

RESULTS: We included five studies for a total of 4030 patients. One study was of high, one of moderate and three of low quality. When all five studies were pooled together, which was felt to be the most appropriate representation, there was not a significant reduction in the incidence of infection (RR 0.69, 95% CI 0.442-1.090). Prophylactic antibiotics did not reduce 90-day (RR 1.130, 95%CI 0.949-1.345) or 180-day (RR 0.960, 95%CI 0.770-1.198) mortality. No differences were noted regarding length of hospital stay or antibiotic-related adverse events but information regarding these variables was minimally described in the included studies.

CONCLUSION: Based on the results of this systematic review, there is no compelling evidence to alter current guidelines to implement prophylactic antibiotics following acute stroke in adult patients.

P07
A Cost-Effectiveness Analysis of a Decolonization Protocol for Staphylococcus aureus Prior to Knee Arthroplasty in Alberta, Canada
E RENNERT-MAY1,2, JM Conly1,2, B Manns1,2
1University of Calgary, Calgary, AB, 2Alberta Health Services, Calgary, AB

OBJECTIVES: While recent research suggests that decolonization of Staphylococcus aureus (S. aureus) reduces complex post knee arthroplasty (KA) infection rates, studies examining its cost-effectiveness are
lacking. Using the perspective of a provincial healthcare system, we conducted a cost-effectiveness analysis of a decolonization protocol (DP) for S. aureus prior to KA, compared to usual care.

METHODS: A simple tree decision model using TreeAge Pro (TreeAge Software Inc 2016) was created to simulate patients undergoing KA. The S. aureus complex joint infection rate from primary KA without decolonization was based on the Alberta Health Services (AHS) Infection Prevention and Control surveillance database. The effectiveness of decolonization using intranasal 2% mupirocin ointment plus chlorhexidine 4% washes (or 2% cloths) at preventing S. aureus joint infections was based on a large pre-/post-intervention trial (Schweizer et al., JAMA, 2015). The relative risk of developing a complex S. aureus infection was 0.48 with the intervention. Costs of medications and hospital care (CDN$ 2015) for those developing KA infections were obtained from the Alberta Blue Cross formulary and the Canadian Institute for Health Information case mix groupers, respectively. Sensitivity analyses were conducted to account for variability with the intervention and possible resistance to chlorhexidine and/or intranasal mupirocin.

RESULTS: The DP was cost-effective with reduced complex S. aureus KA infections (0.18% vs 0.37%) and savings of $65 per person decolonized. The model was robust to sensitivity analyses conducted within plausible ranges. The best and worst case scenarios resulted in savings of $121 and $10 per person decolonized. Yearly cost savings in Alberta were approximately $350,000 when a budget impact analysis was conducted.

CONCLUSIONS: Decolonization for S. aureus reduced the risk of KA infections in our model, and resulted in net annual savings from an AHS perspective. This model could potentially be applied to other Canadian populations undergoing KA and explored in hip arthroplasty settings.

P08
Hand Hygiene Knowledge, Attitudes, and Practices among Hospital Inpatients: A Mixed Methods Study
JA SRIGLEY1,2, S Cho3, C O’Neill4, C Lee3,4,5,6, D Mertz3,4

1BC Children’s & Women’s Hospitals, Vancouver, BC, 2University of British Columbia, Vancouver, BC, 3McMaster University, Hamilton, ON, 4Hamilton Health Sciences, Hamilton, ON, 5St. Joseph’s Healthcare Hamilton, Hamilton, ON, 6Island Health Authority, Victoria, BC

OBJECTIVE: Health care-associated pathogens may be acquired via patients’ own unclean hands, but the importance of patient hand hygiene has been minimally studied. Data on patient hand hygiene rates are scarce, and little is known about the facilitators and barriers of hand hygiene among inpatients. This study aimed to assess the hand hygiene knowledge, attitudes, and practices of adult inpatients at four acute care hospitals in Hamilton, ON.

METHODS: A mixed methods approach was used, with the initial phase consisting of a cross-sectional survey distributed in inpatient rooms for a one-week period. In the second phase, structured interviews were conducted with randomly selected inpatients. Qualitative data were analyzed independently by two researchers using the Theoretical Domains Framework.

RESULTS: A total of 268 surveys were completed, with 66.4% of patients reporting always performing hand hygiene after toileting and 49.2% reporting always performing hand hygiene before eating. The majority of patients (74.6%) stated that they did not want to receive more information about hand hygiene while in hospital. There were 23 patient interviews analyzed. Key themes identified include Knowledge; Environmental Context and Resources; Memory, Attention and Decision Processes; and Social Influences.
Abstracts

**CONCLUSIONS:** Self-reported patient hand hygiene compliance is suboptimal and there are knowledge gaps among patients as to when to perform hand hygiene, but patients are not receptive to receiving traditional educational interventions. Future interventions to improve patient hand hygiene should focus on other behaviour change domains including Environmental Context and Resources (e.g. access to hand sanitizer at the bedside), Memory, Attention and Decision Processes (e.g. posters or other reminders), and Social Influences (e.g. role modelling).

**P09**

*Corynebacterium kroppenstedtii* in Breast Abscess and Granulomatous Mastitis: Not to Be Dismissed as a Mere Skin Contaminant

C HOGAN¹, Y Longtin², K Weiss³

¹McGill University Health Centre, Montréal, QC, ²Jewish General Hospital, Montréal, QC

**BACKGROUND:** *Corynebacterium kroppenstedtii* was first described in 1998 and has since been reported in less than sixty cases worldwide including four in Canada. Emerging evidence supports an association between this pathogen and breast abscess/granulomatous mastitis. *Corynebacterium* species often pose a challenge to isolate in the laboratory and may be dismissed as potential skin contaminants.

**CASE:** A previously healthy 29-year-old female from Nicaragua with no past surgical history presented in August 2016 with a 4-day history of spontaneous left breast tenderness and erythema. A surface ultrasound showed a 2 cm cyst. After having failed two outpatient treatment courses of first-line antibiotics with cephalixin and cefadroxil, she underwent a breast biopsy that showed polymorphonuclear and macrophage cell infiltration compatible with an abscess but no organisms. The culture revealed slight growth of *C. kroppenstedtii*, confirmed by MALDI-TOF MS, and slight growth of *Propionibacterium acnes*. She developed ongoing pus discharge, erythema and pain post-biopsy. She was initially treated with IV ertapenem and PO levofloxacin for 7 days, followed by levofloxacin monotherapy for 10 days. *C. kroppenstedtii* isolates are usually susceptible to most antibiotics; however, resistance to penicillin, clindamycin and fluoroquinolones has been reported. This isolate was susceptible to levofloxacin and vancomycin, but resistant to clindamycin, clarithromycin and TMP-SMX. She clinically improved markedly with almost complete healing of her breast wound over the subsequent 2 months.

**CONCLUSION:** Although a rare presentation, clinicians should be aware of the emerging association between *C. kroppenstedtii* and breast abscess/granulomatous mastitis. In the proper clinical context, corynebacteria should be properly identified to the species level, by Coryne API, 16S rRNA PCR or MALDI-TOF MS, and *C. kroppenstedtii* not merely dismissed as a skin contaminant. Moreover, future studies may expand the association to other *Corynebacterium* species (including *C. pseudotuberculosis* and *C. amycolatum*) as further cases are investigated.

**P10**

Cumulative Antimicrobial Susceptibilities of Anaerobic Bacterial Isolates at a Tertiary Care Hospital in Vancouver, BC (2013–2016)

M Payne¹,², C LOWE¹,², I Sekirov², M Romney¹,², S Champagne¹,²

¹Pathology and Laboratory Medicine, Providence Health Care, Vancouver, BC, ²Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC

**OBJECTIVES:** In most clinical laboratories, anaerobic susceptibility testing is selectively performed as it is labour intensive and resistance to common anaerobic antibiotics is rare. Susceptibility testing is typically only performed for severe infections, and for isolates from sterile sites. Resistance rates in anaerobes have been increasing, particularly to clindamycin and penicillin. We reviewed our anaerobic susceptibility results over a 4-year period to develop an anaerobic antibiogram for use by our clinicians and antimicrobial stewardship team.

**METHODS:** Retrospective review of anaerobic susceptibility testing on clinical isolates at a tertiary care hospital laboratory in Vancouver, BC. Testing was performed by E test methodology and interpretations were based on CLSI Clinical Breakpoints (M100S). Only the first isolate from each patient was included in the analysis.

**RESULTS:** During the study period, 578 anaerobic bacteria had susceptibility results available. Specimen types were composed of: 159 blood cultures, 59 body fluids, and 360 wound cultures.
OBJECTIVE: This study designed and evaluated two plasmids controls: a 43-target plasmid for cmPCR (pSpn-CM1) and a 23-target plasmid for rmPCR (pSpn-RM1).

METHODS: Each plasmid was designed and synthesized as chimeric DNA sequences with all target primer binding sites sequences, as well as probe binding sites in pSpn-RM1. Additional targets (lytA and cpsA) were included in both pSpn-CM1 and pSpn-RM1 for quantification following propagation and purification in *Escherichia coli*. The pSpn-CM1 and pSpn-RM1 plasmids were tested against each cmPCR and rmPCR reaction respectively.

RESULTS: When tested using the cmPCR reactions, all targets of expected band sizes (including the cpsA internal control) could be amplified reproducibly from pSpn-CM1 with good amplicon visibility at a concentration of $10^4$ copies/µl. For the rmPCR reactions, all targets were reproducibly amplified with pSpn-RM1 at concentration of $10^3$ copies/µl, and the PCR efficiency for each target was equivalent to DNA extracted from representative *S. pneumoniae* serotypes.

CONCLUSIONS: These modifiable and quantifiable multitarget plasmids simplify the preparation of controls for PCR-based serotyping of *S. pneumoniae*, allowing good quality control and standardization of PCR methods and reagents. While these plasmids were developed for pneumococcal disease surveillance, the rationale and design concepts could be extended to other highly multiplexed PCR assays.

### Anaerobic Susceptibility by Organism Group, 2013-2016

<table>
<thead>
<tr>
<th>Organism Group</th>
<th>N</th>
<th>Clinda</th>
<th>Mero</th>
<th>Metro</th>
<th>Penicillin</th>
<th>Pip/tazo</th>
</tr>
</thead>
<tbody>
<tr>
<td>Anaerobic GPC</td>
<td>89</td>
<td>62</td>
<td>100</td>
<td>99</td>
<td>97</td>
<td>100</td>
</tr>
<tr>
<td>Actinomyces spp.</td>
<td>62</td>
<td>74</td>
<td>98</td>
<td>5</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Bacteroides fragilis group</td>
<td>150</td>
<td>51</td>
<td>93</td>
<td>100</td>
<td>0</td>
<td>94</td>
</tr>
<tr>
<td>Clostridium spp.</td>
<td>66</td>
<td>57</td>
<td>100</td>
<td>98</td>
<td>83</td>
<td>100</td>
</tr>
<tr>
<td>Fusobacterium spp.</td>
<td>22</td>
<td>86</td>
<td>100</td>
<td>100</td>
<td>95</td>
<td>100</td>
</tr>
<tr>
<td>Prevotella spp.</td>
<td>42</td>
<td>50</td>
<td>100</td>
<td>100</td>
<td>33</td>
<td>100</td>
</tr>
<tr>
<td>Propionibacterium spp.</td>
<td>74</td>
<td>90</td>
<td>99</td>
<td>97</td>
<td>99</td>
<td></td>
</tr>
</tbody>
</table>

N, number of isolates; Clinda, clindamycin; Mero, meropenem; Metro, metronidazole; Pip/tazo, piperacillin-tazobactam

*Anaerobic GPC: Peptostreptococcus spp. (n= 54), Peptococcus spp. (N= 2) and Finegoldia spp.(n= 33)

CONCLUSION(S): Our data showed high rates of clindamycin resistance for anaerobic Gram positive and negative organisms. Low rates of meropenem and piperacillin-tazobactam resistance were identified for the *B. fragilis* group. Metronidazole remains active against all anaerobes with exception of non-spore forming Gram positive bacilli.

### P11

**Multitarget Plasmid Controls for Conventional and Real-Time PCR Serotyping of *Streptococcus pneumoniae***

J Schembri1, H Gillis1,2, SA McNeil1,2,3, JJ LEBLANC1,2,3

1Dalhousie University, Halifax, NS, 2Canadian Center for Vaccinology (CCFV), IWK Health Centre, Halifax, NS, 3Nova Scotia Health Authority (NSHA), Halifax, NS

BACKGROUND: Serotyping of *Streptococcus pneumoniae* is an integral part of disease surveillance, and over 92 serotypes have been characterized by traditional serotyping methods (Quellung reaction). Molecular serotyping methods for *S. pneumoniae* are now increasingly being used that rely on conventional multiplex PCR (cmPCR) and real-time multiplex PCR (rmPCR). Given that cmPCR consist of 8 multiplex reactions with 40 targets, and rmPCR consists of 7 triplex reactions, generating positive controls for these assays can be challenging.
Abstracts

**P12**
**Comparison of the In Vitro Activity of Telavancin and Vancomycin Against Methicillin-Resistant Staphylococcus aureus (MRSA) Isolated from Blood Cultures across Canada: TELA-CHESS 2016**

M BAXTER, HJ Adam, C Lowe, SM Poutanen, K Nichol, DJ Hoban, GG Zhanel

1University of Manitoba, Winnipeg, MB; 2Diagnostic Services Manitoba, Winnipeg, MB; 3Providence Health Care, Vancouver, BC; 4University Health Network, Toronto, ON; 5Sinai Health Systems, Toronto, ON; 6University of Toronto, Toronto, ON

**OBJECTIVE:** Telavancin is a new lipoglycopeptide with a spectrum of activity similar to vancomycin but with enhanced activity versus MRSA. Canadian microbiologists, ID physicians and clinical pharmacists have limited experience with telavancin, and it is not currently available to clinical microbiology laboratories on existing automated testing devices. In order to build awareness of the activity of telavancin in the laboratory testing setting, we initiated a national study called TELA-CHESS (Telavancin - Canadian Hospital Etest Surveillance Study).

**METHODS:** 23 tertiary care hospital laboratories were recruited across Canada. Using Etest methodology, participating sites evaluated the activity of telavancin against 30 MRSA isolates obtained from blood cultures in 2015. Corresponding MIC results for vancomycin, previously obtained from the site's clinical testing, were also submitted to the coordinating site. Antimicrobial susceptibility (%S) was interpreted according to CLSI (M100-S26).

**RESULTS:** The activity (μg/mL) of telavancin and vancomycin is summarized below.

<table>
<thead>
<tr>
<th>Geographic Region* (n)</th>
<th>Telavancin</th>
<th>Vancomycin</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MIC&lt;sub&gt;50&lt;/sub&gt;</td>
<td>MIC&lt;sub&gt;90&lt;/sub&gt;</td>
</tr>
<tr>
<td>National (630)</td>
<td>0.032</td>
<td>0.047</td>
</tr>
<tr>
<td>Western (235)</td>
<td>0.032</td>
<td>0.047</td>
</tr>
<tr>
<td>Central (275)</td>
<td>0.032</td>
<td>0.047</td>
</tr>
<tr>
<td>Eastern (120)</td>
<td>0.047</td>
<td>0.094</td>
</tr>
</tbody>
</table>

*Western: BC, Alberta, Saskatchewan, Manitoba; Central: Ontario; Eastern: Quebec, New Brunswick, Nova Scotia

**CONCLUSIONS:** Telavancin was found to be 32 fold more active than vancomycin versus a national collection of blood isolates of MRSA. Regional data for both telavancin and vancomycin was very similar to data observed nationally. MRSA isolated from blood cultures remain highly susceptible (>99%) to telavancin and vancomycin.

**P13**
**In Vitro Activity of Fosfomycin (FOS) against Antimicrobial-Resistant Escherichia coli (EC) Isolated from Outpatient Urine Samples: CANWARD Surveillance Study 2007-2015**

JA Karlowsky, HJ Adam, M BAXTER, GG Zhanel

1University of Manitoba, Winnipeg, MB; 2Diagnostic Services Manitoba, Winnipeg, MB

**OBJECTIVE:** FOS is approved for the treatment of acute cystitis in women due to susceptible isolates of EC and Enterococcus faecalis. In vitro susceptibility to FOS is not routinely determined in most clinical laboratories in Canada. We determined the in vitro activity of FOS against a collection of EC grown from outpatient urine samples and described its activity against isolates resistant to other antimicrobial agents.

**METHODS:** 1,207 isolates of EC from outpatient urine samples submitted to the CANWARD surveillance study from 2007 to 2015 were tested using the CLSI broth microdilution method. MICs were interpreted using CLSI (M100-S26) breakpoints.
RESULTS:

<table>
<thead>
<tr>
<th>E. coli phenotype (n, isolates)</th>
<th>% Susceptible/MIC&lt;sub&gt;90&lt;/sub&gt; (µg/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>FOS</td>
</tr>
<tr>
<td>All (1,207)</td>
<td>99.2/4</td>
</tr>
<tr>
<td>NIT-resistant (12)</td>
<td>100/32</td>
</tr>
<tr>
<td>AMC-resistant (40)</td>
<td>100/4</td>
</tr>
<tr>
<td>CIP-resistant (228)</td>
<td>96.5/4</td>
</tr>
<tr>
<td>SXT-resistant (302)</td>
<td>99.0/4</td>
</tr>
<tr>
<td>Resistant to CIP and AMC (13)</td>
<td>100/4</td>
</tr>
<tr>
<td>Resistant to SXT and AMC (9)</td>
<td>100/4</td>
</tr>
<tr>
<td>Resistant to SXT and CIP (128)</td>
<td>98.4/4</td>
</tr>
<tr>
<td>ESBL-positive (61)</td>
<td>95.1/4</td>
</tr>
<tr>
<td>MDR (12)</td>
<td>100/8</td>
</tr>
</tbody>
</table>

NIT, nitrofurantoin; AMC, amoxicillin-clavulanate; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole; MDR, resistant to ≥3 antimicrobial classes.

CONCLUSION: For all isolates of EC, FOS and NIT had % susceptible rates ≥10% higher than the other agents tested. % susceptible to FOS was ≥10% higher than to NIT against isolates resistant to both SXT and CIP, ESBL-positive isolates, and MDR isolates.

P14
Threat Scoring for Emerging Infectious Disease Events to Enable Public Health Decisions in Canada
L VRBOVA1, RG Thomas-Reilly2, A Demarsh2

1Public Health Agency of Canada, Toronto, ON, 2Public Health Agency of Canada, Ottawa, ON

BACKGROUND: Emerging infectious disease (EID) events worldwide are identified and analysed by public health institutions worldwide, but are frequently done so in an ad hoc manner. A systematic approach is required to identify EID events warranting the investment of scarce public health resources.

METHODS: In order to develop a scoring tool for EID events, we adapted a multi-criteria decision analysis (MCDA) tool, which was originally created to prioritize infectious disease surveillance systems. The Threat Scoring for Emerging Infectious Diseases (TSEID) tool was piloted and critiqued by 28 experts in a workshop. Twelve initial reports of EIDs from various early warning sources (e.g. ProMED), representing a spectrum of low to very high-risk events, were used to test the tool. Mean scores were calculated for each scenario, using both weighted and unweighted scores, and overall risk levels were assigned based on quartiles. The tool was revised based on expert feedback on the criteria, in addition to ratings from a smaller working group.

RESULTS: The TSEID tool is an MCDA tool with 9 criteria in 4 dimensions (see Table). The criteria have 3-point rating options (low, medium, and high risk) and associated weighting. Risk perception/tolerance is included separately. The TSEID is currently being piloted to identify events of concern that require additional public health actions (e.g. rapid risk assessment).

CONCLUSIONS: Initial results demonstrate the benefit of TSEID in clarifying specific attributes of concern for individual events, in addition to providing a final threat score, which is useful for reporting and briefing purposes.

