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**ORAL PRESENTATIONS**

**Thursday, March 30**
**16:00 – 17:00 SESSION A**

**A01**
Evaluating the use of 18F-FDG PET/CT in the workup of *Staphylococcus aureus* bacteremia: a cost-utility analysis

Sean WX Ong1,2,3, Alice Zhabokritsky1, Nick Daneman1,2, Steven YC Tong1,4, Harindra Wijeysundera1,2
1University of Toronto, Toronto, ON, Canada; 2Sunnybrook Health Sciences Centre, Toronto, ON, Canada; 3University of Melbourne, Melbourne, VIC, Australia; 4Royal Melbourne Hospital, Melbourne, VIC, Australia

**OBJECTIVES:** The use of fluorine-18 fluorodeoxyglucose positron emission tomography/computed tomography (18F-FDG PET/CT) in the evaluation of patients with *Staphylococcus aureus* bacteremia (SAB) is associated with decreased mortality in observational studies. However, uptake is limited by cost and availability. We aimed to evaluate the cost-utility of PET/CT among adults hospitalized with SAB in Ontario.

**METHODS:** A cost-utility analysis was conducted using a probabilistic Markov cohort model assessing three diagnostic strategies: (1) PET/CT in all patients, (2) PET/CT in high-risk patients only, and (3) standard workup (without PET/CT) for all patients. The analysis was from the Ontario healthcare payer perspective using a lifetime horizon, with costs and utilities discounted at 1.5%/year. Primary outcomes were quality-adjusted life years (QALYs), costs, and an incremental cost-effectiveness ratio (ICER). Deterministic and probabilistic sensitivity analyses were conducted to evaluate parameter uncertainty.

**RESULTS:** Current standard of care resulted in an average of 17.09 QALYs at a cost of $209,510 per patient. This was dominated by PET/CT in high-risk patients with average 17.34 QALYs and cost of $199,561. Compared to PET/CT in high-risk patients only, PET/CT for all patients had an ICER of $72,794; however, there was a high degree of uncertainty comparing these two strategies with the existing data inputs. Results were most sensitive to the specificity of standard low-risk workup and PET/CT for detecting metastatic foci. At a willingness-to-pay threshold of $50,000/QALY, PET/CT in high-risk patients was the most cost-effective strategy in 56.9% of simulations (vs 40.2% for PET/CT in all patients).

**CONCLUSIONS:** Our findings suggest that a strategy of using PET/CT in high-risk patients is more cost-effective than the current standard of care of no PET/CT. Randomized controlled trials should be conducted to compare the use of PET/CT in all patients versus high-risk patients only.

**A02**
Impact of an adaptive palivizumab immunoprophylaxis implementation strategy on the annual respiratory syncytial virus epidemics coverage in Québec, Canada

Coralie Hardy1, Naïm Ouldali1, Antoine Lewin2, Marc Lebel1, Christian Renaud3
1Service d’infectiologie, département de pédiatrie, Centre hospitalier universitaire Sainte-Justine, Montréal, QC, Canada; 2Héma-Québec, Montréal, QC; 3Héma-Québec, Montréal, QC, Canada

**OBJECTIVES:** Since the COVID-19 pandemic, Respiratory Syncytial Virus (RSV) seasonal patterns significantly changed. Palivizumab - the current therapy - offers a temporary protection and the challenge is to synchronize the epidemic with the immunization campaign. We aimed to estimate the impact of an adaptive campaign based on real-time RSV surveillance on the epidemic coverage.

**METHODS:** We used a continuous hospital-based surveillance system of RSV, from July 2012 to March 2022, to compare two strategies of palivizumab campaign. The classic palivizumab campaign covers the same period every year, independently of the RSV circulation (1st November - 31st March) subsequently named “preestablished” palivizumab strategy. This strategy was compared to a new “adaptive” approach implemented in Quebec during 2021-22 RSV season. This approach relied on starting palivizumab administration according to the real-time RSV epidemics surveillance system. The main outcome was the proportion of RSV cases covered by the “adaptive” palivizumab immunization strategy in 2021-22 season, compared to the proportion of RSV cases that would have been covered by the “preestablished” palivizumab strategy the same year. The 2021-22 season was defined from week 31, 2021, to week 30, 2022.

**RESULTS:** In 2021-22, an unusually important RSV circulation was detected in September: 263 positive RSV tests on 3,416 patients (16.0% vs 5.5% in 2020). The “adaptive” strategy covered 70.3% (95% CI 69.5-71.0) of RSV cases detected in comparison with the “preestablished” palivizumab strategy covered 70.7% (95% CI 69.6-71.7) of RSV cases detected. In comparison, the “preestablished” palivizumab strategy was less effective in 2021-22 season with 67.8% (95% CI 66.9-68.7) of RSV cases detected.
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would have covered 29.1% (95% CI 28.1-30.2) of detected RSV cases in 2021-22 season.

CONCLUSIONS: An “adaptive” palivizumab strategy, based on real-time RSV surveillance allowed a better coverage of the RSV circulation in 2021-22, compared to a “preestablished” palivizumab strategy. In a context of worldwide changing viral epidemics this “adaptive” strategy may optimize the protection of children at risk of severe RSV infection.

A03
Retrospective cohort analysis of appropriate antibiotic use for community-acquired pneumonia in Canadian older adults

Ariana Saatchi1, Jennifer N Reid1, Salimah Z Shariff2, Marcus Povitz3, Michael Silverman4, David M Patrick1, Andrew M Morris5, James McCormack6, Manon Haverkate7, Fawziah Marra1

1University of British Columbia, Vancouver, BC, Canada; 2ICES Western University, London, ON, Canada; 3University of Calgary, Calgary, AB, Canada; 4University of Western Ontario, London, ON, Canada; 5British Columbia Centre for Disease Control, Vancouver, BC, Canada; 6University Health Network and University of Toronto, Toronto, ON, Canada

OBJECTIVES: This retrospective cohort study is the first in Canada to examine appropriate antibiotic use for community-acquired pneumonia (CAP) in older adults, by agent, dose, and duration. With the highest incidence rates reported in the most elderly populations, appropriate antibiotic use is essential to protect this vulnerable population.

METHODS: All outpatient physician visits for CAP (aged ≥65 years) identified between January 1, 2014, to December 31, 2018, in British Columbia (BC) and Ontario. Categories of prescribing were derived from existing literature and constructed for clinical relevance. Categories included: guideline adherent (first line agent, fully adherent dose/duration), clinically appropriate (non-first line agent but presence of comorbidities/drug interactions), effective but unnecessary (first line agent, excess dose/duration), undertreatment (first line agent, subtherapeutic dose/duration), and not recommended (non-first line agent in absence of comorbidities/drug interactions). Proportions of use were examined by prescribing category. Temporal trends in prescribing quality were examined using Poisson regression.

RESULTS: Over the study period 51,981 and 138,157 unique patients were identified in BC and Ontario, respectively. There were 118,606 and 317,835 total episodes of CAP per province with 46% of patients prescribed an antibiotic in BC, and 52% in Ontario. Clinically appropriate prescribing was seen in 33,486 cases in BC (60.7%) and 122,245 (74.2%) in Ontario, accounting for the most antibiotics issued, across all study years. Excess duration was the hallmark characteristic for effective but unnecessary prescribing (BC: 92%; ON: 99%). The most common duration prescribed was 7 days, followed by 10. Not recommended prescribing was minimal in both provinces, with 4% of use in Ontario, and 7% in BC.

CONCLUSIONS: Overall, three quarters of CAP-related prescribing for older adults was appropriate in Ontario, but only two thirds in BC. Shortening durations—in favour of increasing evidence for 3 to 5-day treatment presents a focused target for stewardship efforts.

A04
Characterization of mobile genetic elements present in Carbapanemese producing organisms in British Columbia, Canada using genomic analysis

Aishwarya Sridhar1,2, Dan Fornika1, Shannon Russell1, Darcy Sutherland1,2, Chris Kwan1, James Zlosnik1, William Hsiao3, Linda Hoang1,2,4

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OBJECTIVES: Carbapenemase-producing organisms (CPOs) pose serious threats to patient care and infection control as carbapenems are used as a last resort against severe nosocomial infections. Carbapenemase genes harboured on mobile transposable elements can spread through either clonal or plasmid-mediated transmission. We conducted a retrospective genomic analysis of 2800 isolates identified through the BC Provincial CPO surveillance program between 2008 - 2022 from healthcare facilities and community laboratories to understand various modes of CPO transmission.

METHODS: Whole genome sequencing was performed at the BC Centre for Disease Control - Public Health Laboratory. Raw reads were checked for quality, assembled, and species identified. MLST, carbapenemase allele typing, transposable elements typing, annotation and replicon-relaxase were predicted using MLST, Abricate, TETyper, bakta and MOB-suite. Clonal transmission analysis was performed using Snippy, Gubbins and SNP-dists. Pan-genome
MLST, maximum likelihood trees were produced using Roary and IQ-TREE.

RESULTS: The 2800 (environmental and clinical) isolates spanned 16 different genera of bacteria and 334 sequence types (ST). Six carbapenemase genes comprised of 25 alleles were identified, the majority belonging to NDM-1 (27%), NDM-5 (31%), KPC-3 (19%), OXA-181 (12%). KPCs, NDMs and OXA-181 were all identified on Tn4401, IS26 and Tn2013. A neighbor-joining tree revealed that reconstructed plasmids with the same plasmid backbone clustered together. The most common plasmid backbones observed were IncN-MOBF (KPC-3), IncL/M-MOBF (NDM-1), IncFIA-IncFIC-MOBF (NDM-5) and IncX3-MOBF (OXA-181). Clonal transmission and epidemiological analysis of sequences with the same species ST and carbapenemase allele showed ≤ 60 pairwise SNPs.

CONCLUSIONS: This study shows that CPOs circulating in BC healthcare settings and the community since 2008 have shown both clonal and plasmid-mediated dissemination of the carbapenemase allele.

ORAL PRESENTATIONS

Thursday, March 30
16:00 – 17:00 SESSION B

B01
Using a Massive-Scale database (N3C) to determine the utility of Remdesivir in the COVID-19 pandemic

Stephen Bokay Lee1,2, Shubrandu Sanjoy2, Evan French3
1University of Saskatchewan, Regina, Canada; 2Saskatchewan Health Authority, Regina, SK, Canada; 3Virginia Commonwealth University, Richmond, VA, USA

OBJECTIVES: Remdesivir, a repurposed antiviral, was investigated for COVID-19. However, the evidence has been mixed and guidelines have varied in their recommendations. Using a massive real world COVID-19 database, we studied whether remdesivir is beneficial in improving COVID-19 outcomes (DUR-32D7405, IRB/REB 21-41).

METHODS: The National COVID Cohort Collaborative (N3C) is repository encompassing 17.6 billion row-level data points from 15 million patients across 76 US institutions. N3C data is ingested through four data models (OMOP, PCORnet, TriNetX, ACT) and harmonized into OMOP 5.3.1. Data was made available in the Palantir Enclave and our samples extracted using enclave tools and SQL. Hospitalized who were aged ≥ 18+ and diagnosed with COVID-19 were extracted then divided to those who underwent remdesivir therapy and standard care. The primary outcome of interest was 28-day mortality.

RESULTS: A total of 301,101 hospitalizations with COVID-19 were identified; among these, the mean age was 56.7±17.9 years. 20.6% received remdesivir and 79.4% standard care. The 28-day mortality rate was 7.9%. The multivariable logistic regression analyses indicate that higher odds of 28-day mortality were observed in men, older-aged, white race and those with pre-COVID comorbidities: congestive heart failure, myocardial infarction, chronic lung disease, kidney disease, cancers, liver disease, peripheral vascular disease, rheumatologic disease, dementia and hemiplegia. Lower risk of 28-day mortality for those who had received remdesivir as compared to those who did not (adjusted OR: 0.85, 95% CI 0.82-0.88, p<0.001).

CONCLUSIONS: Throughout the pandemic, the role of remdesivir in inpatients was unclear. Despite commonplace use in many institutions, evidence for its utility is mixed, and even large guideline bodies differ on recommendations. Here we used real world data from the largest known sample of patients to determine whether remdesivir has an effect. Using this sample, we were able to determine that remdesivir has a significant, albeit small, reduction in mortality.

B02
Real-world effectiveness of nirmatrelvir/ritonavir use for COVID-19: A population-based cohort study in Ontario, Canada

Kevin L Schwartz1,2, John Wang1, Mina Tadrous3,4, Bradley J Langford1,4, Nick Daneman1,2, Valerie Leung1,5, Tara Gomes6,7, Lindsay Friedman1, Peter Daley7, Kevin A Brown1,2
1Public Health Ontario, Toronto, ON, Canada; 2ICES, Toronto, ON, Canada; 3Leslie Dan Faculty of Pharmacy, University of Toronto, Toronto, ON, Canada; 4Dalla Lana School of Public Health, University of Toronto, Toronto, ON, Canada; 5Toronto East Health Network, Toronto, ON, Canada; 6Li Ka Shing Knowledge Institute of St. Michael’s Hospital, Toronto, ON, Canada; 7Memorial University, St. John’s, NL, Canada

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CONCLUSIONS: Throughout the pandemic, the role of remdesivir in inpatients was unclear. Despite commonplace use in many institutions, evidence for its utility is mixed, and even large guideline bodies differ on recommendations. Here we used real world data from the largest known sample of patients to determine whether remdesivir has an effect. Using this sample, we were able to determine that remdesivir has a significant, albeit small, reduction in mortality.
OBJECTIVES: Our objective was to evaluate the real-world effectiveness of nirmatrelvir/ritonavir to prevent severe COVID-19 while Omicron and its subvariants predominate.