Threat Scoring for Emerging Infectious Diseases (TSEID) Criteria

<table>
<thead>
<tr>
<th>Impact</th>
<th>Exposure</th>
<th>Transmission</th>
<th>Additional factors</th>
</tr>
</thead>
<tbody>
<tr>
<td>Disease severity</td>
<td>Introduction to Canada</td>
<td>Transmission</td>
<td>Extraordinary event</td>
</tr>
<tr>
<td>Societal impact</td>
<td>Canadians abroad</td>
<td>Rapid spread</td>
<td>Trusted information</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Intervention</td>
</tr>
</tbody>
</table>
Emendation of the Genus *Clostridium* and Validation of the Description of ‘*Clostridium neonatale*’ Species Novum, as a Member of that Genus

KA BERNARD1,2, A-M Bernier3

1National Microbiology Laboratory, Winnipeg, MB, 2University of Manitoba, Department of Medical Microbiology, Winnipeg, MB, 3Universite Saint Boniface, Winnipeg, MB

**INTRODUCTION:** The genus *Clostridium* was recently emended to limit it to ~110 species from Clostridiales Cluster I which were 'closest to' the type species, *C. butyricum* [2016 IJSEM 66:1009]. In parallel, features of a cluster of bacteria recovered in 1999-2000 from infants with necrotizing enterocolitis (NEC), provisionally named ‘*Clostridium neonatale*’, were recently revisited with the intent of validating its description, which best fit Cluster I by 16S. We found while doing these analyses that a number of validly-named *Clostridium* species were missing from the emended genus description. Therefore, in this study we highlighted those omissions with the intent of clarifying which species actually fit the genus *Clostridium sensu stricto* as well as provide relevant features for ‘*C. neonatale*’.

**MATERIALS AND METHODS:** Some characteristics of NEC-derived bacteria had been outlined previously [Alfa 2002 CID 35:S101]. Data were re-assessed for biochemical and cellular fatty acid (CFA) features; ASTs by CLSI methods. Protein spectra were analysed (after extraction) by MALDI-TOF (Microflex, Bruker). Additional characterization was done using whole genome sequencing (WGS) on an Illumina. Species best fitting *Clostridium* Cluster I were detected by examining 16S and allied taxa which other -wise fit Cluster I but were missing from the 2016 publication.

**RESULTS AND DISCUSSION:** By 16S, ‘*C. neonatale*’ isolates had >99.8% to each other but <98.0% to other species in the genus *Clostridium sensu stricto*. All were saccharolytic, hydrolysed esculin, motile, did not reduce nitrate and had CFAs typical for Cluster I *Clostridium* spp. MALDI results provided unambiguous identification and may prove to be a useful ID method. By WGS, genomes were 4.6-4.7x10^6 bps with a G+C content of 28.3-28.5%, consistent with this genus. ‘*C. neonatale*’ strains were susceptible to 15 antibiotics. We found >20 species of *Clostridium* and allied taxa which otherwise fit Cluster I but were missing from the 2016 publication, including the important human pathogen, *C. perfringens*. We will formally recommend that at least 3 species presently assigned to the genus *Eubacterium* (*E. budaya, E. combesii* and *E. nitritogenes*), be reassigned to the genus *Clostridium sensu stricto* based on these analyses, as recommended for *C. (E.) moniliforme and C. (E.) tarantellae* as well as for two *Sarcina* and one *Anaerobacter* species, in the 2016 publication.

**P16**

**Genotypic Analysis of *Borrelia burgdorferi* Isolated in British Columbia**

M-K LEE1, MI Uyaguari Diaz1,2, M Croxen1, S Man1, K Fernando1, Q Wong1, M Morshed1,2

1BC Centre for Disease Control - Public Health Laboratory, Vancouver, BC, 2Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC

**OBJECTIVES:** The aim is to investigate the diversity of *Borrelia burgdorferi* isolated from British Columbia (BC) using multi-locus sequence typing (MLST) and sequence type (ST) results were compared with the global MLST data base.

**METHODS:** *Borrelia burgdorferi* genomic DNA (n=48) was purified from cultured spirochetes (isolated either from ticks and mice tissues) using a Qiagen DNA Extraction Kit. DNA libraries were constructed using the Nextera XT DNA library preparation kit and quality was assessed on an Agilent Bioanalyzer. Genome sequencing was performed on Illumina MiSeq using reagent kits V3 with 300 bp paired-end output. The quality of the reads was assessed by FastQC. Genomes were assembled and MLST was determined based on the *Borrelia* MLST schemes from pubmlst.org.

**RESULTS:** A total of 21 MLST types were seen among 48 *B burgdorferi* isolates. Approximately 30% (n=14) of BC isolates belonged to 5 ST types, which can also be found in other parts of Canada. Twenty percent (n=10) of BC isolates belonged to 5 different ST types, which were found in BC and in the USA but not in other provinces. Of the remaining 50% of isolates (n=24), 11 STs were typed. Among them, most displayed minor sequence variants (one or two single nucleotide variants, SNV, in one or two loci). Others have SNV in multiple loci, which represented the more diverse sequence information from known ST.
CONCLUSION(S): BC *B. burgdorferi* isolates showed diverse MLST genotypic patterns. There were few MLST patterns that were unique to BC. Further study is underway to analyse *ospC* alleles to cross validate these findings.

P17

**A New *Borrelia* Species Discovered in BC Ticks**

A Dibernardo¹, M-K Lee², R Lindsay¹, E Galanis³,⁴, DM Patrick¹,², M McLaws³, B Henry¹,⁵, M Krajden²,⁶, M Morshed²

¹National Microbiology Laboratory, Winnipeg, MB, ²BC Centre for Disease Control - Public Health Laboratory, Vancouver, BC, ³BC Centre for Disease Control - Communicable Disease Prevention Services, Vancouver, BC, ⁴University of British Columbia - School of Population and Public Health, Vancouver, BC, ⁵Ministry of Health, BC, Victoria, BC, ⁶University of British Columbia - Department of Pathology and Laboratory Medicine, Vancouver, BC

**OBJECTIVE:** *Borrelia burgdorferi sensu lato* is a widespread and diverse bacterial group of which the predominate genospecies in North America is *B. burgdorferi sensu stricto*. A new pathogenic genospecies, *Borrelia mayonii*, was first reported in patients from the midwestern United States and subsequently identified in blacklegged ticks, *Ixodes scapularis*, collected in northwestern Wisconsin and Minnesota.

**MATERIALS AND METHODS:** Both BCCDC Public Health Laboratory and National Microbiology Laboratory (NML) conduct tick surveillance for pathogenic *Borrelia*. DNA is extracted from ticks and amplified with *Borrelia*-specific 23S primers. Positive samples are tested with *ospA* and *glpQ* primers to detect *B. burgdorferi* and *B. miyamotoi*, respectively. Samples negative for both confirmatory assays are tested by *flaB* and IGS nested PCR and sequencing, and *oppA* gene melt curve analysis.

**RESULTS:** We report the first detection of a *B. mayonii*-like agent in Canada in three *Ixodes angustus* ticks. The *flaB* sequence data was 99% similar to that of *B. mayonii* and the melt curve profiles were also consistent with the Tm of this agent. The infected *I. angustus* ticks were collected in British Columbia from two dogs and a child between 2013 and 2016. All three hosts were asymptomatic and Lyme disease serology on the child was negative. The prevalence of this *B. mayonii*-like agent is presumed to be very low since these were the only three positive samples detected among approximately 14,000 ticks tested by BCCDC Public Health Laboratory and the NML during this time period.

**CONCLUSIONS:** The *B. mayonii*-like agent can be detected using the existing PCR testing algorithm; however, serological platforms specific for this pathogen are not commercially available. Physicians need to be aware of the broad spectrum of Lyme disease presentations and consider testing and treatment where clinically appropriate. Continued tick surveillance will help understand the epidemiology of this *B. mayonii*-like spirochete.

P18

**Rapid Identification of Methicillin-Resistant and Methicillin-Susceptible *Staphylococcus aureus* Isolates Directly From Positive Blood Cultures Using the BD MAX™ StaphSR Assay**

V Porter¹, M Chouinard¹, AE Simor¹,²

¹Department of Microbiology, Sunnybrook Health Sciences Centre, Toronto, ON, ²Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON

**BACKGROUND:** Staphylococci are among the most common blood culture isolates detected in hospitalized patients. Rapid identification of *S. aureus* isolates and oxacillin resistance from positive blood cultures could result in more appropriate antimicrobial utilization and improved patient outcomes. The BD MAX™ StaphSR assay (BD Diagnostics, Quebec, Canada) was designed for direct detection of methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) from nasal swabs. Few evaluations have been done using this test from positive blood cultures. This study evaluates the accuracy of the BD MAX™ StaphSR assay to identify MSSA and MRSA directly from positive blood cultures.

**METHODS:** Clinical blood cultures with Gram stains showing Gram-positive cocci in clusters, identified prospectively in our microbiology laboratory, were used. A 15µl aliquot from the blood culture bottles (processed by the BACTEC™ 9240 system, BD Diagnostic Systems) was directly inoculated into BD MAX™ StaphSR Sample Buffer Tubes for processing on the BD MAX™ System. Results were compared with standard laboratory procedures for staphylococcal identification and antimicrobial susceptibility testing.
Abstracts

RESULTS: 103 positive blood culture specimens were tested, including 37 with *S. aureus*, 63 with coagulase-negative staphylococci, and 3 with other bacterial species. All but one *S. aureus* isolate were correctly identified by the BD MAX™ assay (sensitivity 97.3%, specificity 100%); on repeat testing the erroneous isolate was correctly identified. Methicillin susceptibility was correctly determined in all *S aureus* isolates including all 8 MRSA (sensitivity 100%, specificity 100%).

CONCLUSION: The BD MAX™ StaphSR assay is easy to perform, can accurately detect MRSA and MSSA from positive blood cultures, and provides rapid (real-time) results in <2 hours, compared to conventional laboratory methods taking 1-3 days.

P19
Utilizing Opiate Substitution Therapy (OST) as a Tool for Long-term Engagement in HCV Infected People Who Inject Drugs (PWID)
A Alimohammad, G Kiani, T Raycraft, R Shahi, A Singh, B Conway
Vancouver Infectious Diseases Centre, Vancouver, BC

BACKGROUND: In the era of highly effective all-oral HCV treatment regimens, adherence and long-term follow-up are key to achieving a sustained virologic response (SVR), and reducing rates of recurrent viremia (RV) after successful therapy among individuals at ongoing risk of HCV infection. Opiate substitution therapy (OST) can be an effective tool to address these issues, especially if delivered within a multidisciplinary setting - especially if dealing with active people who inject drugs (PWID). We have evaluated this approach at our centre.

METHODS: An observational evaluation was conducted among HCV-infected patients seen at the Vancouver Infectious Diseases Centre (VIDC), where they had access to a multidisciplinary model of care addressing medical, psychiatric, social and addiction-related needs prior to, during and after HCV therapy. A part of addressing patients’ addiction related needs includes enrollment in OST programs on site, or at nearby locations. All HCV-infected PWID on all-oral regimens that completed therapy were included in this analysis. The endpoint was the occurrence of RV, as a determinant of re-engagement in risk behaviors.

RESULTS: To date, 40 PWID have completed all-oral HCV therapy at VIDC with an SVR rate of 93%. Fourteen of these individuals were under some form of OST, either on daily, or weekly dispensed medication. Ten were receiving methadone and four were on suboxone therapy. With a median follow-up of 1.5 years in this cohort, there have been no cases of RV.

CONCLUSION: OST is an important tool to maintain HCV-infected PWID in care after successful therapy. In our hands, such individuals appear to remain in care and we have yet to detect a single case of recurrent HCV infection in our population. Longer term follow-up in multidisciplinary care (including OST) will help in the design and evaluation of optimal approach in this population of “core transmitters” of HCV infection.

P20
Cost-Efficiency Analysis of the Potential Addition of MRSA Chromogenic Media in the Management of Skin-Soft Tissue Infections: An Attempt to Decrease the Use of Vancomycin
C Bogaty1, P Lagace-Wiens1,2

OBJECTIVES: Skin-soft tissue infections (SSTI) are a common pathology seen in emergency departments. Due to the concern for methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin is increasingly being prescribed as part of empiric therapy. MRSA chromogenic media (MRSASelect, Bio-Rad) can potentially diagnose the presence of MRSA after 24 hours of incubation, allowing for a quicker diagnosis compared to routine cultures. This study was undertaken to evaluate the frequency with which vancomycin is prescribed empirically in the treatment of SSTI and assess the potential cost-savings of adding MRSA chromogenic media in the processing of wound cultures.

METHODS: A retrospective chart review was conducted on all wound cultures submitted between July 1st and September 26th, 2016 to St. Boniface Hospital microbiology laboratory (Winnipeg, Manitoba) from the emergency department. The rate of MRSA positivity in wound cultures was compared to the use of empiric vancomycin. The cost of administering vancomycin over a 24-hour period (nursing and drug costs) in MRSA
positive and negative patients was further compared to the costs of adding an additional MRSA chromogenic media to the routine processing of wound cultures (costs of the plate and work-load units).

RESULTS: There were 118 wound cultures submitted for analysis, of which 21 were found to be MRSA positive (17.8%). 45 patients (38.1%) were empirically treated with vancomycin, of which only 6 were found to be MRSA positive (13.3%); 10 received only a single dose of vancomycin and were therefore excluded from the cost-efficiency analysis. Of the remaining MRSA positive patients, 9 received an MRSA-active oral agent, and 6 received no MRSA-active antibiotics. During this three-month period, the potential costs of screening using a MRSA chromogenic media would have been $265.50, compared to $3168.54 for the empiric continuation of vancomycin in MRSA negative patients.

CONCLUSIONS: Vancomycin was included in the empiric treatment of 38.1% of patients presenting with a SSTI to a Winnipeg hospital, of which only 13.3% actually required the antibiotic. The use of MRSA chromogenic media in the processing of wound cultures could allow cost-savings by permitting the earlier discontinuation of empiric vancomycin.

P21 Cascade of Care of HIV Patients Followed at a Canadian STI Clinic
P SMYCZEK1,5, J Gratrix2, S Hewitt1, P Parker1, S Plitt3,5, KA Simmonds4,5, A Singh1,5
1Alberta Health Services-Edmonton STI Clinic, Edmonton, AB, 2Alberta Health Services- Centralized STI Services, Edmonton, AB, 3Public Health Agency of Canada, ON, Ottawa, ON, 4Alberta Health, Edmonton, AB, 5University of Alberta, Edmonton, AB

OBJECTIVE: This program evaluation of HIV care provided by the STI clinic in Edmonton, Alberta examined components of the cascade of care including the proportion of patients retained in care and the proportion with suppressed viral load (VL). We also examined reasons for loss-to-follow-up for those not currently under care.

METHODS: At the end of 2015, demographic and clinical care variables were extracted from a regional HIV program database for patients being followed by the Edmonton STI Clinic. We determined the proportion under current care (a visit in 2015) and those suppressed (<200 copies/mL) on their last recorded VL. A chart review was completed for clients with no clinic visit in 2015 to determine potential reasons for loss of engagement in care. Simple descriptive analyses were completed.

RESULTS: 435 HIV patients were registered to receive treatment and follow-up at the Edmonton STI Clinic; nearly three-quarters (70.6%; n=307) had a visit in 2015. Of the remaining 128 patients, 64.1% (n=82) had moved out of Northern Alberta, 20.3% (n=26) were deceased, 3.9% (n=5) were in a correctional facility, 2.3% (n=3) returned to care in 2016, and 9.4% (n=12) were lost to follow-up. Of the 307 patients in current care, 94.1% (n=289) had a suppressed VL.

CONCLUSIONS: Only a small proportion (9.4%) of patients attending our clinic were lost to follow up and the proportion retained in care with a suppressed VL was high (94%). A personalized, client centered approach resulting in positive patient – provider relationships and an easily accessible downtown location are considered important contributing factors to our high retention in care rates.

P22 Appropriateness of Empiric Antibiotic Therapy in Patients with Gram-negative Bacteremia: A Multi-sited Retrospective Study
R LEE1,2, C Graham1, T Fernandes1,2, A Sengar1,2
1Trillium Health Partners, Toronto, ON, 2Leslie Dan Faculty of Pharmacy at the University of Toronto, Toronto, ON

BACKGROUND: Gram-negative bacteremia (GNB) is a major cause of infection-related mortality, particularly in the setting of increasing antibiotic resistance. Current literature demonstrates that delayed administration of appropriate empiric antibiotic therapy negatively impacts mortality in this population; however, few studies have investigated strategies to minimize this delay.

OBJECTIVES: To determine the proportion of patients with GNB who did not receive appropriate empiric therapy and to measure average ‘time to appropriate therapy’. Secondary objectives were to measure baseline rates of empiric antibiotic use and all-cause mortality.

METHODS: A retrospective chart review was conducted at [an unidentified institution]. Eligible patients included adults who were admitted to hospital and had a blood
culture positive for at least one gram-negative organism between July-December 2015. Data were retrieved from hospital electronic databases and analyzed using Chi-square and 2-sample t-tests. Subgroup analyses were performed in patients with antibiotic-resistant GNB.

RESULTS: A total of 382 GNB episodes were eligible for study inclusion. Nearly 1 in 5 patients (19.1%) did not receive appropriate empiric therapy. Significantly more patients in the antibiotic-resistant subgroup received inappropriate empiric therapy compared to the non-resistant group (41% vs. 3.2%, p<0.001). Time to appropriate therapy was significantly longer in patients who received inappropriate versus appropriate empiric therapy (41.1 vs. 1.4 hrs, p<0.001) and in the resistant versus non-resistant subgroup (16.9 vs. 1.8 hours, p<0.001). Of the 37 patients who received inappropriate empiric therapy with piperacillin-tazobactam, 38% were infected with an extended-spectrum beta-lactamase-producing (ESBL) organism. A non-significant trend towards increased mortality was observed in patients who received inappropriate empiric therapy.

CONCLUSIONS: A significant proportion of patients are receiving inappropriate empiric therapy. Further studies are necessary to improve empiric antibiotic prescribing for GNB while preserving susceptibility to broad-spectrum antibiotics.

P23
Impact of MALDI-TOF and Short-Incubation Subcultures on Time to Identification and Antimicrobial Susceptibility Testing of Gram-Negative Bacilli from Positive Blood Cultures in a Clinical Microbiology Laboratory
N MATIC1, BM Willey2, E Cudek2, P Lo2, SM Poutanen1,2
1Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, 2Department of Microbiology, University Health Network & Mount Sinai Health System, Toronto, ON

BACKGROUND: The microbiology laboratory plays an essential role in the timely diagnosis of bacteremias. Matrix-assisted laser desorption ionization time-of-flight mass spectrometry has the potential to reduce identification turn-around-time (TAT), theoretically reducing time to appropriate antimicrobial therapy. For blood cultures in our laboratory, identification (ID) and antimicrobial susceptibility testing (AST) had been previously performed by VITEK 2 (bioMérieux) using overnight subcultures. In 2013, VITEK MS (bioMérieux) (MALDI) was adopted for ID from short-incubation subcultures which were checked every 4-7 hours for adequate growth; VITEK 2 AST was also encouraged to be performed from these plates.

OBJECTIVES: This quality audit evaluated the impact of the use of MALDI on short-incubation plates on ID and AST TATs in our laboratory compared to VITEK 2.

METHODS: Positive blood cultures with Gram-negative bacilli identified on Gram stain between 0600 and 2100 were included. MALDI ID TATs (time from Gram stain positivity to ID) and AST TAT (time from Gram stain positivity to reported AST) were calculated from 126 prospective isolates from May to September 2016. VITEK 2 ID and AST TATs were calculated from retrospective review of 134 isolates from March to October 2011.

RESULTS: The average VITEK 2 ID and AST TAT was 38h:6min (range 20h:57min - 68h:6min). This is compared to the average MALDI ID TAT of 7h:45min (range 1h:43min - 25h:8min) (P<0.0001, t test), and MALDI AST TAT of 36h:45min (range 22h:9min - 54h:40min) (P=0.1799, t test). Notably, 82% of prospective isolates were loaded on MALDI after the expected 4-7 hour check, but only 39% of prospective isolates had Vitek-2 AST loaded at the time of MALDI. Additionally, an average delay of 11h:54min was observed between the time AST results were available in VITEK 2 and the time laboratory personnel reported these results after purity plate review. A pilot audit revealed preliminary reporting of AST results before purity plate review would result in no very major errors.

CONCLUSIONS: The introduction of MALDI has significantly improved ID TATs of Gram-negative blood culture isolates in our laboratory by an average time of 30h:23min. No change in AST TAT was noted. Optimization of AST load times throughout the workday and automatic release of preliminary AST results could improve AST TAT.
P24
What is the Utility of Collecting Urine Cultures for Mycobacterium in Tuberculosis Patients?
A MCFARLANE1, D Kunimoto1, G Tyrrell2,3

1Division of Infectious Diseases, University of Alberta, Edmonton, AB, 2Division of Diagnostic and Applied Microbiology, Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, AB, 3Provincial Laboratory for Public Health, Edmonton, AB

OBJECTIVES: Practice varies regarding the submission of urine for mycobacterial (MB) culture in tuberculosis (TB) patients. Results often do not change management, but may utilize significant lab resources. This study aimed to define the practice of urine MB culture submission in TB patients, and to determine risk factors associated with positive cultures.