METHODS: We conducted a population-based cohort study in Ontario, Canada including all residents >17 years of age who tested positive for SARS-CoV-2 by PCR between 4 April and 31 August 2022. We compared nirmatrelvir/ritonavir treated patients to unexposed patients and measured the primary outcome of hospitalization from COVID-19 or all cause death, and a secondary outcome of all cause death, at 1-30 days. We used weighted logistic regression to calculate weighted odds ratios (wOR) with 95% membership intervals (CIs) using inverse probability of treatment weighting (IPTW) to control for confounding.

RESULTS: The final cohort included 177,545 patients with 8,876 (5.0%) exposed and 168,669 (95.0%) unexposed individuals. The groups were well balanced with respect to demographic and clinical characteristics after applying stabilized IPTW. Hospitalization or death was lower in the nirmatrelvir/ritonavir treated group compared to unexposed individuals (2.1% vs 3.7%, wOR 0.56; 95%CI, 0.47-0.67). In the secondary analysis, the relative odds of death was also significantly reduced (1.6% vs 3.3%, wOR 0.49; 95%CI, 0.39-0.62). The number needed to treat to prevent one case of severe COVID-19 was 62 (95%CI 43 to 80). Findings were similar across strata of age, drug-drug-interactions, vaccination status, and comorbidities.

CONCLUSIONS: Nirmatrelvir/ritonavir was associated with significantly reduced risk of hospitalization from COVID-19 and death in this observational study, supporting ongoing use of this therapeutic to treat patients with mild COVID-19 at risk for severe disease.

B03 Epidemiology of Pseudomonas aeruginosa in intensive care units: Are sink drains to blame?

Cheryl Volling1, Laura F Mataseje2, Lucía Graña-Miraglia3, Xiaoai Hu3, Sofia Anceva-Sami1, Brenda L Coleman3, Mark Downing4, Susy Hota4, Alainna J Jamal4, Jennie Johnstone1, Kevin Katz6, Jerome A Leis7, Angel X Li4, Vinayaa Mahesh8, Roberto Melano9, Matthew Muller10, Sarah Nayani10, Samir Patel10, Aimee Paterson1, Mare Pejkovska1, Daniel Ricciuto10, Asfia Sultana1, Tamara Vikulova1, Zoe Zhong1, Allison J McGeer1, David S Guttman1, Michael R Mulvey2

1Sinai Health System, Toronto, ON, Canada; 2National Microbiology Laboratory, Winnipeg, MB, Canada; 3University of Toronto, Toronto, ON, Canada; 4Unity Health, Toronto, ON, Canada; 5University Health Network, Toronto, ON, Canada; 6North York General Hospital, Toronto, ON, Canada; 7Sunnybrook Health Sciences Centre, Toronto, ON, Canada; 8Pan American Health Organization, Washington, DC, USA; 9Public Health Ontario Laboratory, Toronto, ON, Canada; 10Lakeridge Health, Oshawa, ON, Canada

OBJECTIVES: To describe the epidemiology of Pseudomonas aeruginosa (PA) in ICUs and estimate the proportion of PA ICU/healthcare-associated infections (PA-HAI) attributable to ICU sink drains.

METHODS: Prospective cohort study within a sink drain trial in 6 ICUs in Canada, where serial drain, faucet and air samples were screened for PA. HAIs were defined using CNISP/NHSN criteria. Patients' admission rectal swabs were eligible for PA screening if length-of-stay was >7 days, OR if they had 'late' swabs (collected >48 hours post-admission) OR PA clinical isolate(s) collected. Suspected ICU-acquired PA was defined as PA-positive 'late' swab(s) or clinical isolate(s) with only negative preceding swabs. Whole genome sequencing (WGS) was conducted using the Illumina platform and phylogenetic analysis performed. Suspected sink-to-patient transmission was defined as ICU-acquired PA closely related (<40 SNV) to sink (drain/air/faucet) isolates previously obtained from a room occupied by the patient.

RESULTS: Over the 10-month study, 819/4263 admissions had an admission swab screened, with 169 (20.6%) positive for PA. Seventy-three episodes of PA-HAI occurred among 61 admissions. The rate of PA-HAI was 3.37/1000 patient-days: higher following positive admission swabs (7.14 vs. 2.28/1000 patient-days, p<0.0001). PA-HAI contributed to death in 31.5% (23/73) of episodes. Fifty-seven admissions with suspected ICU-acquired PA were identified; 34/73 (46.6%) of PA-HAIs occurred in these patients. Close relationships were identified between isolates from 4 admissions with 5 PA-HAI (6.8%) and 1 readmission with PA bacteremia and isolates previously recovered from sinks in their rooms.

CONCLUSIONS: PA-HAI was more likely in patients colonized at admission, though nearly half may have acquired PA in the ICU. Five admissions appeared to have acquired PA from ICU sinks, contributing to more than 7% of PA-HAIs, though sampling limitations may have underestimated environmental-patient relationships. Sinks may be an under-recognized source of HAIs.
B04 The effect of double-masking on particulate filtration, inhalation resistance, and fit of three models of masks

Jesse Cooper¹, Marie Kim⁰, Marshall Chester¹, Torin Brockington-Tyhy¹, Emma Finlayson-Trick¹, Titus Wong¹²

¹Vancouver Coastal Health Authority, Vancouver, BC, Canada; ²University of British Columbia, Vancouver, BC, Canada

OBJECTIVES: Throughout the COVID-19 pandemic, some groups have proposed double-masking in attempts to further prevent COVID transmission compared to single (or no) masking. Currently, there is conflicting evidence as to whether this practice provides improved protection to the user, which has created inconsistent guidance. Our study sought to evaluate three performance measures [particulate filtration efficiency (PFE), inhalation resistance, and fit factor] for three types of masks [medical mask (MM), commercially available single-use mask (CM), and a reusable mask (RM)] when worn singularly or doubled.

METHODS: Each mask model was tested singularly and as a double mask for PFE (TEB-APR-STP-0059), inhalation resistance (TEB-APR-STP-0007) and fit factor (CSA Z94.4 Annex C). For the fit factor assessment, six subjects were used from the National Institute of Occupational Safety and Health (NIOSH) Bivariate Facial Panel to capture a range of facial sizes and shapes. All testing was performed in an ISO-accredited testing laboratory.

RESULTS: For all three mask models, the three performance measures (mean PFE, inhalation resistance, and fit factor) increased when double-masked and the increase in fit for all the models was statistically significant. Although double-masking increased PFE and inhalation resistance for all samples, a small number of subjects observed a decrease in fit factor when double-masking. Interestingly, the MM performed better than the CM with regards to PFE, however, the CM had significantly higher fit factor results compared with the MM.

CONCLUSIONS: Double-masking increased mean and median PFE, inhalation resistance, and fit factor within all three mask models. Our study showed that PFE performance does not necessarily translate to increased protection when worn by an individual, highlighting the importance of donning techniques. Further studies are needed to determine the clinical impact of singular vs double-masking.