METHODS: Local TB and laboratory databases helped identify all patients with TB of any organ system from 2005-2014 who had at least one urine specimen submitted for MB culture. Additional clinical and laboratory data were extracted. Factors associated with positive urine tuberculosis cultures were determined via a case-control analysis.

RESULTS: 370 TB patients (23% of provincial TB cases) had 646 urines for MB culture submitted. 84 specimens were culture positive (13%), from 55 patients (15% of patients). The average time to positivity was 18 days. 277 patients also had a urinalysis submitted. Only 3% of the positive patients had a sole diagnosis of genitourinary TB.

Selected Factors Associated with Urine Culture Positivity

<table>
<thead>
<tr>
<th>Risk factor</th>
<th>Odds Ratio (95% CI)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Foreign born</td>
<td>1.92 (0.86-4.26)</td>
<td>0.11</td>
</tr>
<tr>
<td>HIV positive</td>
<td>3.60 (0.91-14.20)</td>
<td>0.06</td>
</tr>
<tr>
<td>Diabetes mellitus</td>
<td>1.30 (0.48-3.54)</td>
<td>0.61</td>
</tr>
<tr>
<td>No or trace blood on urinalysis</td>
<td>0.42 (0.22-0.82)*</td>
<td>0.01</td>
</tr>
<tr>
<td>No or trace WBC on urinalysis</td>
<td>0.29 (0.15-0.58)*</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

* An odds ratio <1 suggests decreased odds of urine culture positivity.

CONCLUSION: A urinalysis without either significant white blood cells or red blood cells was associated with a significantly lower risk of urine MB culture positivity. This data can help guide clinicians regarding culture submission, depending on the indication. Clinicians should also decide whether urine culture would alter diagnosis or management, before submitting a specimen. Limitations of this study include a lack of information regarding genitourinary symptoms and the indication for culture submission.

P25
Galactomannan Screening Protocol in High-Risk Hematology Patients: Adherence and Outcomes
S Harricharan1, K Biederman1, AM BOMBASSARO1,2, A Lazo-Langner1,2, A Elsayed1,2, A Fulford1,2, J Delport1,2, A Xenocostas1,2

1London Health Sciences Centre, London, ON, 2Western University, London, ON

OBJECTIVES: Early detection of invasive fungal disease in high risk hematology patients through the use of non-invasive tests, such as galactomannan (GM) for aspergillosis, has stimulated interest in targeted versus empiric antifungal therapy. A twice weekly GM screening protocol was implemented at our tertiary care centre. The primary study objective was to determine protocol adherence. Secondary objectives were to compare use of selected resources and clinical outcomes before and after protocol implementation.

METHODS: This was a retrospective cohort study comparing pre and post-GM implementation phases. Adults undergoing induction chemotherapy for acute leukemia (myeloid or lymphoid) and matched related allogeneic stem cell transplants were eligible. Patients could be enrolled more than once and were evaluated as episodes. Post-implementation episodes were assessed for protocol adherence. Pre and post-implementation episodes were compared for use of broad spectrum antifungals (BSAF), consultations (Infectious Diseases, Respiratory) and diagnostics (computed tomography scans, bronchoalveolar lavage) until discharge, peripheral leukocyte recovery, next chemotherapy cycle or death, whichever came first. Clinical outcomes (all-cause mortality, “alive and not on BSAF”) were determined 6 weeks later at the final assessment.

RESULTS: Of 182 episodes consecutively screened, 70 were enrolled per phase. Clinical characteristics were similar between phases. Full or partial protocol
adherence was observed in 61/70 (87%) post-implementation episodes, with full adherence in 40 (57%). Fewer episodes received BSAF, consultations and diagnostics in the post compared to the pre-protocol phase, 7% versus 27% (p=0.002), 26% versus 46% (p=0.014) and 31% versus 46% (p=0.083), respectively. While mortality was similar, more post than pre-implementation episodes were alive and not on BSAF, 98% versus 79% (p<0.001).

CONCLUSIONS: Implementation of a GM screening protocol was associated with significantly fewer episodes receiving BSAF and consultations. Also, significantly more episodes were alive and not on BSAF at the final assessment. GM screening should be continued with efforts to enhance adherence.

P26 ABSTRACT WITHDRAWN

P27
Z-PROFILE: Real-World Utilization and Effectives of Elbasvir/Grazoprevir in Adult Patients with Chronic Hepatitis C in Canada

B CONWAY, E Tam, C Fraser, J Tremblay, B Trottier, A Ramji, S Borgia, K Stewart, JB Trepanier, Y Chalabi

1Vancouver Infectious Diseases Centre, Vancouver, BC, 2LAIR Centre, Vancouver, BC, 3The Cool Aid Community Health Centre, Vancouver, BC, 4Centre Sida Amitié, St-Jérôme, QC, 5Clinique Médicale du Quartier Latin, Montréal, QC, 6GI Research Institute (GIRI), Gastroenterology Division, Vancouver, BC, 7William Osler Health System, Brampton, ON, 8Saskatchewan Infectious Disease Care Network, Saskatoon, SK, 9Merck Canada Inc., Kirkland, QC

BACKGROUND: Direct-acting antivirals represent the standard of care for chronic hepatitis C infection. Canada was the first country worldwide to approve elbasvir/grazoprevir (EBR/GZR) for genotypes (GT) 1 and 4, with/without ribavirin, and for GT3 with sofosbuvir. Currently, reimbursement is available through private payers, with public reimbursement anticipated soon. The aim of this study is to describe the patient profile and real-world effectiveness of EBR/GZR in patients with chronic hepatitis C in Canada.

METHODS: A multicenter retrospective cross-sectional chart review of HCV-infected patients treated with EBR/GZR in selected Canadian health care providers. This interim analysis included patients initiating EBR/GZR treatment between January and November 2016.

RESULTS: In this interim analysis, 102 patients from 8 sites were included. The mean age was 52.6 years, 60.8% were male, 78.4% Caucasian and 5.9% Aboriginal. Genotype distribution included patients infected by GT1a (n=58, 56.9%), GT1b (n=18, 17.6%), GT2 (n=1, 1%), GT3 (n=15, 14.7%), GT4 (n=3, 2.9%), and GT6 (n=1, 1.0%). Pre-treatment fibrosis evaluation revealed a fibrosis stage of F0-1 (n=60, 58.8%), F2 (n=15, 14.7%), F3 (n=8, 7.8%), F4 (n=18, 17.6%) and 1 missing. Prior HCV treatment was reported for 22 (21.6%) patients. Of these, 21 (95.5%) were previously treated with an IFN-containing regimen. Baseline resistance-associated substitutions (RAS) testing was performed for 13 (12.7%) patients. No NS5A substitutions were identified. Eighty-nine patients (87.3%) were prescribed 12 weeks of EBR/GZR and the other 13 patients received 16 weeks of EBR/GZR with RBV. Sofosbuvir was prescribed with EBR/GZR for all 15 patients with GT3. Sustained virological response (SVR12) data will be presented.

CONCLUSION: In this Canadian cohort, the majority of individuals treated had early stage fibrosis and were predominantly infected by GT1 as reflected by the distribution in Canada.

P28
Copper Alloy Tail Pieces Reduce Bacterial Contamination of Sink Surfaces and Adjacent Air in an Intensive Care Unit


1Mount Sinai Hospital, Toronto, ON, 2Oakville Stamping and Bending, Oakville, ON

BACKGROUND: Antibiotic-resistant nosocomial infections in the ICU are a growing concern. There is increasing evidence that hand hygiene sinks and drains may be a reservoir for infections due to Enterobacteriaceae and afermenting gram negative organisms.

METHOD: Hand hygiene sinks in patient rooms in our 16-bed medical/surgical ICU were randomized to 2 different drain designs; one with copper alloy or chrome tailpieces. From September-December 2016, cotton swabs were used to sample the drains (40cm²), basins (366cm²), and rims (39cm²) of hand hygiene sinks in patient rooms in our 16-bed medical/surgical ICU; impactors were used to sample air adjacent to each sink. Swabs were transferred immediately to 1ml neutralizing
Performance Characteristics of a ddPCR assay for the detection of influenza virus.

METHODS: Tenfold dilutions of influenza A/California/07/2009 (H1N1) were prepared in negative mid-turbinate sample / viral transport media matrix (1-100,000 PFU/ml). After RNA extraction, linear range, analytical sensitivity and precision were determined using one-step RT ddPCR kit and QX200™ Droplet Digital™ PCR instrument (BioRad). Accuracy was assessed using a panel of positive (24) and negative (18) samples (RVPfast, Luminex Diagnostics). Statistical analysis was performed using GraphPad Prism. All results are reported in RNA copies per microliter of sample (copies/µl).

RESULTS: Viral quantification using ddPCR was linear between 19.8-55,766.7 copies/µl (r=0.998). The limit of detection was determined to be 14.5 copies/µl (Probit regression analysis). At lower concentrations, primers and probes produced a background average of 9.6 copies/µl (SD=4.3 copies/µl)). Precision was studied in terms of repeatability and the measurement variability was found to be ±10% at high concentrations and ±20% at lower concentrations. Sensitivity was calculated to be 100% while specificity was 61.1%, where 7 samples negative by RVPfast were found to be low positive (15-40 copies/µl) by ddPCR.

CONCLUSIONS: We describe an efficient ddPCR assay for influenza virus with a low limit of detection. Further optimization is required to achieve sufficient specificity for clinical use.
METHODS: A 1-day PPS was conducted on November 3rd, 2016 on all 10 inpatient paediatric wards. Lists of inpatients on antimicrobials at 8:45 am on the survey date were obtained from the Pharmacy Department. Patient-level data collected included demographics, microbiological results, prescribed antimicrobial agents and clinical indications. Denominators included the total number of inpatients at 8:45 am, stratified by ward and service. Appropriateness assessment was made by a survey team member (paediatric infectious diseases physician or pharmacist).

RESULTS: Of 122 inpatients, 44 (36%) were prescribed at least one antimicrobial. Of those, 36 (30%) were on at least one systemic antibiotic. The highest proportions of antimicrobial use were found on the Hematology–Oncology [6/9 (66.7%)], Orthopedics [2/3, (66.7%)], General Paediatrics [13/26 (50%)] and General Surgery [4/9 (44.4%)] services. The most common indications for antimicrobials were medical prophylaxis (22.2%), intra-abdominal infections (18.1%) and bacterial lower respiratory tract infections (12.5%). Of the 50 systemic antibiotic prescriptions, the most common were aminopenicillins [n=9 (18%)], piperacillin-tazobactam [n=6 (12%)] and aminoglycosides [n=6 (12%)]. Excluding surgical prophylaxis, 64 of 66 (97%) antimicrobial prescriptions were indicated. Of those, 27% (n=17) were judged inappropriate, most frequently due to incorrect dosing (52.6%) or choice of agent (26.3%). Most inappropriate use occurred in the neonatal intensive care unit (31.6%), Hematology–Oncology (21.1%) and General Surgery (15.8%).

CONCLUSIONS: The prevalence of antimicrobial use in our centre is comparable to other Canadian paediatric institutions. Stewardship interventions like audit and feedback and practice guidelines should be developed to increase appropriate use.

P31
Development and Evaluation of Molecular Screening Assay for Legionella in Water
D Yu1, F Tsang1, D Eisler1, C Tchao1, S Man1, V Yu2, B Auk1, N Prystajecky1,2

1British Columbia Centre for Disease Control Public Health Laboratory, Vancouver, BC, 2University of British Columbia, Vancouver, BC

BACKGROUND: Legionella bacteria are a public health concern due to their ability to cause both mild (Pontiac fever) and severe (Legionnaires’ disease) illnesses, as well as their ubiquity in water and soil. Environmental investigations of legionellosis cases are challenging because the organism is fastidious and slow growing in culture. Furthermore, extensive environmental testing is often required due to the range of possible sources of Legionella. To improve laboratory throughput, we evaluated and implemented a molecular screening assay for water samples.

METHODS: One litre of water was filtered through a 0.2μm polycarbonate filter and DNA was extracted from the filter using NucliSENS easyMag. A panel of three singleplex qPCRs were used to detect Legionella species (pan-Leg), Legionella pneumophila (Lp) and L. pneumophila serogroup 1 (sg1), targeting the ssrA, mip and sg1 genes, respectively. To assess for PCR inhibition, a qPCR targeting the ITS2 gene of Oncorhynchus keta was used. The assay was evaluated for limit of detection, sensitivity and specificity. Commercial and residential water samples were tested (n=36) by culture and this molecular screening assay for the presence of Legionella.

RESULTS: The assay was shown to be 100% sensitive and 100% specific against of a panel of Legionella and non-Legionella strains. The limit of detection was determined to be 100 CFU for the pan-Leg and sg1 assays and 1000 CFU for the Lp assay. The molecular screening assay detected Legionella in 39% of samples (Ct range 20.0 – 39.5), L. pneumophila in 8% of samples (Ct range 25.9-27.8) and L. pneumophila serogroup 1 in 6% of samples (Ct range 24.3-32.9). All Legionella cultures were negative. Inhibition was not detected in any samples.

CONCLUSIONS: We have demonstrated that the qPCR panel using an easyMag extraction is suitable for screening water samples for Legionella. This assay will improve turn-around-times for presumptive positives and create efficiencies for culture set-up.
P32  
Antimicrobial Susceptibilities of *Escherichia coli* in Canadian Hospitals through the Analysis of Annual Antibiogram Summaries  
G GERMAN1, L Pelude2, J Minion3, SM Poutanen4, B Lee5, I Davis6, K Suh7, N Thampi8, O Larios9, M-A Lefebvre10, C Ellis11, C Lavallée12, GG Zhanel13, K Amaratunga14, MR Mulvey14 and Canadian Nosocomial Infection Surveillance Program  
1Health PEI, Charlottetown, PE, 2Public Health Agency of Canada, Ottawa, ON, 3Regina Qu’Appelle Health Region, Regina, SK, 4University Health Network, Toronto, ON, 5Stollery Children’s Hospital, Edmonton, AB, 6QEI Health Sciences Centre, Halifax, NS, 7The Ottawa Hospital, Ottawa, ON, 8Childrens Hospital of Eastern Ontario, Ottawa, ON, 9South Health Campus, Alberta Health Services, Calgary, AB, 10Montreal Children’s Hospital, Montréal, QC, 11The Moncton Hospital, Horizon Health Network, Moncton, NB, 12Hôpital Maisonneuve-Rosemont, Montréal, QC, 13University of Manitoba, Winnipeg, MB, 14Public Health Agency of Canada, Winnipeg, MB  

OBJECTIVE: Antimicrobial resistance (AMR) is a growing concern as it limits our ability to treat infections in animals and humans. Although multiple systems exist to monitor AMR in Canada, they are limited in the number of isolates tested. In an attempt to improve our understanding of AMR in Canadian hospitals, we have initiated a pilot study to collect existing AMR data from hospital antibiograms.  

METHODS: All participating Canadian Nosocomial Infection Surveillance Program sites were asked to submit annual hospital antibiogram data. Antibiogram data sets were standardized and percent susceptibility was calculated for each antibiotic.  

RESULTS: A total of 32 hospital sites representing 9 provinces submitted antibiogram information from November 2013 to March 31, 2016. Considerable variability existed in the datasets with respect to drugs and organisms tested, specimen types, and patient populations analysed. Due to variability in the timeframes covered by the datasets, only the calendar year of 2015 was analysed which represented 21 hospitals from six provinces and included: BC (N=4), AB (N=6), SK (N=2), ON (N=7), QC (1) and NB (N=1). Overall susceptibility rates were: ampicillin, 56.2% (N=57080); amoxicillin-clavulanate, 83.2% (N=46536); piperacillin-tazobactam, 94.9% (N=54180); ceftriaxone, 91.6% (N=51818); meropenem, 99.6% (N=43370); ciprofloxacin, 81.4% (N=55529); gentamicin, 92.2% (N=42036); tobramycin, 92.9% (N=36133); nitrofurantoin, 95.4% (N=53385), and trimethoprim-sulfamethoxazole, 77.5% (N=57085). There were differences observed when compared with 2015 *E. coli* CANWARD data (N=559; www.can-r.com) that included susceptibility rates for ciprofloxacin (73.2%), ceftriaxone (86.8%), and amoxicillin-clavulanate (77.6%).  

CONCLUSIONS: Lack of standardized antibiogram data sets made comparisons difficult. Attempts should be made to standardize timeframe/year definition, patient status (e.g. inpatient or adult vs. paediatric), specimen type. Nevertheless, hospital antibiogram information represents a potentially rich untapped data source for AMR surveillance and stewardship. The data sets analysed in this study may give a more accurate reflection of susceptibility rates due to their large size.  

P33  
Uptake of Provincial (PEI) Empiric Guidelines Likely a Cause for Reduced *C. difficile* and Drug Resistant Uropathogens Based on Community and Hospital Antibiotic Use Changes  
G GERMAN, J Boswell  
Health PEI, Charlottetown, PE  

BACKGROUND: Canadian data on outcomes for antimicrobial stewardship and antimicrobial use is limited especially in the community hospital and outpatient settings. Since May 2013 Prince Edward Island antibiotic stewardship program has developed in collaboration with local physicians comprehensive empiric guidelines using local antibiotic susceptibility data. The guidelines are based on the SIRS criteria and designed to be used in long term care, primary care, and acute care. Two key themes include avoiding fluoroquinolones in the community for simple infections and preferentially using levofloxacin over moxifloxacin in the acute care setting. The guidelines were embedded throughout the provincial acute care clinical information system and reinforced at quarterly educational events. We wanted to explore the possible benefits of using the empiric treatment guidelines.  

METHODS: Provincial *Clostridium difficile* (Cdiff) cases were provided by the Department of Health and Wellness. The number of multi-drug resistant gram negative urine isolates (non-susceptible ≥3 classes) was extracted from the Cerner Millennium lab information system.
RESULTS: On PEI, there has been a 28% reduction of C.diff laboratory acquired cases between 2013 and 2015. The proportion of multidrug resistant (MDR)-uro-pathogens to total positive results had decreased by 11%. Community prescriptions for moxifloxacin decreased by 54%, levofloxacin increased by 44% ciprofloxacin decreased by 13%, while total quinolones decreased by 20%. As a comparator, nitrofurantoin increased by 26%. At the QE Hospital grams of moxifloxacin decreased by 63%, levofloxacin increased by 216%, ciprofloxacin decreased by 2%, and clindamycin decreased by 19%, while total antibiotic use in grams increased by 15%.

CONCLUSIONS: It appears that development, dissemination, and uptake of guidelines has changed utilisation of targeted antibiotics, which has likely contributed to reduced C. difficile and drug resistant uropathogens. Future steps would include providing geographical area antimicrobial use information and targeted feedback.

P34 Clinical Impact of Cerebrospinal Fluid (CSF) Gram Stain and Culture, a Retrospective Cohort Study
J Joyce1, D Garcia2, P DALEY2

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

BACKGROUND: Microbiologic test results should influence diagnosis and management. In some cases, tests do not change empiric or targeted antibiotic therapy, and these tests may not be clinically useful.

METHODS: CSF specimens were collected from a tertiary microbiology laboratory between January 1, 2013 and December 31, 2013. Specimens were excluded if collected from children or indwelling ventricular drains, if Gram stain was not performed, if collected outside the two teaching hospital locations, or if charts or antibiotic treatment data were not available. Clinical information, antibiotic treatment prior to CSF collection, antibiotic treatment after CSF Gram stain results, and antibiotic treatment after CSF culture results were collected.

RESULTS: 242 CSF specimens were received during the study period. 120 were excluded (84 from children, 2 from indwelling ventricular drains, 12 collected at outside hospitals, 21 data missing, 1 duplicate). The mean age of included patients was 48.7 years ± 16.8 years. 73/122 (59.8%) specimens were collected from males. The main indications for collection were to rule out meningitis (58/122, 47.5%), to investigate a focal neurological symptom (20/122, 16.4%), and for headache (18/122, 14.8%). 98/112 (87.5%) specimens had less than 25 white blood cells/µL (10 specimens were not tested). 2/122 (1.6%) CSF Gram stains revealed organisms. 4/122 (3.2%) of CSF cultures were positive (2 pathogens and 2 contaminants). 49/122 (40.2%) patients were given empiric antibiotics. In 13/49 cases there were antimicrobial changes temporally associated with the CSF Gram stain result (26.5%, NNTest=122/13 = 9). In 28/49 cases, there were antimicrobial changes temporally associated with the CSF culture result (57.1%, NNTest = 122/28 = 4).

CONCLUSIONS: CSF Gram Stain and CSF culture are rarely positive. Most patients with suspected meningitis are treated empirically. CSF culture has a lower NNTest than CSF Gram stain. Changes in antibiotic treatment may represent utility of microbiology tests, however changes may be caused by other unmeasured clinical factors. Further analysis could include appropriateness of antibiotic changes.

P35 Dengue Transmission Dynamics: Epidemiological and Geographic Identification of High Risk Settings in Medellin, Colombia
M CARABALI1, D Calle2, E Henao3, G Parra3, JS Kaufman1, BN Restrepo2

1McGill University, Montréal, QC, 2Universidad CES-ICMT, Medellin, Antioquia, Colombia, 3Public Health Office, Medellin, Antioquia, Colombia

Dengue is a vector-borne disease transmitted to humans by Aedes mosquitoes, the same vector of zika. Medellin is the second largest city in Colombia with more than 2.6 million inhabitants and its annual dengue incidence ranged 161-745 cases per 100,000 inhabitants during the last 10 years. To identify areas with high-risk dengue transmission, we used routinely collected entomological and surveillance data from Medellin between 2008-2013. Using time-series analysis we determine dengue
seasonality for year, month and epidemiological weeks for each neighbourhood and district of the city. Poisson and negative binomial regressions were fit to identify: a) areas with sustained rates of dengue cases throughout the study period, and b) areas with persistent elevated entomological indexes. A dengue risk index (DRI) was constructed using epidemiological, entomological and socio-economic data. Information was analysed using R and maps were generated with ArcGIS software. Overall, 20,477 cases were reported during the study period. From 249 neighbourhoods, 44% (n=109) reported cases every year. The lowest and highest incidences were observed in years 2008 and 2010, with 28.6 and 659.4 cases per 100,000 inhabitants, respectively. Years 2010 and 2013 were considered epidemic. An increased number of cases was typically observed in April with a second peak occurring around September-October of every year. In 2010, the maximum number of cases occurred from the 14th-39th epidemiological weeks, and in 2013, from the 21st-38th epidemiological weeks. Four out of 16 urban districts, located in northeast part of the city had high DRI throughout the study period. These findings provide epidemiological and geographical information of high-risk areas of dengue transmission, useful for decision makers to address specific vector control strategies, and to help the preparedness of health services for upcoming outbreaks.

**P36**

**Real-time PCR for the Detection and Speciation of Plasmodium Infections**

T LEE¹, K Adie¹, T Lo¹, M Lee¹, B Auk¹, Q Wong¹, N Prystajecky¹,², M Morshed¹,²

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

**OBJECTIVES:** The parasite of the genus *Plasmodium* is the infectious agent of malaria which causes an estimated 1 million deaths annually worldwide. Of the five *Plasmodium* species, infections with *P. falciparum* are the most serious, fatal if untreated, requiring STAT detection and speciation. To improve turn-around-time, sensitivity, and specificity, three laboratory-developed multiplexed real-time PCR assays for the Applied Biosystems 7500 FAST Taqman platform were validated for the detection and speciation of *Plasmodium* infections.

**METHODS:** A total of 84 clinical extracts (56 *Plasmodium* positive and 28 *Plasmodium* negative) were tested with our laboratory developed real-time PCR assays; a triplex for the detection of all *Plasmodium* species, *P. falciparum* speciation, and an IPC, plus two additional duplexes for speciation of *P. vivax*/*P. knowlesi* and *P. ovale*/*P. malariae*. Results were compared to microscopic diagnosis (current gold standard) and discordant results were tested by two alternative melt-curve analysis real-time PCR assays. In silico analysis was completed by a probe BLAST using the NCBI database with base pair mismatches analysed by IDT Biophysics web tool.

**RESULTS:** Extract testing results demonstrated 95.2% analytical specificity to *Plasmodium* positive samples and the species identified by microscopy. In total, 4 samples had discordant smear results and real-time PCR results. Upon testing with the referee melt-curve assays, three of the four discordant samples were correctly identified by this assay, including one previously unidentified mixed infection. In silico analysis identified no cross reactivity, including Ebolavirus.

**CONCLUSIONS:** The real-time PCR assays described in this report is a reliable method for identification and speciation of *Plasmodium* infections. It can be used as a QA/QC protocol to supplement the gold standard of microscopic diagnosis or can be used to reliably differentiate malaria from other infectious agents.

**P37**

**Automated Workflow for Bacterial Whole Genome Sequencing in a Public Health Laboratory**

T LEE¹, R Azana¹, V Tang¹, KA MacDonald¹,², B Auk¹, N Prystajecky¹,³, L Hoang¹,², M Croxen¹

¹BCCDC Public Health Laboratory, Vancouver, BC, ²National Microbiology Laboratory, Winnipeg, MB, ³University of British Columbia, Vancouver, BC

**OBJECTIVES:** Manual library preparation for Whole Genome Sequencing (WGS) of bacterial isolates is labour intensive, time consuming, and has the potential for error due to many pipetting steps. Use of automated library preparation can address these challenges and provide consistency in the quality of libraries produced. An automated library preparation instrument, Illumina’s NeoPrep, was evaluated at BCCDC Public Health Laboratory. Several extraction methods were evaluated, taking into consideration existing workflows, access to instruments, and cost, with the final workflow presented.
METHODS: Nucleic acid was extracted from clinical Salmonella, Listeria, and Enterobacteriaceae isolates by Qiagen QIAamp DNA Mini Kit and subsequently sheared by the Diagenode Bioruptor Pico or Covaris M220 ultrasonicator. Sheared DNA profiles were assessed by Agilent Tape Station and DNA yields quantified by Qubit. All libraries were prepared using the Illumina TruSeq Nano DNA kit for NeoPrep. Libraries were sequenced on a MiSeq using a V2 500 cycle reagent kit and depth of coverage was estimated.

RESULTS: Samples sheared using the Bioruptor Pico and the Covaris M220 ultrasonicator were successfully sequenced with at least 30x depth of coverage using this workflow. The success of sequencing DNA libraries generated by the Illumina NeoPrep depends on various factors, including DNA quality, proper shearing and technical pipetting onto the NeoPrep.

CONCLUSIONS: We have identified a workflow process for bacterial culture extraction, DNA shearing, and library preparation on the NeoPrep for routine WGS at the BCCDC Public Health Laboratory.

P38 Development and Validation of a Real-time, Reverse Transcription PCR Assay for Rapid and Low-cost Genotyping of Hepatitis C Virus Genotypes 1a, 1b, 2, and 3a
T LEE1, A Olmstead2, R Chow1, K Gunadasa1, B Auk1, M Krajden1,2, A Jassem1,2
1BCCDC Public Health Laboratory, Vancouver, BC, 2University of British Columbia, Vancouver, BC

BACKGROUND: Hepatitis C virus (HCV) infection affects millions of people and leads to liver fibrosis, cirrhosis, and hepatocellular carcinoma. Treatment regimen selection requires HCV genotype (Gt) and Gt 1 subtype determination. Use of a paired, duplex laboratory developed, reverse transcription (RT)-PCR assay was validated as a low-cost, high-throughput screening approach for major HCV Gt and subtypes in North America.

METHOD: A total of 155 HCV-positive blood specimens tested at the BCCDC Public Health Laboratory (PHL) were run in parallel with the laboratory developed real-time RT-PCR assay (paired, duplex) and the existing commercial line probe assay (LiPA). Discordant results were tested by sequencing and an alternative PCR assay.

RESULTS: The laboratory developed real-time RT-PCR assay had a 95% overall sensitivity, with individual Gt sensitivity and specificity of 98-100% for Gt 1a/3a and 85-98% for Gt 1b/2 respectively. The RT-PCR assay detected mixed HCV Gts in clinical and spiked samples with no false-positive reactions for rare Gts 4, 5, or 6. Implementation of this laboratory developed test RT-PCR assay, with algorithmic reflex LiPA testing, was calculated to be 8–13% of the cost of using LiPA alone, and could also save 1.5 hours of hands-on time.

CONCLUSIONS: Use of a laboratory developed RT-PCR assay for HCV genotyping has the potential to reduce reagent cost and labour in high-volume testing settings.

P39 The Canadian Nosocomial Infection Surveillance Program (CNISP) a Historical Perspective: 1995 to 2016 and Beyond
JM LANGLEY1,2, C Frenette1,4, D Gravel5, G Golding6, MR Mulvey6, K Amaratunga5, L Pelude5, and Canadian Nosocomial Infection Surveillance Program
1IWK Health Centre, Halifax, NS, 2Dalhousie University, Halifax, NS, 3McGill University Health Centre, Montréal, QC, 4McGill University, Montréal, QC, 5Public Health Agency of Canada, Ottawa, ON, 6Public Health Agency of Canada, Winnipeg, MB

OBJECTIVES: To describe the history of the Canadian Nosocomial Infection Surveillance Program (CNISP), a national surveillance system reporting on the epidemiology, molecular characterization and antimicrobial resistance of healthcare- associated infections since 1995.

METHODS: Retrospective review of CNISP data, publications, protocols and meeting notes was conducted to describe the history of CNISP.

RESULTS: In 1994, 18 hospitals from 7 provinces agreed to participate in CNISP. In 2016, 65 hospitals across 10 provinces collaborate in surveillance. The first CNISP target was methicillin-resistant Staphylococcus aureus (MRSA) in 1995. Since then, CNISP has initiated surveillance on vancomycin resistant enterococcus (VRE), Clostridium difficile infections (CDI), central line associated bloodstream infections (CLABSI), influenza in
hospitalized adults, viral respiratory illness in children, surgical site infections and carbapenem resistant organisms (CRO). In addition, CNISP has done studies on antimicrobial utilization, hospital-wide antibiograms and point prevalence of HAI. The network has evaluated the quality and representativeness of its data, surveyed infection control practices, and the National Microbiology Laboratory (NML) has molecularly characterized and identified antimicrobial resistance patterns for MRSA, CDI, VRE and CROs. CNISP has produced more than 260 scientific peer-reviewed publications and presented at national and international conferences.

CONCLUSIONS: For more than 20 years CNISP has been a successful collaboration between the federal government and sentinel acute-care hospitals across Canada. CNISP surveillance has provided a measure of the burden of illness, established benchmark rates and identified potential risk factors in relation to HAIs in Canada. CNISP surveillance provides key information that helps to improve the health of Canadians and improve patient safety.

P40
Disseminated Chronic Histoplasmosis Presenting as Acute Splenic Rupture in a Patient with Rheumatoid Arthritis Treated with Biologic Therapy
JN KANJI1,2,4, SZ Brown1,3, R Rennie1,2

1University of Alberta, Edmonton, AB, 2Provincial Laboratory for Public Health (Microbiology), Edmonton, AB, 3DynaLife Dx, Edmonton, AB, 4Misericordia Hospital, Covenant Health, Edmonton, AB

INTRODUCTION: Systemic infection due to Histoplasma capsulatum can be difficult to diagnose in patients with severe immunosuppression due to lack of an inflammatory response. The dimorphic mould often involves multiple areas of the body, especially the reticuloendothelial system. We report a case of chronic disseminated histoplasmosis in a patient on biologic therapy who first presented with acute splenic rupture.

CASE DESCRIPTION: A 54-year-old female with rheumatoid arthritis (RA) treated with golimumab, leflunomide, and methotrexate was referred for 6 months of fevers and persistent dry cough. Five months prior, she had presented with left upper quadrant pain and was diagnosed with spontaneous splenic rupture on computed tomography (CT) of the abdomen requiring splenectomy (no aetiology found). Two months after, she underwent mediastinoscopy to biopsy several lung nodules. Pathology revealed granulomatous inflammation and budding yeast forms consistent with H. capsulatum (Gomori methenamine silver (GMS)). Retrospective staining of splenic tissue blocks with GMS and periodic acid-Schiff stain (PAS) demonstrated rare fungal spores morphologically identical to those in the mediastinal biopsies without evidence of splenic granulomatous changes. Serum Histoplasma antigen testing was positive, but urine antigen and serology testing were negative. The patient received induction liposomal amphotericin B and one year of itraconazole with good results. Biologic therapy was re-started due to refractory RA symptoms. The patient remains on suppressive itraconazole.

DISCUSSION: While splenic calcifications and granulomas are not uncommon in patients with resolved or previously treated H. capsulatum infection, unexplained splenic rupture as a presenting manifestation of disseminated infection is rare. To our knowledge, this has only been reported once before, also in a patient on biologic therapy for autoimmune disease. This case highlights the lack of symptoms and seroconversion that may be seen in those on such medications. Clinicians should consider disseminated histoplasmosis in cases of idiopathic splenic rupture in patients who are severely immunosuppressed and pursue tissue or antigen based diagnostics as serology may be falsely negative.
community hospital, a review was performed to identify potential contributing factors.

**METHODS:** A retrospective chart review of primary THAs and TKAs was performed by two nurses from the department of Infection Prevention and Control (IPC) between 01 January – 30 June 2015. Standard National Healthcare Safety Network SSI surveillance definitions were applied, and all SSIs were reviewed by an IPC physician. Twenty-seven variables based on the Safer Healthcare Now campaign of the Canadian Patient Safety Institute were identified and evaluated. Data was analysed using two-tailed Fisher’s exact test followed by bivariate exact logistic regression using complete case data.

**RESULTS:** During the 6 month period, 321 elective arthroplasties were performed (116 THAs, 205 TKAs), of which 63% patients had a BMI ≥30 (59/116 THAs, 143/205 TKAs). PJIs were identified (3 THA, 5 TKAs). Use of untinted chlorhexidine skin preparation was the only factor associated with a PJI (OR 16.2, 95% CI 1.37-191.2, p < 0.03). The majority of patients with a PJI had their dressing removed prior to hospital discharge (7/8, 88%), no drain placed (7/8, 88%), and no preoperative hair removal (5/8, 63%). Surgical network analysis revealed 40% of operating room staff attended ≥1 patient who developed an SSI. Orthopaedic infection rates were 2.61/100 procedures (THAs) and 2.23/100 procedures (TKAs).

**CONCLUSIONS:** Our study revealed higher odds of developing a PJI when using untinted chlorhexidine. This chart review is limited by the small number of SSIs identified, thus limiting any major conclusions. Given the lack of significant variables, this raises questions of whether difficult to measure variables such as surgical technique, haemostasis, and operating room environment (like ventilation and traffic) contributed to the PJIs.

**P42**

**Bone Marrow Transplant Room Makeovers: Re-engineering Patient Rooms Can Lead to a More Sanitary Environment**

E Bryce¹, A Stefanovic¹, T WONG¹, T Woznow¹, R Broady¹, L Hoang², M Croxen²

¹Vancouver Coastal Health, Vancouver, BC, ²BC Centre for Disease Control, Vancouver, BC

**OBJECTIVES:** To evaluate novel environmental engineering solutions to minimize microbial burden in the rooms of patients undergoing bone marrow transplantation.

**METHODS:** This one-year pilot project (Oct 2015-Oct 2016) examined the environment of nine patients undergoing myeloablative (allogeneic) transplantation who were randomized to stay in a re-engineered or a standard bone marrow transplant (BMT) room. Re-engineered rooms had copper installed on seven high-touch surfaces, wall-mounted ultraviolet C light in the patient washroom, titanium dioxide paint on walls, filtered tap water, as well as no-touch soap, alcohol based hand rub and paper towel dispensers. Both re-engineered and standard rooms received regular cleaning and UV-C light disinfection upon patient discharge as per protocol. Weekly RODAC cultures and ATPB (Adenosine Triphosphate – Bioluminescence) measurements on high touch surfaces as well as standard cultures (Blood Agar Plates) of water and air samples were performed throughout the patient’s admission.

**RESULTS:** Average RODAC CFU/plate were 62.6 +/- 279.9 (n=147) and 6.32 +/- 16.6 (n=175;p=0.0083) while average ATPB RLU were 434.4 +/- 675.5 (n=147) and 62.9 +/- 280.9 (n=182;p=0.0001) for standard and re-engineered rooms, respectively. The average CFU/BAP on air samples was 14.2 +/- 11 (n=21) and 15.6 +/- 25.2 (n=25;p=0.8145) for standard and re-engineered rooms. Filtered water counts were 26.5 +/- 36.5 CFU/BAP (n=20) and 0.08 +/- 0.28 CFU/BAP plate (n=25;p=0.0007 for re-engineered rooms. Minimal tarnishing was noted on copper surfaces.

**CONCLUSIONS:** This pilot project demonstrates that lower microbial counts and ATPB measurements were consistently sustained on high-touch surfaces. Lower microbial counts were also observed in filtered water samples in re-engineered rooms over the one-year pilot project period.
P43  
Detection of *Clostridium difficile* Colonization Using Rectal Swabs and Lab-Developed LAMP Assay

Y YU1, A Hadzic2, D Mertz2, P Jayaratne1,2, M Smieja1,2

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

**OBJECTIVE:** *Clostridium difficile* infection (CDI) is a nosocomial infection, associated with increased healthcare utilization, morbidity, and mortality. Studies have shown that detecting and isolating *C difficile* carriers was associated with a significant decrease in the incidence of healthcare-associated CDI, but the use of commercial assays was a major cost. In this pilot study, we used an inexpensive Loop Mediated Isothermal Amplification (LAMP) method to estimate the prevalence of *Clostridium Difficile* colonization in asymptomatic high-risk patients using rectal swabs.

**METHOD:** During October to December 2016, infection prevention and control (IPAC) personnel identified 383 nasal/rectal swabs collected for methicillin-resistant *Staphylococcus aureus* (MRSA) surveillance of patients from high risk inpatient units (including Medicine, Oncology and Nephrology) at the Hamilton Health Sciences (3 hospital sites) and St. Joseph's Healthcare Hamilton (1 hospital site). Flocked swabs in Amies transport medium (eSwab, Copan Italia) were initially set up for MRSA screening, followed by *C. difficile* tcdC gene LAMP test, which was developed for routine *C. difficile* diagnosis in the clinical laboratory. Briefly, swabs were vortexed, mixed with lysis buffer, and boiled at 95°C for 15 minutes. Following additional vortexing and centrifugation, the supernatant was used for DNA amplification. The LAMP assay was performed on a Rotor-Gene Q (Qiagen).

**RESULTS:** Out of the 383 specimens tested, 40 were positive for the tcdC gene. After excluding 10 patients having positive *C. difficile* test within the previous 30 days, colonization was 30 out of 373 (8.0%). Prevalence varied from 6.9% to 11.1% for the four hospital sites, which included one pediatric and three adult sites.

**CONCLUSION:** Our study demonstrates that rectal swabs coupled with an inexpensive lab-developed LAMP assay can efficiently detect *C. difficile* colonization. This may be a valuable tool in future studies to evaluate infection control strategies and antimicrobial management in the prevention of *C. difficile* diarrhea.

P44  
Detection of Enteropathogens in Children with Acute Gastroenteritis Presenting with Isolated Vomiting — APPETITE Study

B LEE1, XL Pang1, R Zhuo1, B Parsons1, L Chui1, J Xie2, K Lowerison1, L Osterreicher1, S Ali1, S Freedman2

1University of Alberta, Edmonton, AB, 2University of Calgary, Calgary, AB, 3Alberta Health Services, Calgary, AB

**BACKGROUND:** Since diarrheal stool samples are the recommended specimen for testing in children with acute gastroenteritis, etiological investigations are rarely performed in children with AGE who present with isolated vomiting.

**OBJECTIVE:** To identify enteropathogens in children with AGE and isolated vomiting.

**METHODS:** Children <18 years of age with ≥3 episodes of vomiting in 24 hours and <7 days of symptoms were recruited in 2 pediatric emergency departments (PEDs), a public health clinic, and via a provincial nursing advice phone line. Rectal swabs and stool samples were collected and tested using the Luminex xTAG Gastrointestinal Pathogen Panel, an in-house 5 virus panel and enteric bacterial culture. Data regarding vomiting and diarrhea frequency and duration were collected at the time of enrolment (i.e. specimen acquisition).

**RESULTS:** Between December 2014 and October 2016, 1,646 study participants were tested according to our study algorithm: 888 (54%) presented with both vomiting and diarrhea, 559 (34%) had isolated vomiting, 190 (12%) had isolated diarrhea, 9 (0.5%) were missing these data. Of the participants presented with isolated vomiting, stool specimens were submitted from 372 (67%) children and rectal swab from 555 (99%). 51% (286/559) of these participants had one or more virus detected with the most common being norovirus (NoV) (n=164, 50%), followed by adenovirus (Adv) (60, 18%), rotavirus (Rota) (53, 16%), sapovirus (47, 14%) and astrovirus (5, 2%). More than one virus was detected in 39 cases and the combination of NoV and Adv was the most common (n=16). 12% (69/559) tested positive for *C. difficile* (Cdiff). Of these 69 cases, 41 (59%) had both
CONCLUSIONS: Over 50% of children with isolated vomiting had a pathogenic enteric virus identified in stool specimens or rectal swabs, representing a significant pathogen-based disease burden not previously included in healthcare planning, e.g., Rota vaccine evaluation. NoV was the predominant agent identified followed by Adv and Rota.
RESULTS: BioNumerics v7.6 wgMLST schemas and IRIDA’s SNVPhyl pipeline produced concordant clustering results for the enteric organisms assessed by both methods. Known outbreak isolates were appropriately clustered by both methods. SNV analysis, however, was more discriminatory for *Salmonella* Heidelberg. Both methods were easy to use and provided phylogenetic results within several hours. Neither method required much knowledge of bioinformatics or genomics.