ORAL PRESENTATIONS

Friday, March 31
10:30 – 11:30 SESSION C

C01 Microbiology of blood-stream infections in Ontario, Canada during COVID-19 pandemic: a retrospective, observational study

Mohammad Rubayet Hasan¹², Yasmeen M Vincent¹², Daniela L Leto¹², Huda Almohri¹²

¹LifeLabs, Toronto, ON, Canada; ²McMaster University, Hamilton, ON, Canada

OBJECTIVES: The changing epidemiology of bloodstream infections (BSI) in recent decades has been driven by many factors. Most recently, BSI epidemiology in the community and hospitals may have been impacted by mobility restrictions and increased rate of hospitalizations associated with COVID-19. In this study, we assessed the microbiology of BSI in Ontario during the COVID-19 pandemic compared to the pre-pandemic period.

METHODS: Retrospective data from blood cultures (n = 252,874) performed by Lifelabs Medical Laboratories in Ontario from January 2016 to December 2021 collected from patients attending primary care facilities and 32 hospitals across the province were utilized. Blood culture positivity rates for most frequently isolated bacterial pathogens were compared between the pre-COVID-19 period (July 2018 to March 2020) and the COVID-19 period (April 2020 to December 2021) for both community and hospitals. Chi-Square test was used to determine if the differences in proportions were significantly different.

RESULTS: Overall positivity rates of blood cultures received from the community decreased from 0.84 % to 0.67% (p=0.018) but those received from hospitals increased from 2.74% to 9.41% (p=0.000) during COVID-19. *Escherichia coli*, *Staphylococcus aureus*, Coagulase negative *Staphylococcus* species, *Salmonella* species, *Klebsiella* species and *Enterococcus* species were among the most frequently isolated organisms in blood cultures in the pre-COVID-19 period. For hospitals, the isolation rates of different organisms increased by 2-8 fold during COVID-19. For the community, no significant changes were observed except that the isolation rate of *Salmonella* species was significantly lower (p=0.0001) during COVID-19. The rates of positive blood cultures with MRSA and ESBL/AmpC producing Enterobacteriales significantly increased for hospitals, but...
C02 Rapid change in the genetic mechanism of reduced susceptibility to ciprofloxacin in *Salmonella enteritidis* from human infections and potential linkage to animal and food sources

Michael R Mulvey1,2, Amrita Bharat1,3, Ketna Mistry1, Linda Hoang1, Linda Chui1, Jessica Minion2, David Alexander4, Samir Patel7, Sadjia Bekal8, Sameh El Bailey6, Gregory J German14, David Haldane11, George Zahariadis1, Kim Zeibel1,2, Agnes Agunos6, Brent P Avery14, Richard J Reid-Smith14, Carolee Carson14

1National Microbiology Laboratory, Winnipeg, MB, Canada; 2Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, Canada; 3BC Centre for Disease Control Public Health Laboratory, Vancouver, BC, Canada; 4Alberta Provincial Laboratory for Public Health, Edmonton, AB, Canada; 5Saskatchewan Disease Control Laboratory, Regina, SK, Canada; 6. Diagnostic Services Manitoba, Winnipeg, MB, Canada; 7Public Health Ontario Laboratories, Toronto, ON, Canada; 8Laboratoire de santé publique du Québec, INSPQ, Ste-Anne-de-Beaupré, QC, Canada; 9Saint John Regional Hospital, Saint John, NB, Canada; 10Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada; 11Department of Pathology and Laboratory Medicine, Queen Elizabeth II Health Sciences Centre, Halifax, NS, Canada; 12Newfoundland Public Health Laboratory, St. John’s, NL, Canada; 13National Microbiology Laboratory, Guelph, ON, Canada; 14Centre for Foodborne, Environmental and Zoonotic Infectious Diseases, Guelph, ON, Canada

**OBJECTIVES:** Reduced susceptibility in *Salmonella enteritidis* (SE) to ciprofloxacin is a concern and we conducted this study to better understand the mechanisms of this resistance.

**METHODS:** SE isolates were collected through the Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS) between April 2017 and December 2021. Whole genome sequencing was conducted as part of PulseNet Canada and NML Guelph Reference Services Unit. AMR prediction and sequence type was determined using StarAMR. Phylogenetic analysis was conducted using the SNVPhyl pipeline.

**RESULTS:** 10,285 human isolates were analyzed with 2,284 (22.2%) having gyr mutations related to a predicted ciprofloxacin reduced susceptibility (cip-RS). 1,336 (58.5%) carried gyrA (D87Y) while 788 (34.5%) carried gyrA (D87N). There were no double mutations observed in gyrA and gyrB which would produce a predicted ciprofloxacin resistant phenotype. The proportion of isolates harbouring gyrA (D87N) decreased over the study period as follows: 2017 (237, 39.8%); 2018 (259, 31.0%); 2019 (200, 18.4%); 2020 (71, 11.9%); and 2021 (21, 5.4%), whereas the isolates harbouring the gyrA (D87Y) increased over the study period as follows: 2017 (72, 12.1%); 2018 (165, 19.8%); 2019 (397, 36.5%); 2020 (392, 65.9%); and 2021 (310, 82.9%). SNV-based phylogenomic analysis revealed the gyrA (D87N) isolates from 2017 formed a cluster (0 to 25 SNVs), whereas isolates of gyrA (D87Y) from 2021 formed a distinct cluster (0-7 SNVs) that differed by at least 420 SNVs from the 2017 gyrA (D87N) cluster. Analysis of SE predicted gyrA cip-RS in food and animal isolates from 2021 (N=16) revealed all isolates contained gyrA (D87Y) and clustered with the human 2021 gyrA (D87Y) isolates (0-21 SNVs).

**CONCLUSIONS:** Ciprofloxacin reduced susceptibility in SE is a concern as it may limit treatment of adult invasive infections. In addition, the finding that Canadian animal/food isolates are closely related may suggest transmission between animals/food and people.

C03 Incidence of vaccine-preventable invasive pneumococcal disease in younger adults with co-morbidity in the post-PCV13 era

Zoe Zhong1, Altynay Shigayeva1, Jeffrey C Kwong2, Walter HB Demczuk1, Irene Martin1, Huda Almohri3, Mark Downing4, Jonathan B Gubbay4, Kazi Hassan4, Kevin Katz4, Reena Lovinsky4, Larissa M Matukas5, Tony Mazzulli4, Anne Opavsky6, Agron Plevnishi7, Jeff Powis10, Daniel Ricciuto11, David Richardson12, Allison J McGee1

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**OBJECTIVES:** Cost-effectiveness analyses support routine use of 15- or 20-valent conjugate pneumococcal vaccines for the community, MRSA rates remained unchanged and ESBL/AmpC rates decreased significantly.