CONCLUSIONS: Both IRIDA and BioNumerics 7.6 were able to provide an automated method of phylogenetic analysis for enteric pathogens. Both methods would be easy to use in a public health setting, by technicians with little bioinformatics expertise.

### P48

**Outbreak of Group A Streptococcus (GAS) in a Shelter for Homeless Men, Toronto, Canada**

M FINKELSTEIN1,3, A McGeer1,5, H Sachdeva1,3, C Dohoo2, R Stuart1, E Kaplan4, D Hayden3, E Rea1,3, E Gournis1,3

1University of Toronto, Toronto, ON, 2Public Health Agency of Canada, Vancouver, BC, 3Toronto Public Health, Toronto, ON, 4University of Minnesota Medical School, Minneapolis, MN, USA, 5Mount Sinai Hospital, Toronto, ON

**INTRODUCTION:** Group A Streptococcus (GAS) is a frequent cause of outbreaks in health care institutions yet outbreak reports in the literature from homeless shelters are rare even though homeless/under-housed individuals are at increased risk of severe GAS infection. Since March 2016, Toronto Public Health has investigated an outbreak of GAS in a large men’s shelter with a high proportion of long-stay residents. Here we describe the epidemiology of the outbreak and public health actions taken to control it.

**METHODS:** A confirmed case was a client or staff member of the 543 bed shelter after Feb. 1, 2016, with laboratory confirmed infection with *emm*74 or *emm*101 GAS. Outbreak control measures included: optimization of infection control activities and wound care, early case finding, screening residents and staff using wound, throat or nares swabs, treatment of screen-positive residents and staff, exclusion of staff, enhanced resident access to influenza vaccine and harm reduction supplies, unit-based antibiotic prophylaxis with cephalaxin...
Abstracts

102

Resistance Patterns of enterobacteriaceae in Urines are Similar in Symptomatic and Asymptomatic Patients

F AL DHUFAIRI1,6, C Ellis3, L Maze Dit Mieusement4, A McGeer5, D Mertz1,2

1McMaster University, Hamilton, ON, 2Hamilton Health Sciences, Hamilton, ON, 3The Moncton Hospital, Horizon Health Network, Moncton, NB, 4Mount Sinai Hospital, Toronto, ON, 5University of Toronto, Toronto, ON, 6Prince Mohammed Medical City, Al Jouf, Saudi Arabia

OBJECTIVES: Antibiograms are being used to guide empiric treatment. However, roughly 50% of urine cultures informing urine antibiograms are from patients with asymptomatic bacteriuria (ABU), which may limit the generalizability for treatment decisions in patients with urinary tract infections (UTI). Hence, we aimed to compare the antimicrobial resistance patterns in patients with ABU to patients with symptomatic UTI.

METHODS: We retrospectively reviewed urine cultures with significant growth of the most common enterobacteriaceae (E. coli, K. pneumoniae, K. oxytoca, P. mirabilis, P. vulgaris) among inpatients with data on symptoms available from three different hospital sites: Hamilton Health Sciences, Hamilton (n=217), Mount Sinai Hospital, Toronto (n=69), and Moncton, NB (n=346). Rates of resistance, based on CLSI, were compared between UTI and ABU patients reporting odds ratios (OR) and 95% confidence intervals (CI).

RESULTS: Of 632 positive cultures, 310 (49.1%) were collected from ABU patients. E. coli was the most common pathogen (n=221, 71.3% in UTI and n=230, 71.4% in ABU patients) followed by K. pneumoniae (n=55, 17.7% and n=55, 17.1%, respectively). Ceftriaxone resistance (21.7%) was significantly more common at Mount Sinai than at the two other hospital sites (6.4% in Moncton and 4.6% in Hamilton; p<0.001).

CONCLUSIONS: Our findings confirm that resistance patterns in enterobacteriaceae from patients with ABU can be used in antibiograms to guide empiric treatment choices in UTI patients. Although some strains are known to be more likely to result in ABU, the resistance patterns in a clinical setting are very similar to those found in UTI patients.

Comparison of resistance patterns in UTI versus ABU patients

<table>
<thead>
<tr>
<th>Antibiotic</th>
<th>n(%) resistance UTI</th>
<th>n(%) resistance ABU</th>
<th>OR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ampicillin</td>
<td>180 (55.9)</td>
<td>163 (52.6)</td>
<td>1.1</td>
<td>0.8-1.6</td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>25 (7.8)</td>
<td>22 (7.1)</td>
<td>1.1</td>
<td>0.6-2.0</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>65 (20.2)</td>
<td>58 (18.7)</td>
<td>1.1</td>
<td>0.7-1.6</td>
</tr>
<tr>
<td>TMP/SMX</td>
<td>57 (17.7)</td>
<td>44 (14.2)</td>
<td>1.3</td>
<td>0.8-2.0</td>
</tr>
<tr>
<td>Nitrofurantoin</td>
<td>76 (23.6)</td>
<td>73 (23.5)</td>
<td>1.0</td>
<td>0.7-1.4</td>
</tr>
</tbody>
</table>

Ceftriaxone resistance (21.7%) was significantly more common at Mount Sinai than at the two other hospital sites (6.4% in Moncton and 4.6% in Hamilton; p<0.001).

CONCLUSIONS: Our findings confirm that resistance patterns in enterobacteriaceae from patients with ABU can be used in antibiograms to guide empiric treatment choices in UTI patients. Although some strains are known to be more likely to result in ABU, the resistance patterns in a clinical setting are very similar to those found in UTI patients.

RESULTS: The outbreak was declared on Mar. 31, 2016 on long stay unit A after four emm74 (a rare type in Toronto) infections were detected and then spread to long-stay unit B and short-stay unit C. As of January, 2017, three rounds of residents/staff screening covered 1,624 persons; two screenings involved public health orders compelling residents and staff to participate. Cases decreased after all unit A residents were prescribed cephalaxin or five days of azithromycin prophylaxis. As of Jan. 13, 2017, 53 confirmed cases (seven invasive) were reported (43 emm74 and 10 emm101), a 26% attack rate on unit A, 10% on unit B and 3% on unit C. All invasive cases were hospitalized but no outbreak-associated deaths occurred. Infection control activities included replacing all mattresses and a deep cleaning of units A/B. Having a wound in the month prior to onset was associated with increased risk of GAS infection (O.R. 2,555; 95%C.I. 77-84,816).

CONCLUSION: There are many potential routes of GAS transmission in a shelter so a response requires multi-modal strategies. GAS shelter outbreaks pose unique challenges for public health response and sharing the lessons learned is important, as the homeless/under-housed population is at risk of complications from GAS infections.

P49

Resistance Patterns of enterobacteriaceae in Urines are Similar in Symptomatic and Asymptomatic Patients

F AL DHUFAIRI1,6, C Ellis3, L Maze Dit Mieusement4, A McGeer5, D Mertz1,2

1McMaster University, Hamilton, ON, 2Hamilton Health Sciences, Hamilton, ON, 3The Moncton Hospital, Horizon Health Network, Moncton, NB, 4Mount Sinai Hospital, Toronto, ON, 5University of Toronto, Toronto, ON, 6Prince Mohammed Medical City, Al Jouf, Saudi Arabia

OBJECTIVES: Antibiograms are being used to guide empiric treatment. However, roughly 50% of urine cultures informing urine antibiograms are from patients with asymptomatic bacteriuria (ABU), which may limit the generalizability for treatment decisions in patients with urinary tract infections (UTI). Hence, we aimed to compare the antimicrobial resistance patterns in patients with ABU to patients with symptomatic UTI.
P51
Evaluation of Chromogenic Screening Agars for the Detection of Carbapenemase Producing Organisms (CPO) and Extended Spectrum Beta Lactamase (ESBL) Producers
L Turnerbull¹, T Dingle¹,², P Naidu¹,²
¹Provincial Laboratory for Public Health, Edmonton, AB, ²University of Alberta, Edmonton, AB

INTRODUCTION: During 2016, the number of requests for CPO and ESBL screening increased dramatically at our institution. Our current chromogenic CPO screening plate is insensitive for the isolation of CPOs other than KPCs; we have no ESBL screening plate in use.

OBJECTIVE: To compare the performance of 7 chromogenic screening agars for the detection of CPO and ESBL producers.

METHODS: Sixty three characterized Enterobacteriaceae isolates were tested against mSUPERCARBA (CHROMagar), CHROMagar KPC (CHROMagar), Brilliance CRE (Oxoid, Thermofischer Scientific), Colorex ESBL (Colorex), Colorex C3Gr (Colorex), Chromogenic ESBL Isolation (Oxoid) and ESBL Isolation Agar (Oxoid). The Enterobacteriaceae isolates included 21 known CPOs, 30 ESBLs and 15 negatives. Ten fold serial dilutions of a 0.5 McFarland were made (10⁸ – 10³ CFU/ml) and 100ul of each dilution was inoculated onto each media type. Plates were incubated for 24h at 35°C and colonies were counted.

RESULTS: The sensitivity of detection of CPOs using mSUPERCARBA was the highest and was able to detect 100% of CPOs including 2 OXA-48 isolates and 1 NMC isolate. The

CONCLUSIONS: The sensitivity of mSUPERCARBA was the highest and was able to detect 100% of CPOs including 2 OXA-48 isolates and 1 NMC isolate. The
Brilliance CRE medium had the highest specificity by detecting fewer ESBL isolates with reduced carbapenem susceptibility. Colorex C3Gr had the highest sensitivities for detecting CPOs and ESBLs but had the lowest specificity. The high sensitivity and low specificity of the CPO and ESBL chromogenic agars make them ideal for screening, but further confirmatory testing is necessary due to high false positivity rates.

P52
Evaluation of BD MAX™ System for Confirmation of Neisseria gonorrhoeae Positive Viper XTR™ Results
H ALMOHRI, D Leto
LifeLabs Medical Laboratory Services, Toronto, ON

Neisseria gonorrhoeae (GC) is an important causative agent of sexually transmitted infection in both men and women that can have a broad range of symptoms. High volume screening testing for GC using the BD ProbeTec™ GC Qx Amplified DNA Assay on the BD Viper™ Analyzer allows for rapid testing of large numbers of specimens. Nucleic acid target for GC on Viper is chromosomal pilin gene inverting protein homologue. N. cinerea, N. subflava and N. lactamica might result in false positive results; therefore, positive results require confirmation prior to finalizing the result. BD MAX targets the gonococcal opcA gene. Objective: To assess the use of BD MAX™ GC rtPCR as a confirmatory method for urine specimens, endocervical and urethral swabs that test positive for GC using BD Viper. A total of 474 of clinical samples that tested positive on the BD Viper™ were tested on the BD MAX™ System using the GC rtPCR Assay. Out of 349 urine samples, 94 (26.9%) turned to be negative for GC, and out of 125 swabs, 71 (56.8%) turned to be negative for GC on BD Max. For Verification a total of 112 random samples were tested; 69 urine samples and 43 swabs. There were 90 concordant results (81% agreement on BD MAX and Viper), 21 discordant results. Of the 43 swabs, 15 (35.7%) that initially tested positive on the BD Viper turned to be negative for GC on the BD MAX, 1 indeterminate swab and 7(10.1%) of the 69 urine samples initially testing positive on the BD Viper, were negative on the BD MAX. The 8 discordant results were matching on gene sequencing, 12 of which were positive and 8 were negative on BD MAX. Twenty Viper positive samples were sent for gene sequencing, 12 of which were positive and 8 were negative on BD MAX. The 8 discordant results were matching on gene sequencing with the BD MAX results and were confirmed negative for GC by gene sequencing. Negative results were found to be N. lactamica and proved to be false positive Viper results.

In conclusion, Positive GC results on BD Viper™XTR should be confirmed using a test with an alternate target.

BD MAX is an acceptable confirmatory test for Viper positive GC results.

P53
Stability of SurePath Liquid Base Cytology Samples for Detection and Genotyping of HPV on Roche cobas® 4800
H ALMOHRI, E Nagai

LifeLab Medical Laboratory Services, Toronto, ON

SurePath contains formalin, which crosslinks HPV DNA to proteins. DNA-protein cross-linking can result in DNA fragmentation and interfere with PCR amplification, thus reducing a test's analytical sensitivity. Concerns of limited stability and reduced sensitivity of HPV testing using samples stored in SurePath preservative have been raised potentially causing false-negative results.

OBJECTIVE: To test the stability of SurePath before and after treatment with Sample Prep buffer SBP for testing on Roche cobas 4800.

METHODS: 44 positive cytology Surepath specimens were tested before and after treatment with Sample prep buffer. 15 samples were tested before and after treatment at 14 days, 30 days and 6 weeks.

RESULTS: 44 samples were on average 35 days old when tested, refrigerated on day 7-8 after collection, and were tested before and after adding the SPB. Results showed improvement in Delta Ct values after adding the SBP. For HPV 16 median delta Ct was -2.95, for HPV 18 -4.55, other HR HPV – 3.2 and B-Globin was -6.2. 5 samples (2 LSIL, 2 HSIL, 1 ASCUS) were tested at 14 days after collection at room temperature before and after addition of SPB. All sample showed improved Ct values except for one bloody sample that turned negative for HR HPV after addition of SPB, Ct value was 39.2 without SBP. At 30 days stability test, another 5 samples (2 LSIL, 2 HSIL, 1 ASCUS) were tested before and after addition of SPB, all Ct results showed improvement and one sample that was negative for HPV 16 without SBP, was tested positive after SBP with Ct value of 35.7. At 6 weeks stability test, 5 samples (2 LSIL, 2 HSIL, and 1 ASCUS) were tested before and after SPB. All results
showed improved Ct values. One sample turned out to be co-infected with HR HPV as well as HPV 16 with SBP, while only HPV 16 was detected without SBP.

CONCLUSION: Addition of SBP to SurePath samples stored at room temperature up to 6 weeks after collection will improve Ct values for the detection of HPV on Roche cobas 4800. Bloody samples may result in false negative results.

P54
Prescriber Tendencies Influence Antibiotic Initiation, Selection and Duration in Long Term Care Facilities
N DANEMAN1,2,3,4,5, MA Campitelli1,5, V Giannakeas1, AM Morris1,6, CM Bell1,4,3,6, CJ Maxwell1,7, L Jeffs8, PC Austin1,5, SE Bronskill1,5

1Institute for Clinical Evaluative Sciences, Toronto, ON, 2Sunnybrook Research Institute, Toronto, ON, 3Sunnybrook Health Sciences Centre, University of Toronto, Toronto, ON, 4Dept. of Medicine, University of Toronto, Toronto, ON, 5Institute Health Policy Management & Evaluation, Toronto, ON, 6Sinai Health System, Toronto, ON, 7University of Waterloo, Waterloo, ON, 8St. Michael’s, Toronto, ON

OBJECTIVE: Understanding the extent to which current antibiotic prescribing behaviour is influenced by clinicians’ historical patterns of practice will help target interventions to optimize antibiotic use in long-term care.

METHODS: We conducted a retrospective cohort study of all physicians who prescribed to Ontario long-term care residents between January 1 and December 31, 2014. We examined variability in antibiotic prescribing across physicians for three measures: initiation of antibiotics, use of prolonged durations exceeding 7 days, and selection of fluoroquinolones. Funnel plots with control limits were used to determine the extent of variation and characterize physicians as extreme low, low, average, high and extreme high prescribers for each tendency. Multivariable logistic regression was used to assess whether a clinician’s prescribing tendency in the previous year predicted current prescribing patterns, after accounting for residents’ demographics, comorbidity, functional status, and indwelling devices.

RESULTS: Across 1,695 long-term care physicians, who prescribed for 93,132 residents, there was wide variability in antibiotic initiation (median 45% of patients; interquartile range (IQR) 32-55%), use of prolonged treatment durations (median 30% of antibiotic prescriptions; IQR 19-46%), and selection of fluoroquinolones (median 27% of antibiotic prescriptions; IQR 18-37%). Physicians’ antibiotic prescribing tendencies in 2014 correlated strongly with tendencies in the previous year. Controlling for individual resident characteristics, prior prescribing tendency was a significant predictor of current practice.

CONCLUSION: Antibiotic prescribers exhibit individual, measurable, historical tendencies towards antibiotic initiation, use of prolonged treatment duration and class selection; prescriber audit-and-feedback may be a promising tool to optimize antibiotic use in long-term care.

P55
New Technology, Best Practice Training and Improved Processes Impact Blood Culture Quality
J VANDERLAAN

Grand River Hospital, Kitchener, ON

Grand River Health operates two acute care hospitals; Grand River (GRH) and St. Mary’s General (SMGH), with combined 758 in-patient beds. In 2015, Grand River implemented the BD BACTEC™ FX and EpiCenter™ Data Management System in the GRH microbiology laboratory and best practice training program for blood culture collection at each site. New technology, staff education and streamlined processes provided an opportunity to improve and better track blood culture Key Performance Indicators (KPIs).

Pre- and post-data was collected from the LIS (n=20,126) and LIS, BACTEC™ FX and EpiCenter™ – Specimen Registration platform (n=22,118), respectively. Data was analyzed for improvement in the following KPIs; contamination, false positive, true positive, overfill and underfill vial rates.

Post-implementation, improvements were observed in several KPIs. Combined contamination and overfill incidence for GRH and SMGH were reduced 41% and 58.3%, respectively. The largest improvement was obtained at SMGH where contamination decreased by 48% (from 2.7% to 1.4%) and overfill rates by 72% (2.2% to 0.6%). In addition, underfill rates were improved at GRH by 17% (from 4.7% to 3.9%). Post implementation, EpiCenter™ Data Management monitored
and generated reports for instrument status, capacity, contamination, positivity rates and blood volume. Blood cultures are vital for identifying pathogens and in directing appropriate antibiotic therapy. Each step in the collection procedure affects the quality of the specimen and potential for errors in the diagnostic result. Overfilled or contaminated blood culture vials are common occurrences that lead to additional laboratory testing and unnecessary antibiotic therapy. Underfilled vials reduce the potential to harvest organisms causing septicemia which impacts patient morbidity and mortality. This study demonstrates that technology and education can improve blood culture quality allowing for alignment with best practices for patient care, KPI monitoring and antibiotic stewardship.


P56
Airborne Survival and Inactivation of Human Pathogens Indoors: Studies with a Room-sized Aerobiology Chamber
B ZARGAR1, MK Ijaz2, JR Rubino2, SA Sattar3
1CREM Co Labs, Mississauga, ON, 2RB, Montvale, New Jersey, USA, 3University of Ottawa, Ottawa, ON

BACKGROUND: The air indoors has profound health implications as it can expose us to pathogens, allergens and particulates either directly or via contaminated surfaces. There is, therefore, an upsurge in marketing of air decontamination technologies, but with no proper validation of their claims. We addressed the gap through the construction and use of a versatile room-sized (24 m³) chamber to study airborne pathogen survival and inactivation.

MATERIALS AND METHODS: Staphylococcus aureus (ATCC 6538) and Klebsiella pneumoniae (ATCC 4352) were suspended in a soil load and separately aerosolized into the chamber with a Collison nebulizer. A muffin fan evenly distributed and kept the bacteria airborne. The aerosols were collected with a programmable slit sampler directly onto Petri plates with Letheen agar. The RH and air temperature inside the chamber were at 50±5% and 20±1°C, respectively. The plates were incubated at 36±1°C for 18-20 h and the CFU counted. Two commercial devices, based on HEPA filters and UV light, were separately placed in the chamber and tested with the efficacy criterion of >3 log10 loss in viability of both the tested bacteria.

RESULTS: The initial levels of CFU/m³ of the air ranged between 4.2 to 5.0 log10. The rates of biological decay for S. aureus and K. pneumoniae were 0.0064±0.00015 and 0.0244±0.009 as log10 CFU/m³/min, respectively. The tested devices met the efficacy criterion in 45 min; both could also reduce repeated airborne challenge to undetectable levels. Further, reductions in airborne bacteria could also reduce their levels on surfaces in the chamber. Mathematical modelling confirmed the experimental data.