**CONCLUSIONS:** Our results suggest that there were shifts in BSI epidemiology in Ontario during the COVID-19 pandemic, both in hospitals and in the community.
(PCV) in adults 65+, those 50-64y with chronic illness, and immunocompromised adults. Whether PCV15/20 should be recommended for some adults aged 20-49 remains uncertain. We measured the incidence of invasive pneumococcal disease (IPD) in adult sub-populations aged 20-49y to support cost-effectiveness analyses.

**METHODS:** We have performed population-based surveillance for IPD since 1995 (pop’n ~4.5 M). Microbiology laboratories serving residents area report sterile site isolates of *Streptococcus pneumoniae* to a central office, with annual audits to ensure completeness. The National Microbiology Laboratory provides serotyping. Population data are from Statistics Canada, and estimates of prevalence of underlying conditions by age from ICES. We analyzed serotype specific IPD incidence for the period 2014-2021 (post-implementation of PCV13 in children).

**RESULTS:** From 1/1/2014 to 31/12/2021, 4561 episodes of IPD occurred; 2126 (47%) in persons 65+y, 1411 (31%) in persons 50-64y, and 1024 (22%) in persons 20-49y. IPD incidence in healthy adults 65+ was 5.1 and 6.7 /100,000/yr. for disease due to PCV15 and PCV20 STs, respectively. In 50–64-year-olds with underlying disease the incidence of PCV15 and PCV20 IPD was 6.6 and 8.2, respectively. In 20–49yo adults, the incidence of disease due to PCV15 and PCV20 STs (/100,000/yr) with/without underlying conditions were: healthy: 0.89 and 1.11; asthma: 0.57 and 0.83; COPD: 0.0 and 1.85; cardiac disease: 1.10 and 2.20; diabetes mellitus 3.36 and 4.29; kidney disease: 5.33 and 8.88; cancer 9.38 and 11.14; who are homeless/underhoused 50 and 67.50; who are receiving dialysis for renal failure 112 and 167; who are HIV positive or have received a solid organ/bone-marrow/stem cell transplant 33.04 and 40.36, respectively.

**CONCLUSIONS:** This information should support cost-effectiveness analysis for PCV15/PCV20 programs in 20–49-year-olds. Programs may be cost-effective for patients with kidney disease or cancer, and homeless/underhoused adults.

**C04**

**Detection of two alphacoronaviruses in bats in eastern Ontario, Canada**

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**OBJECTIVES:** Bats are key hosts for coronaviruses, some of which pose spillover risks to humans and other animals. Surveillance for bat coronaviruses in Canada remains limited, representing a critical blind spot for pandemic preparedness and bat conservation. Therefore, we began screening bats for endemic coronaviruses in Ontario, Canada.

**METHODS:** Oral swabs were collected from 40 big brown bats (*Eptesicus fuscus*), 119 little brown myotis (*Myotis lucifugus*), 31 eastern small-footed myotis (*Myotis leibii*), and 35 tri-coloured bats (*Perimyotis subflavus*) in eastern Ontario, Canada from July to September in 2020 and 2021. RNA from sample pools of 2-4 individuals were extracted and analyzed using a nested pan-coronavirus RT-PCR targeting the highly conserved RNA-dependent RNA-polymerase (RDRP) of the coronavirus genome; samples from positive pools were re-analyzed individually for confirmation. Partial RDRP sequencing was conducted on positive samples and resultant consensus sequences were identified using BLASTn, limiting the search to North American coronavirus sequences. Phylogenetic analysis was performed including alphacoronavirus genomes, with SARS-CoV-2 as an outgroup representing betacoronaviruses.

**RESULTS:** Overall, 2.5% (1/40) *E. fuscus* and 0.8% (1/119) *M. lucifugus* samples were RT-PCR-positive. Two coronaviruses from the alphacoronavirus genus were identified, with 70% similarity between the two. The sequence from the *E. fuscus* sample had 95% similarity to an *Eptesicus* bat coronavirus (EbCov) previously identified from *E. fuscus* in bats in Ontario, Canada.
Our study provides preliminary insights into coronavirus diversity in bats in a previously under-sampled region. This work provides a baseline for more rigorous surveillance, and the opportunity to understand transmission dynamics of endemic coronaviruses in a natural setting.

CONCLUSIONS: Our study provides preliminary insights into coronavirus diversity in bats in a previously under-sampled region. This work provides a baseline for more rigorous surveillance, and the opportunity to understand transmission dynamics of endemic coronaviruses in a natural setting.

ORAL PRESENTATIONS

Friday, March 31
10:30 – 11:30 SESSION D

D01
Evaluation of two inactivation protocols for malaria diagnostic testing for persons under investigation for Ebola Virus Disease

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OBJECTIVES: Diagnostic testing for individuals identified as persons under investigation (PUI) for Ebola Virus Disease (EVD) requires special biosafety precautions. Given the overlap in malaria and EVD, prompt and accurate malaria testing is required. In this study, we investigated the impact of two inactivation protocols for malaria testing: 1) one-hour heat inactivation for malaria rapid diagnostic test (RDT), and 2) adaptation of an extraction protocol with ethanol for malaria quantitative polymerase chain reaction (qPCR).

METHODS: Archived whole blood specimens were selected to represent positives across a range of species and parasitemia values, and negative controls. A one-hour, 60 °C inactivation step was performed on whole blood specimens, followed by in-house laboratory-developed malaria qPCR. Malaria detection results using each inactivation method were compared to standard procedure without inactivation.

RESULTS: For the RDT, a total of 20 samples were tested, including 10 P. falciparum, 5 non-falciparum species, and 5 negative controls. The heat inactivation procedure demonstrated sensitivity and specificity of 100% (20/20) compared to current protocol without inactivation. For the qPCR, a total of 25 specimens were tested, including 11 P. falciparum, 7 non-falciparum species, and 6 negative controls. qPCR results based on this method demonstrated sensitivity and specificity of 100% (25/25) compared to standard testing. However, there was up to 5.0 cycle increase/loss in analytical sensitivity using the ethanol inactivation method.

CONCLUSIONS: The two inactivation protocols investigated in this study align with Canadian biosafety guidelines for handling specimens from PUI for EVD and demonstrated maintained sensitivity for the qualitative detection of malaria by RDT and qPCR. These support overall utility for EVD malaria testing preparedness.

D02
Validation of the Abbott Alinity i-series for testing of Hepatitis B, Hepatitis C, and Human Immunodeficiency Virus using dried blood spots

Ashley DeBaets, Joshua Collantes, Chris Czarnecki, Christine Mesa, Philip Lacap, Karla Cachero, Braedy Farmer, Kohavit Kleitman, John Kim

Public Health Agency of Canada – National Laboratory for HIV Reference Services, Winnipeg, MB, Canada

OBJECTIVES: A substantial increase in STBBI rates during the COVID-19 pandemic has put pressure on regional health authorities to increase diagnostic and surveillance testing. Access to testing in remote, isolated, and at-risk populations can be difficult due to lack of physical and human resources. Using dried blood spots (DBS) can increase access to testing, but laboratories need an efficient way to process large numbers of these samples. The Abbott Alinity i is a multiplex immunoassay instrument designed to provide quick results for multiple targets using a single specimen. We propose a multi-assay approach using DBS samples to simultaneously test for HBV, HCV, and HIV on this instrument.