DISCUSSION/CONCLUSION: The chamber’s general design and operation met the U.S. EPA’s 2012 Guidelines for testing indoor air decontamination technologies. It is also suitable for work with all major classes of airborne pathogens, and for assessing physical and/or chemical means of air decontamination under field-relevant conditions.

P57
Landscape of Antimicrobial Stewardship Programs in Ontario Hospitals: 2016 Snapshot
V LEUNG1, J Hui-Chih Wu1, B Langford1, G Garber1,2,3
1Public Health Ontario, Toronto, ON, 2University of Toronto, Toronto, ON, 3University of Ottawa, Ottawa, ON

OBJECTIVES: In 2013, antimicrobial stewardship became an Accreditation Canada Required Organization- al Practice for facilities providing inpatient acute care, cancer, rehabilitation and complex continuing care services. To gain an understanding of how the landscape of antimicrobial stewardship in Ontario healthcare facilities has evolved and what structural and strategic program elements are currently in place, the Antimicrobial Stewardship Program (ASP) at Public Health Ontario (PHO) conducted a voluntary survey of hospitals in the province.

METHODS: The Ontario ASP Landscape survey was developed by the PHO ASP with input from external stakeholders and was distributed online to hospital corporations targeting front-line ASP clinicians. The survey was open for 5 weeks (September 19th to October 24th 2016). Email and telephone reminders were used to encourage responses. Efforts were made to reconcile unintended duplicate responses. Mental Health and
ambulatory sites were excluded from the analysis. Descriptive analysis was performed at an aggregate level and by hospital type (acute teaching, large community, small community and complex continuing care & rehabilitation).

RESULTS: The overall response rate was 74% (97/131 corporations). Of these, 93% have a formal ASP or are in the process of implementation. Resource allocation for ASPs in Ontario is currently suboptimal. Half of ASPs do not have designated resources; the other half are generally under resourced with respect to physician and pharmacist expertise compared with AMMI Canada ASP Business Case Recommendations. PHO core strategies, considered to be foundational, have been implemented in most hospitals; however, opportunity exists to increase implementation of evidence-based interventions.

CONCLUSIONS: ASPs are evolving in Ontario hospitals. While the majority have a formal ASP with foundational strategies in place, most are not adequately resourced. Future efforts should address ways to improve resource allocation for ASPs in Ontario so that these programs can continue to grow in scope and impact.

PS58
A Comparative Study of Conventional Identification and Disk Susceptibility Testing of Microorganisms to an Automated System Phoenix 100
ST HAKIM1,2, SG Nadeem2, T Bashir2

1Jinnah University for Women, Department of Microbiology, Jinnah University for Women, Karachi, Pakistan, 2Oxford College of Arts, Business and Technology, Scarborough, ON

BACKGROUND: Healthcare-associated infections (HAIs) continue to trouble the healthcare industry. The centers for disease control and Prevention estimates one in 20 patients will contact HAIs every day. Some of the better-known bacteria responsible for HAIs are Enterobacteriaceae, Acinetobacter baumannii, Pseudomonas aeruginosa, Burkholderia cepacia, Stenotrophomonas maltophilia, and Staphylococcus aureus etc [2]. A timely diagnosis is the most effective approach to prevent or control microbial infections. This study was designed to compare the conventional microbiology ID/AST testing with an Automated Phoenix 100 and to evaluate the accuracy, rapidity and efficiency of Automated Phoenix which contributes in the rapid diagnosis of bacterial isolates. This is the first study on comparison of conventional Microbiology method and Automated Phoenix 100 from Pakistan.

MATERIALS AND METHODS: Clinical isolates from indoor and outdoor patients (N=500) were collected including Blood, Urine, Pus, Abscess, Wound, Ear, Eye, Tissue, Tracheal, Sputum etc. Test isolates were Enterobacteriaceae (170), Acinetobacter sp. (120), Pseudomonas aeruginosa (60), MRSA (60), Methicillin Resistant Coagulase Negative Staphylococci (20), Stenotrophomonas maltophilia (20), Burkholderia cepacia (20), Serratia marcescens (10), Providencia rettgeri (100) and Staphylococcus pneumoniae (10).

RESULT: All Specimen were processed according to NSCCLS standards and 24-48 hours old pure cultures were used for both conventional Microbiology method and for Automated Phoenix testing of ID/AST. Results were almost equal with more rapidity. Conclusion: The Phoenix system is efficient for rapid identification and antimicrobial susceptibility testing of bacteria, it decreases antibiotic consumption and improves patient care.

PS59
Using Quality Improvement Methods to Sustain Optimal Antimicrobial Use in the ICU Setting
L Jeffs1, M ZAHRADNIK1, M Law1, M Steinberg2, S Kruger2, Y Nakamachi1, CM Bell1, AM Morris2

1St Michael’s Hospital, Toronto, ON, 2Mount Sinai Hospital, Toronto, ON, 3Brock University, St Catharines, ON

There is growing evidence on the benefits of Antimicrobial Stewardship Programs (ASPs), however less is known about the components, factors, and conditions which influence the sustainability of the projects implemented as part of ASPs. In response, a Quality Improvement (QI) strategy with integrated sustainability planning was developed to improve and sustain optimal antimicrobial use in ICUs. This QI strategy (referred to as ASP-SUSTAIN) used Health Quality Ontario’s sustainability planner and employed iterative plan-do-study-act (PDSA) cycles. Four teams from different hospital ICUs participated in ASP-SUSTAIN that included a series of five interactive learning modules delivered in a Communities-of-Practice model. Each team
implemented a project with the guidance of a mentor that focused on improving antimicrobial use in the ICU setting. A qualitative research design with content analysis was employed involving 6 focus groups (2 at six months and 4 following the completion of the program) with the participating teams. The following themes emerged from the focus group dataset of 25 participants—benefits of participating in ASP-SUSTAIN include: keeping on track and moving forward; hearing from others and brainstorming with team; and identifying areas for improvement. In terms of sustainability the following themes emerged: getting leadership and local stakeholder engagement and buy-in; making it a routine practice; and having a ripple effect. The following challenges were identified by participants: not being able to leverage information technology (IT); lack of physician engagement; having a short time frame for project completion; and lack of clarity on ASP-SUSTAIN expectations. Study findings add to the evolving body of knowledge around the benefits of engaging clinicians and staff in an integrated QI sustainability strategy and the components, factors, and conditions that influence application of QI into practice and the sustainability of QI projects aimed at optimizing antimicrobial stewardship.

**P60**

**Performance of the FilmArray Respiratory Panel for the Detection of Respiratory Pathogens in Bronchoscopy Specimens**

K Locher1, A Stefanovic1, A Jassem2, L Hoang2, T Wong1, E Bryce1, J Grant1, D Roscoe1

1Vancouver General Hospital, Division of Medical Microbiology and Infection Control, Vancouver, BC, 2British Columbia Centre for Disease Control Public Health Laboratory, Vancouver, BC

**OBJECTIVE:** The Biofire FilmArray Respiratory Panel (RP) is a rapid multiplexed molecular assay that simultaneously detects 17 respiratory viruses and 3 bacterial targets approved for the use with nasopharyngeal specimens. We evaluated the performance of the assay using bronchoscopy specimens.

**METHODS:** A total of 85 bronchoscopy specimens (82 bronchoalveolar lavages and 3 bronchial washes) were tested by the FilmArray RP and another assay that detects a similar panel of organisms (Luminex xTAG Respiratory Viral Panel FAST or Luminex NxTAG Respiratory Pathogen Panel) which was validated in-house on bronchoscopy specimens. Seventy were archived specimens that were initially tested by the Luminex method and frozen (- 70 °C) for subsequent testing by FilmArray RP and 15 were fresh specimens. For discordant analysis the Luminex assay was repeated on the same sample and as a resolving test a singleplex in-house PCR for the respective target was done in some cases.

**RESULTS:** Of the 85 specimens concordant results were obtained for 70 samples. Discordant results were observed in 15 (17.6%) of the specimens. The majority of discordant results (14/15) occurred in archived specimens that had been frozen. Fourteen discordant samples were re-tested by Luminex and in some cases an in-house PCR, and in 10/14 samples the FilmArray result was confirmed. One sample was omitted from the analysis due to insufficient volume for repeat testing. Four samples remained discordant. These were all positive by the FilmArray method and remained negative by Luminex and in-house developed PCR. After discordant analysis, the FilmArray assay had an overall agreement of 97.6%, a concordance for positive results of 100% and a concordance for negative results of 91%.

**CONCLUSIONS:** The performance of the FilmArray Respiratory Panel for the detection of respiratory pathogens in bronchoscopy specimens is in high agreement with the detection of the same pathogens by the Luminex respiratory panel.

**P61**

**A Comparison of eSwab™ and M40 Swabs for Testing for Group B Streptococcus Among Pregnant Women**

MH Yudin1,2, M Tadros1,2, J Nadarajah3,2, M Hass2, C Beatty1, V Cirone1, M Lacroix1, L deSouza1, M Geary1,2, LM Matukas1,2

1St. Michael’s Hospital, Toronto, ON, 2University of Toronto, Toronto, ON, 3Markham Stouffville Hospital, Toronto, ON

**BACKGROUND:** eSwab™ may be more sensitive than traditional culture swabs as a result of being able to collect a higher volume of cellular material. We compared culture results and ease of use for self-collected specimens for group B streptococcus (GBS) among pregnant women.

**MATERIALS AND METHODS:** Pregnant women attending the outpatient prenatal clinic at a hospital in Canada from March 2015 to December 2016 were asked...
to collect two vaginal-rectal swab specimens for GBS at 35-37 weeks gestational age: traditional M40 Transys-
tem (Copan Diagnostic Inc., California) and eSwabTM system (Copan Diagnostic, Inc., California). They were also asked to complete a short questionnaire asking about ease of use of eSwabTM. A sample size of convenience was used.

RESULTS: During the study period 185 women were tested. 42/185 (22.7%) M40 swabs were positive and 43/185 (23.2%) eSwabTM were positive for GBS. Seventy-seven per cent of women rated the eSwabTM as easy to use, and only eight per cent had issues with spillage of the fluid in the eSwabTM tube.

CONCLUSIONS: There was no significant difference in GBS culture results among pregnant women using traditional M40 swabs or eSwabTM. Most women reported that eSwabTM were easy to use. Despite literature suggesting a higher sensitivity of eSwabTM, in this population eSwabTM were not superior to traditional M40 swabs.

P62
Mandatory Infectious Disease Consultation and Adherence to an Internal Evidence-based Guideline for Candidemia: A Pre and Post Intervention Study
B GHADAKI1,2, D Mertz1
1McMaster University, Hamilton, ON; 2Niagara Health, St. Catharines, ON

OBJECTIVE: We assessed whether mandatory Infectious Disease (ID) consultation for candidemia leads to improved adherence to an internally developed evidence-based guideline that covers several components including empiric use of an echinocandin.

METHODS: At two tertiary care teaching hospitals in Hamilton, ON, an internal guideline adapted from the IDSA guideline outlining an evidence-based approach to management of candidemia and mandatory ID consultation was implemented in May 2014. We compared patients with candidemia before implementation (control group) from May 2013 to April 2014, to patients after implementation (intervention group) from May 2014 to April 2015. Outcomes included adherence to the internal guideline and patient outcomes.

RESULTS: The control and intervention group consisted of 59 and 54 patients, with a mean age of 63 and 59 years respectively. Similar rates of ICU admission (44% vs. 43%) and Charlson Index (median 2) were seen in both groups. ID involvement was similar with 97% and 100% involvement, and ID consultation within 48 hours of blood culture positivity increased non-significantly from 88% to 93%. Adherence to all components of the internal guideline was low and did not improve significantly (24% in the control and 31% in the intervention group). The individual components that contributed to low adherence were lack of ophthalmology consultation, inappropriate empiric therapy and wrong dose. Post intervention there was a significant increase in ophthalmology consultation (63% vs. 81%, p=0.042), and a non-significant change in the use of appropriate empiric antifungal therapy (54% vs. 70%), and use of the appropriate doses (71% vs. 72%). Clearance of blood cultures, relapse rates and mortality were similar in both groups.

CONCLUSIONS: Mandatory ID consultation supported by an internal guideline for management of candidemia led to improved adherence to specific components of management; however, absence of ID involvement was already rare before implementation. Citing an evidence-based protocol for management of candidemia in addition to mandatory ID consultation led to a decrease in time to ID involvement, and improved adherence to specific components of management.

P63
Escherichia coli Harbouring mcr-1 and blanDM Plasmid Genes in a Returning Traveller from China: The Importance of Coordinated Surveillance
M Croxen1, R Azana1, D Purych2, E Brodkin3, L HOANG1
1BC Centre for Disease Control Public Health Laboratory, Vancouver, BC; 2Fraser Health Authority Medical Microbiology Laboratory, Surrey, BC; 3Fraser Health Authority Infection Prevention and Control, Surrey, BC

OBJECTIVE: Colistin is one of the last antibiotics available to treat infections associated with carbapenemase producing organisms (CPO). Recently, a plasmid-mediated colistin resistance gene, mcr-1, was reported in an E. coli isolate from China and has subsequently been found in various Enterobacteriaceae isolated in foods, animals, and human infections. In BC, CPO screening
Cardiac Aspergillosis is still a fatal disease with a mortality rate of almost 90% and prognosis remains poor. Late diagnosis of the disease, its complications such as cerebral hemorrhage, and delay in the start of appropriate treatment are the major causes of poor outcome. During 13 years, a total of 7 aspergillus cases were diagnosed in our centre – a tertiary care hospital for cardiovascular diseases. In this study, clinical characteristics of aspergillosis including endocarditis, endarteritis(aortitis), graft infection, and abscess are discussed. The diagnosis was confirmed based on culture, or pathologic findings including tissue invasion by hyphae.

**RESULTS:** Three patients survived. Previous heart surgeries included: valvular surgeries (4),CABG (1), heart transplant (1), and tube graft (1). At presentation, all patients had low grade fever and were mild to moderately ill. Time interval between first surgery and infection was 1-12 months. All the patients had vegetations either on valve, perivalvular, or aortic wall. Only Aortic valve or Aortic wall was infected in all the patients. All vegetations were large (>1cm), hypermobile, and often multiple. Destruction of valve leaflets were also observed. Blood cultures in all patients were negative, but vegetation cultures in all patients were positive usually after four days of incubation. The heart transplant patient was excluded from above information as he only developed aspergillus renal abscess, blood culture and urine cultures were negative, and the heart was normal.

**CONCLUSION:** Based on our observations we recommend a pentad of clinical and paraclinical factors as clues for pre-operative pre-emptive diagnosis of fungal-Aspergillus endoarteritis: 1) History of cardiac surgery within last year, 2) Fever, 3) Negative blood cultures, 4) Large emboli, 5) Large(>1cm) hypermobile vegetation. In all patients, fatal embolic and/or rupture of mycotic aneurysm occurred during two weeks after re-operation. This period is extremely important to be aware of, because the fulminant cerebral complications may have very subtle symptoms and prompt intervention is crucial. The use of combination therapy with triazole and Echinocandins could be lifesaving.

**METHODS:** The E. coli isolate was sequenced on an Illumina MiSeq. CPO genomes were analyzed to determine intraspecies relatedness of travel and non-travel associated isolates reported to PICNet’s surveillance program. Plasmid similarity to previous BC isolates and to other publicly available plasmid data was determined.

**RESULTS:** The E. coli belonged to Sequence Type 533 (ST533) and carried the *blaNDM-5* allele. This ST533 had not been previously seen before in the BCCDC CPO database. The mcr-1 gene and *blaNDM-5* were not assembled on a contig with a plasmid replicon, so the plasmid typing could not be discerned. Plasmid types found include IncFIB, IncFIC, IncFI, IncHI, IncHI2, IncHI2A and IncX3.

**CONCLUSIONS:** While the mcr-1 was likely colonizing the patient at the time of admission, it is difficult to determine whether the *blaNDM-5* was imported or locally acquired. Coordinated CPO surveillance of genomics-level data is important to better understand the dynamics of global vs local characteristics of CPO plasmids. Carbapenemase gene detection including mcr-1 detection provides important information for patient management, infection control, and local resistance surveillance.

**P64**

**Invasive Aspergillus Infections Post Cardiac Surgery – New lessons we learned**

N ALMASSI¹, MR Rezaei², N Samiei³, MM Peighambari²

¹Rajaee Heart Center, Tehran, Iran, ²Tehran Heart Center, Tehran, Iran, ³Heart Valve Disease Research Center, Rajaee Heart Center, Tehran, Iran
CONCLUSIONS: Our novel systematic review presents a detailed summary of variables associated with EE in IE; these findings could potentially inform clinical decision-making, by facilitating risk stratification in patients being considered for early surgery.

P66
Neutropenia Rates of Antiviral Prophylaxis in CMV High Risk Solid Organ Transplant Recipients
University of Alberta, Edmonton, AB

BACKGROUND: Solid organ transplant (SOT) patients at high risk for cytomegalovirus (CMV) disease are those seronegative for CMV and receiving an allograft from a seropositive donor (D+/R-). To reduce the incidence of CMV disease, antiviral prophylaxis is indicated for 3 to 6 months in non-lung solid organ transplantation. However, its use is limited by toxicities, particularly myelosuppression.

METHODS: We conducted a retrospective study at the University of Alberta, Edmonton. We included CMV mismatch (D+/R-) adult patients (age ≥18) who received non-lung SOT, between October 2005 and December 2013. Except for kidneys, who received 6 months of antiviral prophylaxis, the remainder of the patients received a total of 3 months. We assessed treatment discontinuation and neutropenia rates of antiviral prophylaxis and its impact on CMV viremia. Follow-up period was 2 years post-transplantation.

RESULTS: We included 152 patients of which 111 (73%) were males. Mean age was 50.28 years. Of all non-lung SOT recipients that received CMV prophylaxis, 67 were liver, 52 kidney, 21 heart, 10 pancreas, 7 of which were simultaneous pancreas-kidney, and 2 multivisceral transplant recipients. Induction treatment with anti-lymphocyte antibody was administered in 22 patients (15%), of which 17 (77%) were heart transplant recipients. A total of 35 (23%) SOT patients had adverse effects, of which 22 (63%) had neutropenia. Eight (36%) of the neutropenia cases, required granulocyte-colony stimulating factor. Neutropenia was more common in liver (19.4%) and in kidney (13.5%) transplant recipients. No episodes of neutropenia were
Abstracts

P68
Investigating the Epidemiology of Resistance and Virulence Genes in Listeria monocytogenes using BioNumerics® 7.6
B WEST, K Vranckx, K De Bruyne, H Pouseele
Applied Maths, Sint-Martens-Latem, Belgium

INTRODUCTION: Listeria monocytogenes is a ubiquitous organism in the environment and a rare cause of human disease. Though listeriosis occurs infrequently, it is characterized by a high case-fatality rate which can exceed 30% percent. However, the virulence of L. monocytogenes is not investigated in routine surveillance as every isolates in food or clinical setting is considered problematic. Determination of resistance is also performed very infrequently as resistance is rarely encountered. Therefore, our knowledge on the frequency of known virulence and resistance genes in L. monocytogenes is limited.

PURPOSE: As more and more whole genomes become available from surveillance, this data can be used to make an extensive study on the epidemiology of known resistance and virulence genes.

METHODS: Publically available sequence read sets of more than 10,000 L. monocytogenes isolates were batched and then sent for reporting purposes. Following implementation of the system on Nov 4, 2016, both manual/traditional and automatic methods for surveillance were performed in duplicate to ensure reliability and accuracy of the system.

RESULTS: Following implementation, there have been zero HAI in our hospital, measured via both traditional and automated surveillance systems making it difficult to evaluate the accuracy of the system.

CONCLUSION: An automated EHR HAI detection system was successfully implemented at our institution. Future work will look at applying further logic to the system, defined by the rules put forth by the National Healthcare Safety Network to improve identification of HAI. Furthermore, our text search analytics will need to be improved to recognize the difference between terms such as “purulence” and “no purulence” when identifying SSI. Once optimized, further metrics will be used to evaluate the effectiveness of our system.
assembled on the BioNumerics Calculation engine using SPAdes. With a blast algorithm integrated in the sequence extraction tool of BioNumerics 7.6, all known virulence and resistance genes were extracted from these whole genome sequences.

RESULTS: The BioNumerics® 7.6 software and its integrated calculation engine offer a powerful platform where whole genome data analysis can be performed and validated against traditional data such as MLST or PFGE, as well as phenotypic data. The virulence genes and resistance genes could be easily extracted and matched the phenotype of the strain, when known. This tool therefore provides the possibility to extract more knowledge in an easier way from publicly available data and prepares for the development of tools similar to ResFinder, VirFinder, etc. applied to Listeria.