METHODS: 200+ matched plasma and directly spotted DBS samples were tested to determine an appropriate cut-off using ROC curve analysis based on the provided...
sensitivity and specificity for each assay. Precision was analyzed for both plasma and DBS eluates. The testing of result stability over time in different storage conditions is ongoing. Cross-reactivity with SARS-CoV-2 and HTLV-1/2 was also examined. Seroconversion panels contrived as DBS were used to compare the Alinity to other commercially available assays. Additionally, an inhibition panel and HBV WHO standard were contrived and tested.

RESULTS: The Alinity provides accurate results with DBS that are comparable to the gold standard – plasma – or other commercially available testing platforms and in-house developed methods. The three assays have acceptable sensitivity/specificity of 94.59%/97.37% for HBV, 95.35%/100.00% for HCV, and 99.04%/99.15% for HIV. Additionally, the variation between technicians, days, and preparation was minimal with the coefficient of variation staying low at concentrations near the cut-off.

CONCLUSIONS: Processing and testing DBS samples has previously been a time and resource consuming activity. The ability to test for HBV, HCV, and HIV from DBS as a single specimen on an open-access platform will decrease hands on time, improving TAT and efficiency.

**D03**

**Increasing perioperative cefazolin utilization for Surgical Site Infection prophylaxis in β-Lactam allergic patients**

Tariq Esmail,1,2 Mark T McIntyre,1,2 David Wong,1,2 Chantelle Nielson,1 Indira Gobin,1 Philip Liu,1 Natalia Lauzon,1 Timothy Jackson,1,2 Alon Vaisman1,2

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OBJECTIVES: A cornerstone of Surgical Site Infections (SSIs) prevention is perioperative administration of cefazolin. Historically, cefazolin was avoided in patients with a self-reported β-lactam allergy (SRBA), resulting in increased exposure to alternative antibiotics, SSI rates, toxicity, and cost. Evidence demonstrates that, using history alone, cefazolin can safely be administered in many of these patients. The aim of this quality improvement project was to increase the proportion of SRBA patients receiving cefazolin as prophylaxis for elective procedures using history alone.

METHODS: This QI intervention was conducted from 2018-2022 in a large multi-site tertiary academic centre. Our multidisciplinary team implemented the modified-ACCEPT (Allergy Clarification for Cefazolin Evidence-based Prescribing Tool), an evidence-based algorithm that safely identifies low-risk β-lactam allergic patients who could receive cefazolin using a simplified two-item questionnaire without the need for skin testing. The algorithm was administered by nurses and pharmacists in the pre-operative clinic. Anesthesiologists received notification of the assessment in the electronic record prior to surgery. Prior to implementation, educational interventions were conducted to increase understanding of antimicrobial prophylaxis. Run charts were used for the evaluation of process measures and statistical process control (p chart) was used to evaluate our outcome measure.

RESULTS: Between January 2018 and May 2022, 6023/59862 SRBA patients underwent surgery (10.1%). Baseline data (January 2018 – March 2019) showed a stable rate of cefazolin administration among SRBA patients at 23.6%, which rose to 50% after educational interventions were performed. After the modified-ACCEPT tool was implemented, there was a significant shift in the proportion of patients receiving cefazolin, up to 68.5%. By the end of the study period, the proportion of SRBA patients receiving cefazolin increased from 24% to 68% ($\chi^2 = 159.7$, p<0.0001) (Figure D03-1).

CONCLUSIONS: Implementation of a simple two-question standardized assessment of β-Lactam allergic patients and educational efforts can effectively increase the use of cefazolin among SRBA patients.
and duplicate for Cobas Liat using the multiplex SARS-CoV-2 and influenza A/B.

RESULTS: Compared to the reference method, Cobas Liat showed a sensitivity of 100 % for the detection of SARS-CoV-2 for all 108 wastewater samples. Given the widespread of SARS-CoV-2 during the study period, we were unable to obtain negative wastewater samples for SARS-CoV-2 and could not assess specificity. Reproducibility was excellent for the duplicate samples of Cobas Liat and triplicate samples of reference tests. The analytic time was greatly reduced with Cobas Liat to 30 minutes, compared to 4 hours for the reference test. Furthermore, we detected influenza A in four consecutive samples, which occurred concurrently with an outbreak in the community. Further subtyping of SARS-CoV-2 and Influenza A strains are in progress.

CONCLUSIONS: Compared to the reference test, the Cobas Liat showed 100% sensitivity to detect SARS-CoV-2 in wastewater samples, with a great reduction of turnaround time from 4 hours to 30 minutes. Simultaneous detection of influenza and SARS-CoV-2 with the multiplex targets of Cobas Liat appears promising.
Combination antibiotic therapy for persistent Staphylococcus aureus bacteremia: A retrospective analysis

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OBJECTIVES: Combination antibiotic therapy has been proposed as effective treatment for persistent Staphylococcus aureus bacteremia. We aimed to describe the utilization of combination therapy for persistent S. aureus bacteremia and compare clinical outcomes in patients treated with combination versus monotherapy.

METHODS: This retrospective cohort study included adults with persistent S. aureus bacteremia treated with any combination of antibiotics compared to monotherapy (2015 to 2022). We defined persistent bacteremia as positive blood cultures for at least 72 hours despite active antibiotics.

RESULTS: Among 100 patients analyzed, 47% received combination therapy and 53% received monotherapy. The median age was 62 years and 64% were males. Patients treated with combination therapy were younger (median 54 vs. 67 years, p=0.005), more often had MRSA bacteremia (58.3% vs. 26.9%, p<0.001), and had a lower Charlson Comorbidity Index (CCI) (median 2 vs. 4, p=0.041). The most frequent combinations were cloxacillin-ertapenem (n=5, 17%) and cloxacillin-rifampin (n=5, 17%) for MSSA and daptomycin-ceftobiprole (n=8, 15%) and vancomycin-daptomycin (n=8, 15%) for MRSA. Combination therapy was initiated a median of 7 (IQR 5 to 10) days after index blood culture result. Patients who received combination therapy had a longer duration of bacteremia compared to monotherapy (median 216 vs. 118 hours, p<0.001). The duration of bacteremia following initiation of combination therapy was a median of 3 (IQR 1 to 4) days. There were no significant differences in hospital mortality, embolic or metastatic complications, microbiological relapse, or adverse events.

CONCLUSIONS: Combination antibiotic therapy was more likely to be initiated in younger patients, those with MRSA bacteremia, and those with fewer comorbidities. Patients receiving combination therapy had a significantly longer duration of bacteremia compared to monotherapy, potentially due to confounding by indication.