P69 Provider Education Strategies to Decrease Ciprofloxacin Prescriptions in Patients with Acute Uncomplicated Cystitis

J DICKTER1, R Guo2, D Nguyen2, K Nguyen2, S Park2, S Ko2, V Chiu2, P Cho2

1City of Hope, Duarte, CA, USA, 2Kaiser Permanente, Fontana, CA, USA

BACKGROUND: Fluoroquinolones are not recommended as first line therapy for treating acute uncomplicated urinary tract infections (AUC), but clinicians continue to prescribe them inappropriately. We investigate whether intervention by clinician education decreases ciprofloxacin prescriptions for AUC.

METHODS: This is a non-blinded quasi-experimental study to assess whether intensive clinician intervention through a multifaceted program of education, oversight and ongoing direct feedback can reduce prescriber choice of ciprofloxacin for AUC. Primary care providers were enrolled in two arms: control group, and intervention group. Prescription habits were compared at baseline (12 months), during the intervention period (8 months), and during the post-intervention period (7 months). For the primary endpoint, our hypothesis is that intensive monitoring and educational interventions will reduce inappropriate prescription of ciprofloxacin. Ciprofloxacin prescriptions were compared using a Chi-square test during the baseline, intervention, and post-intervention periods. Odds ratios (OR) of prescribing ciprofloxacin at baseline, during the intervention period, and during the post-intervention period were calculated.

RESULTS: 116 providers were enrolled. Baseline characteristics for providers in each group were similar. Baseline rates of ciprofloxacin use were comparable: control group 33.7%, intervention group 29.7% [OR, 0.87; 95% confidence interval (CI), 0.57-1.34; p=0.5307]. During the intervention period, there was a statistically significant decrease in ciprofloxacin prescription rates comparing the intervention group at baseline (29.7%) and after intervention (25.0%), (OR, 0.32; 95% CI, 0.22-0.47, p<0.0001). There was also a statistically significant decrease in ciprofloxacin prescription rates comparing the intervention group (25.0%) vs the control group (31.1%), (OR 0.27; 95% CI, 0.15-0.47; p<0.0001). There continued to be a statistically significant decrease in ciprofloxacin prescriptions at baseline (29.7%) compared to the post-intervention group (10.8%), (OR 0.29; 95% CI, 0.2-0.44; p<0.0001).

CONCLUSIONS: We show in a non-blinded quasi-experimental study that intensive prescription monitoring and provider feedback resulted in a significant reduction of ciprofloxacin use, which lasts throughout the intervention period and 7 months thereafter. This study shows the importance of developing education programs to decrease inappropriate fluoroquinolone use.

P70 Severe Human Respiratory Bocavirus Infection; Time to Acknowledge It!

S NASSIR, S Malik

Hereford County hospital, Hereford, UK

BACKGROUND: Human Bocavirus (HBoV) was first isolated in 2005 from respiratory secretions in Sweden. It is thought that, HBoV is the fourth commonest virus found in paediatric respiratory samples after Adenoviruses, Rhinoviruses and Respiratory Syncytial Virus. True pathogenicity of HBoV as a sole pathogen in respiratory tract infections has been largely obscured by the fact that HBoV is frequently found simultaneously with other respiratory viruses. Evidence is now mounting to show that HBoV is an important cause of lower respiratory tract illness and can cause significant respiratory illness in the young paediatric populations. We present the
case of a 16-month-old girl who was previously healthy fully vaccinated. She presented with moderate respiratory distress and quickly deteriorated within 24 hours needing intensive care. The only pathogen grown in her microbiology was of HBoV at a tertiary pediatrics centre. This article adds to evidence of HBoV virulence and this kind of acute deterioration has been described before with HBoV.

**RESULTS:** This virus as in our case, and the other cases mentioned was the sole pathogen isolated and causing the life threatening respiratory infection. In all the cases, the rate of deterioration was dramatically fast and may be a feature of this virus. In our case, the rate of improvement was equally speedy.

**CONCLUSIONS:** The reason for us to write up this case is firstly, microbiology labs do not look for it in the initial virology screen of respiratory secretions. Secondly we were pleasantly surprised with the dramatic rate of improvement. This child with a very alarming CXR needed less than 6 days stay at hospital and 3 of them were in PICU. Hence we looked at the literature to see if the dramatic speed of deterioration and the subsequent rate of improvement was a feature of HBoV. We come across similar cases of life threatening respiratory infections caused by HBoV. The paediatric community is not well aware of this virus, and this indeed is not included in the virology screening panel of many hospitals. The purpose of this report is to raise awareness of this otherwise unfamiliar virus.

**P71**  
**Risk Factors for Mortality in Patients with *Pseudomonas aeruginosa* Bacteremia**  
D YAHAV1,2, Y Weissman1,2, L Leibovici1,2  

1Rabin Medical Center, Beilinson Hospital, Petah-Tikva, Israel,  
2Sackler Faculty of Medicine, Tel Aviv University, Tel-Aviv, Israel

**OBJECTIVES:** To identify risk factors for short term mortality (7 and 30 days mortality) and long term mortality in patients with *Pseudomonas aeruginosa* (PA) bacteremia.

**METHODS:** Retrospective cohort study including 273 adult patients hospitalized between 2009-2015 with *P. aeruginosa* bacteremia. Demographic and clinical data were collected from medical charts. The study hypotheses were tested using standard statistical analyzes.

**RESULTS:** Thirty-day mortality rate was 37.7% (103/273); seven-day mortality rate was 19.1% (52/273); and median survival was 85 days (interquartile range (IQR): 11-622.75). Median age was 71 (IQR: 58-80) years. Variables associated with 30-day mortality in multivariate analysis were: unknown/ pulmonary source (odds ratio (OR) 4.02, 95% confidence interval (CI): 2.144-7.542), lower albumin (OR 2.923; 95% CI: 1.644-5.208), neutropenia (OR 3.032; 95% CI: 1.134-8.107), reduced functional capacity (OR 2.484, 95% CI: 1.319-4.677) and higher Charlson comorbidity index (OR 1.149, 95% CI: 1.014-1.302). In 7-day mortality multivariate analysis, unknown/ pulmonary source (OR 5.816, 95% CI: 2.826-11.97), reduced functional capacity (OR 3.057, 95% CI: 1.509-6.192) and higher Charlson comorbidity index (OR 1.172, 95% CI: 1.022-1.345) were found to be independent predictors of mortality. Multivariate Cox regression analysis revealed that older age (>65), reduced functional capacity, higher Charlson comorbidity index (>6) and unknown/ pulmonary source were independent predictors of long term mortality.

**CONCLUSIONS:** Among patients with PA bacteremia, baseline general condition of the patient, as expressed by functional capacity and comorbidities, is an independent predictor of both short and long term mortality. Pulmonary/ unknown source also predicts short and long term mortality. Low albumin levels and neutropenia predicts 30 days mortality. Baseline condition of patients with PA bacteremia is the main factor in predicting outcome of this fatal infection. Due to the irreversibility of these risk factors efforts should probably focus on prevention of infection.

**P72**  
**Is the Time Ripe to Begin Routine Susceptibility Testing for *Candida albicans* Isolated from Blood Stream Infections?**  
S CHOUDHURY

Tan Tock Seng Hospital, Singapore, Singapore

Antifungal susceptibility (AFS) testing is being increasingly used to guide the management of candidiasis. At our 1500 bedded hospital in Singapore, AFS has conventionally been performed on index bloodstream isolates of non-*albicans* species employing the Sensititre YeastOne™ (TREK Diagnostics, Cleveland OH). In 2014 susceptibility testing was extended to *Candida albicans* at our laboratory to cater to the demand for a more
comprehensive testing. The IDSA 2016 guidelines recommend susceptibility testing to azoles for “all” Candida spp. (strong recommendation; low-quality evidence) from bloodstream infections. This superseded previous guidelines wherein a routine susceptibility test was not warranted for *C. albicans*.

I endeavored to measure its impact on this pathogen deemed largely sensitive to the azoles. Data from the Laboratory Information System was used to identify the susceptibility profiles for all bloodstream isolates of *C. albicans* between Feb 2014 and Dec 2016. During this period 188 patients were candidemic. A susceptibility test was performed on 152 isolates. Patients who had expired or were discharged/transferred to a neighboring facility were excluded from the analysis. While non-*albicans* constituted the majority (*C. glabrata* (n=45), *C. tropicalis* (n=27), *C. parapsilosis* (n=8), *C. krusei* (n=2) and *C. guillermondii* (n=1)), *C. albicans* comprised more than a third (n=53) of all isolates subjected to a susceptibility testing. All but three isolates of *C. albicans* were susceptible to the azoles. Fluconazole/voriconazole MICs for the two susceptible dose-dependent and the resistant strains were 4 mg L⁻¹/0.25 mg L⁻¹ and 8 mg L⁻¹/1 mg L⁻¹ respectively. The three patients with non-susceptible strains had no documented history of exposure to anazole.

Apart from being expensive (approx. 100 USD/isolate), AFS testing remains cumbersome and is labor intensive without automation. Potential cost savings could be enormous since *C. albicans* comprised 40% of the isolates subjected to an in vitro testing. Susceptibility testing for *C. albicans* at our centre may be reserved for patients not responding to empirical therapy and/or with a history of recent exposure to azoles while representative isolates should be tested to monitor emerging resistance.
### AUTHOR INDEX

<table>
<thead>
<tr>
<th>Author</th>
<th>Initials</th>
<th>Page(s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Abdesselam K</td>
<td>B05</td>
<td></td>
</tr>
<tr>
<td>Adachi D</td>
<td>H01</td>
<td></td>
</tr>
<tr>
<td>Adam HJ</td>
<td>G01, H04,S, P02, P04, P12, P13, SP07</td>
<td></td>
</tr>
<tr>
<td>Adhikarl N</td>
<td>P65, SP13, SP38</td>
<td></td>
</tr>
<tr>
<td>Adie K</td>
<td>P36</td>
<td></td>
</tr>
<tr>
<td>Adomako K</td>
<td>A02</td>
<td></td>
</tr>
<tr>
<td>Al Dufairi F</td>
<td>P49</td>
<td></td>
</tr>
<tr>
<td>Alattas N</td>
<td>IP06</td>
<td></td>
</tr>
<tr>
<td>Albaradi BA</td>
<td>SP05</td>
<td></td>
</tr>
<tr>
<td>Alexandre S</td>
<td>I04</td>
<td></td>
</tr>
<tr>
<td>Alfaraidi H</td>
<td>SP06</td>
<td></td>
</tr>
<tr>
<td>Alghamdi S</td>
<td>SP32</td>
<td></td>
</tr>
<tr>
<td>Ali S</td>
<td>A01.S, P44</td>
<td></td>
</tr>
<tr>
<td>Alimohammadi A</td>
<td>P19</td>
<td></td>
</tr>
<tr>
<td>Allen V</td>
<td>A02, SP18</td>
<td></td>
</tr>
<tr>
<td>Allison J</td>
<td>SP26</td>
<td></td>
</tr>
<tr>
<td>Almassi N</td>
<td>P64</td>
<td></td>
</tr>
<tr>
<td>Almohri H</td>
<td>L01, P52, P53</td>
<td></td>
</tr>
<tr>
<td>Al-Salman A</td>
<td>SP16</td>
<td></td>
</tr>
<tr>
<td>Amarantunga K</td>
<td>B04, B05, K05, I04, P32, P39</td>
<td></td>
</tr>
<tr>
<td>Amemiya Y</td>
<td>P29</td>
<td></td>
</tr>
<tr>
<td>Andany N</td>
<td>IP05</td>
<td></td>
</tr>
<tr>
<td>Andonov A</td>
<td>F01</td>
<td></td>
</tr>
<tr>
<td>Aral S</td>
<td>SP18</td>
<td></td>
</tr>
<tr>
<td>Armen H</td>
<td>IP10</td>
<td></td>
</tr>
<tr>
<td>Armstrong I</td>
<td>G05, SP30</td>
<td></td>
</tr>
<tr>
<td>Arnason T</td>
<td>F01</td>
<td></td>
</tr>
<tr>
<td>Aslanian P</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Asplin R</td>
<td>SP25</td>
<td></td>
</tr>
<tr>
<td>Aubin MJ</td>
<td>F02</td>
<td></td>
</tr>
<tr>
<td>Auk B</td>
<td>A05, P31, P36, P37, P38</td>
<td></td>
</tr>
<tr>
<td>Austin PC</td>
<td>P54</td>
<td></td>
</tr>
<tr>
<td>Avery B</td>
<td>G04</td>
<td></td>
</tr>
<tr>
<td>Avril M</td>
<td>SP48</td>
<td></td>
</tr>
<tr>
<td>Azana R</td>
<td>G07, P37, P47, P63</td>
<td></td>
</tr>
<tr>
<td>Aziz T</td>
<td>SP40</td>
<td></td>
</tr>
<tr>
<td>Bernard KA</td>
<td>P15, SP41</td>
<td></td>
</tr>
<tr>
<td>Bernat K</td>
<td>D02</td>
<td></td>
</tr>
<tr>
<td>Bernier A-M</td>
<td>P15</td>
<td></td>
</tr>
<tr>
<td>Bhargava R</td>
<td>IP09</td>
<td></td>
</tr>
<tr>
<td>Bhatia A</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Bhatnagar M</td>
<td>IP10</td>
<td></td>
</tr>
<tr>
<td>Biederman K</td>
<td>P25</td>
<td></td>
</tr>
<tr>
<td>Bignell M</td>
<td>SP14</td>
<td></td>
</tr>
<tr>
<td>Blinn H</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Bloom J</td>
<td>IP08</td>
<td></td>
</tr>
<tr>
<td>Boerlin P</td>
<td>G04</td>
<td></td>
</tr>
<tr>
<td>Bogaty C</td>
<td>P20</td>
<td></td>
</tr>
<tr>
<td>Boissonneault V</td>
<td>J01.S</td>
<td></td>
</tr>
<tr>
<td>Bombassaro AM</td>
<td>P25</td>
<td></td>
</tr>
<tr>
<td>Bonnett J</td>
<td>B02</td>
<td></td>
</tr>
<tr>
<td>Borgia S</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Borgundvaag E</td>
<td>SP30, G05</td>
<td></td>
</tr>
<tr>
<td>Borlang J</td>
<td>F01</td>
<td></td>
</tr>
<tr>
<td>Boswell J</td>
<td>P33</td>
<td></td>
</tr>
<tr>
<td>Boutin C-A</td>
<td>F05.S</td>
<td></td>
</tr>
<tr>
<td>Boychuk LR</td>
<td>P41</td>
<td></td>
</tr>
<tr>
<td>Boyd S</td>
<td>B03.S, SP26</td>
<td></td>
</tr>
<tr>
<td>Boyd D</td>
<td>G04</td>
<td></td>
</tr>
<tr>
<td>Boyle K</td>
<td>P65, SP13, SP38</td>
<td></td>
</tr>
<tr>
<td>Brancato J</td>
<td>D01</td>
<td></td>
</tr>
<tr>
<td>Brazier AJ</td>
<td>SP48</td>
<td></td>
</tr>
<tr>
<td>Bresee L</td>
<td>P06</td>
<td></td>
</tr>
<tr>
<td>Broady R</td>
<td>I06, P42</td>
<td></td>
</tr>
<tr>
<td>Brodkin E</td>
<td>G06, G07, P63</td>
<td></td>
</tr>
<tr>
<td>Bronskill SE</td>
<td>P54</td>
<td></td>
</tr>
<tr>
<td>Brooks A</td>
<td>E03, SP15</td>
<td></td>
</tr>
<tr>
<td>Brooks S</td>
<td>H02</td>
<td></td>
</tr>
<tr>
<td>Broukhansi G</td>
<td>A02</td>
<td></td>
</tr>
<tr>
<td>Brown SZ</td>
<td>P40</td>
<td></td>
</tr>
<tr>
<td>Bryce E</td>
<td>I06, L04, P42, P60</td>
<td></td>
</tr>
<tr>
<td>Bull A</td>
<td>G01</td>
<td></td>
</tr>
<tr>
<td>Burchell A</td>
<td>SP18</td>
<td></td>
</tr>
<tr>
<td>Burzd T</td>
<td>SP41</td>
<td></td>
</tr>
<tr>
<td>Burt K</td>
<td>SP26</td>
<td></td>
</tr>
<tr>
<td>Burton D</td>
<td>H01</td>
<td></td>
</tr>
<tr>
<td>Burton J</td>
<td>SP10</td>
<td></td>
</tr>
<tr>
<td>Bush K</td>
<td>B04</td>
<td></td>
</tr>
<tr>
<td>Caswell D</td>
<td>D03</td>
<td></td>
</tr>
<tr>
<td>Cervera-Alvarez C</td>
<td>I01.S, P66, SP33</td>
<td></td>
</tr>
<tr>
<td>Chahal D</td>
<td>SP01</td>
<td></td>
</tr>
<tr>
<td>Chaili N</td>
<td>D04</td>
<td></td>
</tr>
<tr>
<td>Chalabi Y</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Champagne S</td>
<td>P10, SP35</td>
<td></td>
</tr>
<tr>
<td>Chan W</td>
<td>SP09</td>
<td></td>
</tr>
<tr>
<td>Chandran AU</td>
<td>E02.S</td>
<td></td>
</tr>
<tr>
<td>Charbonney E</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Charlton C</td>
<td>C02</td>
<td></td>
</tr>
<tr>
<td>Chau D</td>
<td>A02</td>
<td></td>
</tr>
<tr>
<td>Chen JC</td>
<td>G07</td>
<td></td>
</tr>
<tr>
<td>Cheng MP</td>
<td>SP31</td>
<td></td>
</tr>
<tr>
<td>Chernesky M</td>
<td>J04, J05</td>
<td></td>
</tr>
<tr>
<td>Cho S</td>
<td>P69</td>
<td></td>
</tr>
<tr>
<td>Choi K</td>
<td>I04</td>
<td></td>
</tr>
<tr>
<td>Chong M</td>
<td>K03</td>
<td></td>
</tr>
<tr>
<td>Choudhury S</td>
<td>P72</td>
<td></td>
</tr>
<tr>
<td>Chouinard M</td>
<td>P18</td>
<td></td>
</tr>
<tr>
<td>Chow R</td>
<td>P38</td>
<td></td>
</tr>
<tr>
<td>Chu K</td>
<td>D04</td>
<td></td>
</tr>
<tr>
<td>Chui L</td>
<td>A01.S, A03, P05, P44</td>
<td></td>
</tr>
<tr>
<td>Church D</td>
<td>L03.S</td>
<td></td>
</tr>
<tr>
<td>Ciccottelli W</td>
<td>A02</td>
<td></td>
</tr>
<tr>
<td>Cirone V</td>
<td>P61</td>
<td></td>
</tr>
<tr>
<td>Clark S</td>
<td>SP21</td>
<td></td>
</tr>
<tr>
<td>Coburn B</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Cohen G</td>
<td>P65, SP13, SP38</td>
<td></td>
</tr>
<tr>
<td>Coleman B</td>
<td>G05, SP30</td>
<td></td>
</tr>
<tr>
<td>Coleman T</td>
<td>SP16</td>
<td></td>
</tr>
<tr>
<td>Collet JC</td>
<td>B04, I04</td>
<td></td>
</tr>
<tr>
<td>Conly JM</td>
<td>B02, B05, P07, SP44, IP10</td>
<td></td>
</tr>
<tr>
<td>Conroy A</td>
<td>IP09</td>
<td></td>
</tr>
<tr>
<td>Conway B</td>
<td>P19, P27</td>
<td></td>
</tr>
<tr>
<td>Cook DJ</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Cook D</td>
<td>D04</td>
<td></td>
</tr>
<tr>
<td>Cooper R</td>
<td>SP19</td>
<td></td>
</tr>
<tr>
<td>Courtice R</td>
<td>SP37</td>
<td></td>
</tr>
<tr>
<td>Craig J</td>
<td>IP05</td>
<td></td>
</tr>
<tr>
<td>Craven L</td>
<td>SP10</td>
<td></td>
</tr>
<tr>
<td>Crocker A</td>
<td>I05</td>
<td></td>
</tr>
<tr>
<td>Croxen M</td>
<td>G06, G07, I06, P16, P37, P42, P47, P63</td>
<td></td>
</tr>
<tr>
<td>Cudek E</td>
<td>P23</td>
<td></td>
</tr>
<tr>
<td>Dagnone R</td>
<td>K04.S</td>
<td></td>
</tr>
<tr>
<td>Dale L</td>
<td>E05</td>
<td></td>
</tr>
<tr>
<td>Daley P</td>
<td>B03.S, P34, SP26</td>
<td></td>
</tr>
<tr>
<td>Dalton BR</td>
<td>B02</td>
<td></td>
</tr>
<tr>
<td>Dalton J</td>
<td>B03.S</td>
<td></td>
</tr>
<tr>
<td>Dagnone R</td>
<td>K04.S</td>
<td></td>
</tr>
<tr>
<td>Daniel P</td>
<td>E05</td>
<td></td>
</tr>
<tr>
<td>Daley P</td>
<td>B03.S, P34, SP26</td>
<td></td>
</tr>
<tr>
<td>Dalton BR</td>
<td>B02</td>
<td></td>
</tr>
<tr>
<td>Dalton J</td>
<td>B03.S</td>
<td></td>
</tr>
</tbody>
</table>