P003

Real-life experience with ceftobiprole in Canada: results from the CLEAR (Canadian LEadership on Antimicrobial Real-life usage) registry

George G Zhanel, Justin Kosar, Melanie R Baxter, Rita Dhami, Sergio Borgia, Neal Irfan, Kelly MacDonald, Gordon Dow, Teagan Rolf von den Baumen, Maxime Dubé, Yoav Keynan, Anna Lee, Zain Chagla, Gabriel Girouard, Andrew Walkty, James A Karlovsky

1University of Manitoba, Winnipeg, MB, Canada; 2Royal University Hospital, Saskatoon, SK, Canada; 3London Health Sciences Centre, London, ON, Canada; 4William Osler Health System, Brampton, ON, Canada; 5Hamilton Health Sciences Centre, Hamilton, ON, Canada; 6The Moncton Hospital, Moncton, NB, Canada; 7Sainte-Croix Hospital, Drummondville, QC, Canada; 8Scarborough Health Network, Toronto, ON, Canada; 9St. Joseph’s Healthcare, Hamilton, ON, Canada; 10Dr-Georges-L.-Dumont University Hospital, Moncton, NB, Canada

OBJECTIVES: Ceftobiprole is an IV cephalosporin with broad-spectrum activity and a favourable safety profile. Published data on the clinical use of ceftobiprole are limited. We report on the use of ceftobiprole in Canadian patients using data captured by the CLEAR registry.

METHODS: A ceftobiprole usage questionnaire was developed using the input of infectious disease / medical microbiology specialists (physicians and pharmacists)
across Canada. The CLEAR registry protocol/questionnaire was submitted and received approval by the University of Manitoba Ethics Committee (April 2019). The CLEAR registry uses the web-based research data management program, REDCap™ (online survey, https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=A8EHM8JJRF) to facilitate clinicians voluntarily entering details associated with their experiences using dalbavancin.

RESULTS: Data were available for 80 patients (as of December 1, 2022). The most common infections treated with ceftobiprole were endocarditis (38.0% of patients), bone/joint infection (26.6%), and hospital-acquired bacterial pneumonia (7.6%). 94.9% of patients had bacteremia and 29.1% were in ICU. Ceftobiprole was primarily used as directed therapy for MRSA infections (96.2% of patients). Ceftobiprole susceptibility testing was performed in isolates from 38.0% of patients. It was used concomitantly with daptomycin in 48.7% of patients and with vancomycin in 26.9%. Ceftobiprole was used following treatment failure (70.9%), resistance detection (12.7%), or adverse effects/intolerance (15.2%) from initially prescribed antimicrobial agents. The dosage regimen was customized in 98.7% of patients based on their creatinine clearance. Treatment duration was primarily >10 days (65.4% of patients) with microbiological success in 92.9% and clinical success in 85.3% of patients. The 30-day mortality was 8.9%. 3.9% of patients reported an adverse effect.

CONCLUSIONS: In Canada to date, ceftobiprole is used as directed therapy to treat a variety of severe infections caused by MRSA. It is primarily used in combination with daptomycin or vancomycin, has high microbiological and clinical cure rates, and an excellent safety profile.

P004
Real-life experience with dalbavancin in Canada: results from the CLEAR (Canadian LEadership on Antimicrobial Real-life usage) registry
George G Zhanel1, Gabriel Girouard2, Rita Dhami3, Melanie R Baxter1
1University of Manitoba, Winnipeg, MB, Canada; 2Dr-Georges-L.-Dumont University Hospital, Moncton, NB, Canada; 3London Health Sciences Centre, London, ON, Canada

OBJECTIVES: Dalbavancin, an IV glycolipopeptide approved for the treatment of Acute Bacterial Skin and Skin Structure Infections (ABSSSI) was recently marketed in Canada. Its long half-life (> 200 hours) allows for single-dose treatment. We report the use of dalbavancin in Canadian patients using data captured by the CLEAR registry.

METHODS: A dalbavancin usage questionnaire was developed using the input of infectious disease/medical microbiology specialists (physicians and pharmacists) across Canada. The CLEAR registry protocol/questionnaire was approved by the University of Manitoba Ethics Committee. The CLEAR registry uses the web-based research data management program, REDCap™ (online survey, https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=TPMWJX98HL) to facilitate clinicians voluntarily entering details associated with their experiences using dalbavancin (link opened October 2022).

RESULTS: Data were available for 3 patients (as of December 1, 2022). Two patients had bone/joint infection (BJI) and 1 had ABSSSI. Dalbavancin was administered in an infectious diseases clinic, an OPAT facility or hospital ward using a short 30 min infusion. In all patients, dalbavancin was used alone as directed therapy versus MRSA. Dalbavancin was used due to failure of previous antimicrobial therapy (2 patients) or due to its convenient single-dose therapy. Two patients received a single 1500 mg dose, while one patient with BJI received 1500 mg IV on day one followed by another 1500 mg on day 8. One patient was an IV drug abuser and homeless while another had mental health issues and treatment adherence was a consideration. In all cases, microbiological eradication/presumed eradication occurred along with clinical cure/improvement with no adverse effects.

CONCLUSIONS: To date, dalbavancin is used as directed therapy to treat on-label (ABSSSI) and off-label (BJI) infections caused by MRSA. It is used alone after failure of previous antimicrobial therapy or for its single-dose treatment convenience. So far high microbiological/clinical cure rates, and an excellent safety profile have been reported.

P005
Real-life experience with IV fosfomycin in Canada: results from the CLEAR (Canadian LEadership on Antimicrobial Real-life usage) registry
George G Zhanel1, Melanie R Baxter1, Maggie Wong2, Yazdan Mirzanejad3, Anna Lee4, Rita Dhami5, Justin Kosar6, Denise Werry7, Neal Irfan8, Jean-Francois Tessier9, Gabriel Girouard10, Carlo Tascini11, Teagan Rolf von den Baumen5,12, Andrew Walkty1, James A Karlowsky1
1University of Manitoba, Winnipeg, MB, Canada; 2Fraser Health, Vancouver, BC, Canada; 3University of British Columbia, Vancouver, BC, Canada; 4Scarborough Health Network, Toronto,
OBJECTIVES: Data on the use of IV fosfomycin in Canada are limited. We report the use of IV fosfomycin in Canadian patients using data captured by the CLEAR registry.

METHODS: The CLEAR registry uses the web-based research data management program, REDCap™ (online survey, https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=F7JXNDFXEF) to facilitate clinicians entering details associated with their clinical experiences using IV fosfomycin.