---

*Journal officiel de l'Association pour la microbiologie médicale et l'infectiologie Canada* 2.Supplément, 2017
<table>
<thead>
<tr>
<th>Abstracts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hoang L G04, G06, G07, I06, J04, P37, P42, P47, P60, P63</td>
</tr>
<tr>
<td>Hoban DJ G01, H04.5, P12, SP07</td>
</tr>
<tr>
<td>Hogan C P09, SP17</td>
</tr>
<tr>
<td>Hollenberg MD SP48</td>
</tr>
<tr>
<td>Holm M E03</td>
</tr>
<tr>
<td>Horsman GB J02</td>
</tr>
<tr>
<td>Hosford K G06</td>
</tr>
<tr>
<td>Hossein-Moghaddam S K04.5</td>
</tr>
<tr>
<td>Hota S C01, L05, I04</td>
</tr>
<tr>
<td>Houston S SP43</td>
</tr>
<tr>
<td>Hovhannisyan G SP16</td>
</tr>
<tr>
<td>Hughes S SP47</td>
</tr>
<tr>
<td>Hui-Chih Wu J P57</td>
</tr>
<tr>
<td>Hull M C05, SP03</td>
</tr>
<tr>
<td>Hutt K K04.5</td>
</tr>
<tr>
<td>Hwang D SP21</td>
</tr>
<tr>
<td>Ijaz MK P56</td>
</tr>
<tr>
<td>Irfan N E03</td>
</tr>
<tr>
<td>Irwin R G04</td>
</tr>
<tr>
<td>Ismail A SP08</td>
</tr>
<tr>
<td>Iugovaz I SP08</td>
</tr>
<tr>
<td>Ivany A K05</td>
</tr>
<tr>
<td>Jacka S P41</td>
</tr>
<tr>
<td>Jackson C D02</td>
</tr>
<tr>
<td>Jadavji T SP04</td>
</tr>
<tr>
<td>Jafri H SP40</td>
</tr>
<tr>
<td>Jain S K04.5</td>
</tr>
<tr>
<td>Jamal A SP30</td>
</tr>
<tr>
<td>Jang D J04, J05</td>
</tr>
<tr>
<td>Jassem A D04, H05, P38, SP35, P60</td>
</tr>
<tr>
<td>Jaworski L F02</td>
</tr>
<tr>
<td>Jayaratne P G03, P43, SP06</td>
</tr>
<tr>
<td>Jayasinghe K G05, SP30</td>
</tr>
<tr>
<td>Jeffs L P54, P59</td>
</tr>
<tr>
<td>Jiao L SP05</td>
</tr>
<tr>
<td>Joffe AM E01.5</td>
</tr>
<tr>
<td>John M B04</td>
</tr>
<tr>
<td>Johnston BL B04</td>
</tr>
<tr>
<td>Johnstone J A02, G05, SP30, SP36</td>
</tr>
<tr>
<td>Joy T SP10</td>
</tr>
<tr>
<td>Joyce J P34</td>
</tr>
<tr>
<td>Juba M P45, P46</td>
</tr>
<tr>
<td>Kabbani D P66, SP33</td>
</tr>
<tr>
<td>Kadivar K D03</td>
</tr>
<tr>
<td>Kadkhoda K D01, D03</td>
</tr>
<tr>
<td>Kain K IP09</td>
</tr>
<tr>
<td>Kalina D SP40</td>
</tr>
<tr>
<td>Kamhuka L IP01</td>
</tr>
<tr>
<td>Kan T K01</td>
</tr>
<tr>
<td>Kandel C SP24</td>
</tr>
<tr>
<td>Kang KT SP47</td>
</tr>
<tr>
<td>Kanji JN I03, I05, P40, P41</td>
</tr>
<tr>
<td>Karlowsky JA H04.5, SP07, P02, P04, P13</td>
</tr>
<tr>
<td>Kasper K C05</td>
</tr>
<tr>
<td>Kassam S P04</td>
</tr>
<tr>
<td>Katz KC A02, B05, G05, I04, K05, SP30</td>
</tr>
</tbody>
</table>
Microbiota Therapeutics Outcomes Program (MTOP)

C01, L05

Mihara K
SP48

Mill C
K03

Milloy M-J
SP03

Milner DA
SP48

Mineau S
I02.5

Minion J
I04, P32

Minnema B
K01

Mishra S
SP18, SP20, SP22

Mohamed M
SP09

Moennddin R
IP08

Montgomery C
J03

Moore D
I04, P30

Moquet N
SP20, SP22

Mori J
G07

Morris AM
P54, P59, IP08

Morris-Rice S
IP07

Morseshed M
J03, P16, P17, P36

Mubareka S
P29, SP45, IP11

Mukkala AN
SP39

Muller M
G05, SP30

Muller MP
IP04

Mulvey MR
G04, G06, G07, I03, P32, P39, SP07

Munirama R
I04

Murphy D
F05.S

Muscedere J
B01

Musianski L
SP27

Musielak L
SP15

Musielak L
IP04

Musley E
P41

N

Nadarajah J
P61

Nadeem SG
P58

Nadolny E
A02

Nagai E
L01, P53

Naidu P
J04, L02.5, P05, P51

Nakamachi Y
P59, IP08

Namasopo S
IP09

Nash J
G04

Nassir E
P70

Natori Y
SP34

Naus M
H05

Nechita V
SP39

Nettel-Aguirre A
A01.S

Ng K
C05, K02, L04

Nguyen T
SP23

Nguyen D
P69

Nguyen K
P69

Nichol K
H04.5, P12

Nix E
H07

Noseworthy E
B04

Nosova E
SP03

Nourimand A
SP39

Nunn A
H05

O

Oda J
I03

O’Donnell S
F03.S

O’Keefe J
B03.S

Olmstead A
P38

Ondro C
B02

O’Neill C
P08, SP19

Opoka R
IP09

Ormiston D
K05

Osoyse C
F01

Osman M
C02

Osterreicher L
A01.S, P44

Ostrow O
E04

P

Paccagnella A
P47

Palayew M
SP17

Palmy L
K01

Pang XL
A01.S, A04, P44

Papenburg J
P30

Paquet-Bolduc B
IP02

Park S
P69

Parker P
P21

Parkinson K
H04.S

Parra G
P35

Parsons B
A01.S, A03, P44

Parvath S
SP10

Patel S
G05, SP14, SP30, SP36, P41

Patel M
SP42

Paterson A
C01, G02, I02.5, L05

Patrick DM
E05, K03, P17

Patriquin G
SP41

Pavletic A
SP25

Payne M
P10, SP35

Pearce C
IP01, IP10

Peighambari MM
P64

Pelude L
B04, B05, K05, P32, P39

Penney C
B03.S, SP26

Peragine C
IP06

Pernica JM
SP06

Petrich A
E04

Pieroni P
P04

Pinto R
B01

Plevneshi E
P28

Pitt S
P21

Popovski Z
P45, P46

Porter C
L04

Porter V
P18, P12

Pouseele H
P68

Poutanen SM
C01, G02, G05, I02.5, L05, P01, P12, P23, P32, SP30

Powis J E
K01

Preiksaitis J
SP43

Press N
C05

Priyantha MAR
SP37

Prystajecky N
A05, P31, P36, P37
<table>
<thead>
<tr>
<th>Name</th>
<th>Affiliation</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Puddicombe D</td>
<td>SP35</td>
<td></td>
</tr>
<tr>
<td>Pudek M</td>
<td>L04</td>
<td></td>
</tr>
<tr>
<td>Purohit PK</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Purych D</td>
<td>P63</td>
<td></td>
</tr>
<tr>
<td>Qiu YY</td>
<td>A04</td>
<td></td>
</tr>
<tr>
<td>Quach C</td>
<td>B04, F03.S, I04, K05, SP11</td>
<td></td>
</tr>
<tr>
<td>Qumosani K</td>
<td>SP10</td>
<td></td>
</tr>
<tr>
<td>Sattar SA</td>
<td>P56</td>
<td></td>
</tr>
<tr>
<td>Savaryn B</td>
<td>E02.S</td>
<td></td>
</tr>
<tr>
<td>Savlov D</td>
<td>E04</td>
<td></td>
</tr>
<tr>
<td>Schembri J</td>
<td>P11</td>
<td></td>
</tr>
<tr>
<td>Science M</td>
<td>B04, I04, K05</td>
<td></td>
</tr>
<tr>
<td>Scott J</td>
<td>IP11</td>
<td></td>
</tr>
<tr>
<td>Sedman J</td>
<td>SP08</td>
<td></td>
</tr>
<tr>
<td>Sehrr B</td>
<td>F02</td>
<td></td>
</tr>
<tr>
<td>Sekirov I</td>
<td>P10</td>
<td></td>
</tr>
<tr>
<td>Seng A</td>
<td>P22</td>
<td></td>
</tr>
<tr>
<td>Senthinathan A</td>
<td>IP08</td>
<td></td>
</tr>
<tr>
<td>Seth A</td>
<td>P29</td>
<td></td>
</tr>
<tr>
<td>Shahinaz S</td>
<td>G05, SP30</td>
<td></td>
</tr>
<tr>
<td>Shafran S</td>
<td>C04.C</td>
<td></td>
</tr>
<tr>
<td>Shah S</td>
<td>K02</td>
<td></td>
</tr>
<tr>
<td>Shahi R</td>
<td>P19</td>
<td></td>
</tr>
<tr>
<td>Shakeri A</td>
<td>SP18</td>
<td></td>
</tr>
<tr>
<td>Sharma P</td>
<td>K03</td>
<td></td>
</tr>
<tr>
<td>Sherazi A</td>
<td>SP16</td>
<td></td>
</tr>
<tr>
<td>Shi P</td>
<td>D05</td>
<td></td>
</tr>
<tr>
<td>Shokoples S</td>
<td>G01, H01</td>
<td></td>
</tr>
<tr>
<td>Shirmilak G</td>
<td>C05, K02</td>
<td></td>
</tr>
<tr>
<td>Silverman M</td>
<td>K02, SP10, SP16, IP07</td>
<td></td>
</tr>
<tr>
<td>Simmonds KA</td>
<td>A03, C02, E01.S, P21</td>
<td></td>
</tr>
<tr>
<td>Simor AE</td>
<td>B05, G05, I04, K05, P18, SP12, SP30, IP05</td>
<td></td>
</tr>
<tr>
<td>Simpson Y</td>
<td>J03</td>
<td></td>
</tr>
<tr>
<td>Singh A</td>
<td>P19, P21</td>
<td></td>
</tr>
<tr>
<td>Sis B</td>
<td>SP43</td>
<td></td>
</tr>
<tr>
<td>Skinner S</td>
<td>C03, SP04</td>
<td></td>
</tr>
<tr>
<td>Sigli W</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Smieja M</td>
<td>J04, J05, P43, SP06, SP29</td>
<td></td>
</tr>
<tr>
<td>Southern Ontario Fecal Transplant (SOFT) Group</td>
<td>C01</td>
<td></td>
</tr>
<tr>
<td>Speare R</td>
<td>F04,S</td>
<td></td>
</tr>
<tr>
<td>Speicher D</td>
<td>SP29</td>
<td></td>
</tr>
<tr>
<td>Srigley JA</td>
<td>B04, G07, K05, P08</td>
<td></td>
</tr>
<tr>
<td>Smithh JD</td>
<td>SP48</td>
<td></td>
</tr>
<tr>
<td>Smyczek P</td>
<td>P21</td>
<td></td>
</tr>
<tr>
<td>Sniatynski M</td>
<td>SP37</td>
<td></td>
</tr>
<tr>
<td>So J</td>
<td>B04, K05</td>
<td></td>
</tr>
<tr>
<td>Tadros M</td>
<td>P61, SP14, IP04</td>
<td></td>
</tr>
<tr>
<td>Talamo L</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Tam B</td>
<td>SP14</td>
<td></td>
</tr>
<tr>
<td>Tam E</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Tan C</td>
<td>SP13</td>
<td></td>
</tr>
<tr>
<td>Tan DHS</td>
<td>SP18</td>
<td></td>
</tr>
<tr>
<td>Tan C</td>
<td>P65, SP38</td>
<td></td>
</tr>
<tr>
<td>Tang V</td>
<td>P37</td>
<td></td>
</tr>
<tr>
<td>Tannenbaum D</td>
<td>IP08</td>
<td></td>
</tr>
<tr>
<td>Tapiero B</td>
<td>F03.S</td>
<td></td>
</tr>
<tr>
<td>Tardig F</td>
<td>H02</td>
<td></td>
</tr>
<tr>
<td>Tarr P</td>
<td>A01.S</td>
<td></td>
</tr>
<tr>
<td>Tat-Ko J</td>
<td>SP10</td>
<td></td>
</tr>
<tr>
<td>Taylor G</td>
<td>B04, I03, I04, I05, P05</td>
<td></td>
</tr>
<tr>
<td>Tchao C</td>
<td>A05, P31</td>
<td></td>
</tr>
<tr>
<td>Terrick J</td>
<td>P04</td>
<td></td>
</tr>
<tr>
<td>Thakur SD</td>
<td>J02</td>
<td></td>
</tr>
<tr>
<td>Thampi N</td>
<td>B04, I02.S, K03, P32</td>
<td></td>
</tr>
<tr>
<td>Thirion D</td>
<td>B05</td>
<td></td>
</tr>
<tr>
<td>Thomas S</td>
<td>P28, P67</td>
<td></td>
</tr>
<tr>
<td>Thomas-Reilly RG</td>
<td>P14</td>
<td></td>
</tr>
<tr>
<td>Thompson G</td>
<td>K04.S</td>
<td></td>
</tr>
<tr>
<td>Tijet N</td>
<td>SP36</td>
<td></td>
</tr>
<tr>
<td>Tilley P</td>
<td>SP47</td>
<td></td>
</tr>
<tr>
<td>Ting J</td>
<td>SP47</td>
<td></td>
</tr>
<tr>
<td>Tipples G</td>
<td>A04</td>
<td></td>
</tr>
<tr>
<td>Toye R</td>
<td>G04</td>
<td></td>
</tr>
<tr>
<td>Tremblay J</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Trepanier JB</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Trim X</td>
<td>SP28</td>
<td></td>
</tr>
<tr>
<td>Trottier S</td>
<td>IP02</td>
<td></td>
</tr>
<tr>
<td>Trottier B</td>
<td>P27</td>
<td></td>
</tr>
<tr>
<td>Truong C</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Tsang R</td>
<td>H07</td>
<td></td>
</tr>
<tr>
<td>Tsang C</td>
<td>IP01</td>
<td></td>
</tr>
<tr>
<td>Tsang F</td>
<td>A05, P31</td>
<td></td>
</tr>
<tr>
<td>Tullis E</td>
<td>SP21</td>
<td></td>
</tr>
<tr>
<td>Turenne C</td>
<td>P02</td>
<td></td>
</tr>
<tr>
<td>Turnbull L</td>
<td>G01, P05, P51</td>
<td></td>
</tr>
<tr>
<td>Tyndall M</td>
<td>J03</td>
<td></td>
</tr>
<tr>
<td>Tyrrell G</td>
<td>I01.S, L02.S, P24</td>
<td></td>
</tr>
<tr>
<td>Ugartes-Torres A</td>
<td>L03.S</td>
<td></td>
</tr>
<tr>
<td>Ulanova M</td>
<td>H07</td>
<td></td>
</tr>
<tr>
<td>Urch B</td>
<td>IP11</td>
<td></td>
</tr>
<tr>
<td>Usman H</td>
<td>H01</td>
<td></td>
</tr>
<tr>
<td>Uyagauri Diaz M</td>
<td>P16</td>
<td></td>
</tr>
<tr>
<td>Abstracts</td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------</td>
<td></td>
<td></td>
</tr>
<tr>
<td>West B</td>
<td>P68</td>
<td></td>
</tr>
<tr>
<td>Wiens R</td>
<td>I03</td>
<td></td>
</tr>
<tr>
<td>Wijesundara NM</td>
<td>SP46</td>
<td></td>
</tr>
<tr>
<td>Wilcox E</td>
<td>B01</td>
<td></td>
</tr>
<tr>
<td>Willey BM</td>
<td>G02, G05, I02,S, L05, P01, P23, SP30</td>
<td></td>
</tr>
<tr>
<td>Wilson E</td>
<td>SP44</td>
<td></td>
</tr>
<tr>
<td>Wisely L</td>
<td>G02, G03, P28, SP28</td>
<td></td>
</tr>
<tr>
<td>Wong S</td>
<td>D05</td>
<td></td>
</tr>
<tr>
<td>Wong L</td>
<td>G06, G07</td>
<td></td>
</tr>
<tr>
<td>Wong T</td>
<td>G07, I06, L04, P42, P60, SP01</td>
<td></td>
</tr>
<tr>
<td>Wong A</td>
<td>I04</td>
<td></td>
</tr>
<tr>
<td>Wong J</td>
<td>J03</td>
<td></td>
</tr>
<tr>
<td>Wong Q</td>
<td>J03</td>
<td></td>
</tr>
<tr>
<td>Wong B</td>
<td>J04, SP18</td>
<td></td>
</tr>
<tr>
<td>Wong Q</td>
<td>P16, P36</td>
<td></td>
</tr>
<tr>
<td>Wood E</td>
<td>SP03</td>
<td></td>
</tr>
<tr>
<td>Woznow T</td>
<td>I06, P42</td>
<td></td>
</tr>
<tr>
<td>Wu W</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Wudel B</td>
<td>C05</td>
<td></td>
</tr>
<tr>
<td>Wylie J</td>
<td>J04</td>
<td></td>
</tr>
<tr>
<td>Wyndham K</td>
<td>P41</td>
<td></td>
</tr>
<tr>
<td>Xenocostas A</td>
<td>P25</td>
<td></td>
</tr>
<tr>
<td>Xie J</td>
<td>A01.S, P44</td>
<td></td>
</tr>
<tr>
<td>Yahav D</td>
<td>P71</td>
<td></td>
</tr>
<tr>
<td>Yang A</td>
<td>P65, SP13, SP38</td>
<td></td>
</tr>
<tr>
<td>Yang N</td>
<td>SP39</td>
<td></td>
</tr>
<tr>
<td>Yau Y</td>
<td>SP02</td>
<td></td>
</tr>
<tr>
<td>Yen M</td>
<td>IP12</td>
<td></td>
</tr>
<tr>
<td>Yip L</td>
<td>P29, SP45</td>
<td></td>
</tr>
<tr>
<td>Young P</td>
<td>A02</td>
<td></td>
</tr>
<tr>
<td>Yu D</td>
<td>P31</td>
<td></td>
</tr>
<tr>
<td>Yu V</td>
<td>P31</td>
<td></td>
</tr>
<tr>
<td>Yu Y</td>
<td>P43</td>
<td></td>
</tr>
<tr>
<td>Yudin MH</td>
<td>P61</td>
<td></td>
</tr>
<tr>
<td>Yuen K</td>
<td>A03</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Z</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zagorovsky K</td>
</tr>
<tr>
<td>Zahradnik M</td>
</tr>
<tr>
<td>Zapernick L</td>
</tr>
<tr>
<td>Zargar B</td>
</tr>
<tr>
<td>Zern C</td>
</tr>
<tr>
<td>Zhanel GG</td>
</tr>
<tr>
<td>Zhang Y</td>
</tr>
<tr>
<td>Zhang L</td>
</tr>
<tr>
<td>Zhao B</td>
</tr>
<tr>
<td>Zhi S</td>
</tr>
<tr>
<td>Zhou R</td>
</tr>
<tr>
<td>Zhou H</td>
</tr>
<tr>
<td>Zhuo R</td>
</tr>
<tr>
<td>Ziegler C</td>
</tr>
<tr>
<td>Zulfiqar A</td>
</tr>
</tbody>
</table>