RESULTS: Data were available for 59 patients treated with IV fosfomycin. Infections treated included: bacteremia/sepsis +/- a documented site of infection (25.4% of patients), complicated urinary tract infection (20.3%), ventilator-associated bacterial pneumonia (16.6%), hospital-acquired bacterial pneumonia (13.6%), complicated intraabdominal infection (10.2%), endocarditis (3.4%), bone/joint infections (3.4%), community-acquired bacterial pneumonia (3.4%), and central nervous system infection (1.7%). IV fosfomycin was used to treat Gram-negative (88.1%) or Gram-positive (10.2%) infections. The most common pathogens treated were carbapenem-resistant Enterobacteriales (CRE) (44.1%), MDR Pseudomonas aeruginosa (18.6%), vancomycin-resistant Enterococcus faecium (VRE) (5.1%), and MRSA (3.4%). IV fosfomycin was used primarily as directed therapy (88.1% patients) and typically prescribed as part of combination therapy (86.4%). Fosfomycin was prescribed due to resistance to other antimicrobial agents (69.5%), clinical failure of previous therapy (18.6%), or adverse effects associated with use of previous agents (10.2%). Microbiological success (eradication/presumed eradication) occurred in 77.4% and clinical success (clinical cure/improvement) occurred in 62.5% of patients; overall, 15.3% of patients died due to their infection. Adverse effects were not documented in 73.1% of patients and no patient discontinued therapy due to an adverse effect.

CONCLUSIONS: In Canada, IV fosfomycin is used primarily as directed therapy to treat a variety of severe infections caused by Gram-negative and Gram-positive bacteria. It is primarily used in patients infected with bacteria resistant to other agents and as part of combination therapy. Its use is associated with relatively high microbiological and clinical cure rates, and an excellent safety profile.

P006
Treating hospital-acquired, ventilated hospital-acquired and ventilatory-associated bacterial pneumonia in Canada with ceftolozane/tazobactam (C/T): Real-life experience from the CLEAR (Canadian LEadership on Antimicrobial Real-life usage) registry

George G Zhanel1, Rita Dhami2, Melanie R Baxter1, Maggie Wong1, Yazdan Mirzanejad1, Justin Kosar1, Carlos Cervera2, Neel Irfan1, Sergio Borgia1, Robert Ariano3, Michel Savoie10, Andrew Walkty1, James A Karlowsky1

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OBJECTIVES: We report the use of ceftolozane/tazobactam (C/T) in Canada to treat hospital-acquired bacterial pneumonia (HABP), ventilated hospital-acquired bacterial pneumonia (VHABP) and ventilatory-associated bacterial pneumonia (VABP) using the national CLEAR registry.

METHODS: A C/T usage questionnaire was developed to facilitate clinicians voluntarily entering details of their clinical experiences using C/T.

RESULTS: Data were available for 44 patients (as of December 6, 2022) treated with C/T. C/T was used for HABP (45.5% of patients), VHABP (9.1%) and VABP (38.6%). 9.1% of patients had bacteremia; 77.3% were in an ICU. C/T was used primarily as directed therapy but on occasion as empiric therapy for documented or eventually documented Pseudomonas aeruginosa infections (97.7% of patients). C/T susceptibility testing was performed on isolates from 90.7% of patients. C/T was used in combination with another antimicrobial active versus Gram-negative bacilli in 40.9% of patients (IV or aerosolized aminoglycosides [44.4%], IV or aerosolized colistin/polymyxin B [22.2%]...
Abstracts

and fluoroquinolones [16.6%]). C/T was used primarily because of resistance to previously prescribed antimicrobial agents (88.6%). The dosage regimen was customized in all patients based on their creatinine clearance. Treatment duration was primarily >10 days (43.2% of patients) with 44.4% microbiological success and 58.6% clinical success. Overall, 30-day mortality was 18.2%. 8.3% of patients had adverse effects not requiring drug discontinuation.

CONCLUSIONS: In Canada, C/T is used both as directed and empiric therapy when treating HABP, VABP and vHABP severe infections caused MDR P. aeruginosa. It is commonly used in combination with other antimicrobials and is associated with relatively good clinical cure rates and an excellent safety profile.

P007
Baseline prevalence of antimicrobial resistance in patients who develop a surgical site infection in hip and knee arthroplasty: A brief report

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OBJECTIVES: In Alberta, a decolonization strategy is used prior to hip and knee replacements. The decolonization strategy in Alberta includes both topical chlorhexidine gluconate (CHG) and mupirocin ointment (MO). Currently in Alberta, there is no understanding of the baseline prevalence of antimicrobial resistance (AMR) in respect the decolonization strategy. The objective is to assess the baseline prevalence of antimicrobial resistance in patients in Alberta who develop an SSI positive for SA or NAS after hip and knee replacement.

METHODS: This study assessed the carrying genes related to MO and CHG: Mup and qac. Wound tissues were collected from patients who developed a complex SSI post hip and knee arthroplasty, and any specimens positive for S. aureus or NAS. Positive specimens were tested for resistance in both MO and CHG between January 2020 to July 2021.

RESULTS: In total, we had 43 positive specimens for SSIs from our two major hip and knee clinics. Of our 43 positive specimens, 16 were positive for NAS and none were positive for SA. Of the 16 specimens positive for NAS, 10 were carrying the gene qac and 6 were carrying the gene MupA.

CONCLUSIONS: Our study investigated the baseline prevalence of AMR of patients in Alberta who develop an SSI positive for SA or NAS post hip and knee replacements. Our results had 43 positive specimens, and 16 of those specimens were positive for NAS. Our study has provided the baseline prevalence of AMR in patients who develop an SSI post hip and knee replacements in Alberta. Not only does this study give us an understanding of prevalence in Alberta, but this study can be used for ongoing AMR monitoring in the province.

P008
Clinical characteristics and management of neurosurgical device-associated ventriculitis and meningitis: a retrospective observational study

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1Department of Pharmacy, Hamilton Health Sciences, Hamilton, ON, Canada; 2Division of Infectious Diseases, Department of Medicine, McMaster University, Hamilton, ON, Canada; 3Department of Microbiology, Hamilton Regional Laboratory Medicine Program, Hamilton, ON, Canada

OBJECTIVES: To characterize the diagnostic characteristics, management, and outcomes of neurosurgical device associated ventriculitis/meningitis (NDAVM).

METHODS: Retrospective observational study of adults admitted between 2015-2021 consulted to infectious diseases for suspected NDAVM.

RESULTS: 95 patients were included (73 drain- and 22 shunt-associated infections). Median age was 54 years (interquartile range (IQR), 39, 62.5) and median Charlson Comorbidity Index was 2 (IQR 1, 4). 90% required ICU or step-up care for a median of 21 days (IQR 14, 39). The most common indication for device insertion was intracranial hemorrhage (58%). 89% of infections manifested within
Herpes zoster (HZ) occurs upon reactivation of latent varicella zoster virus. Patients with an immunocompromising (IC) condition are at increased risk of HZ and its complications. This study aims to summarize the available evidence on the HZ-related burden of disease in people with IC conditions and descriptively compare it with the HZ burden in the general population.

METHODS: A systematic literature search was performed in Embase and PubMed (Jan 2002-Jan 2022), supplemented by a grey literature search. Studies were eligible if they included outcomes of interest, including HZ incidence, recurrence and HZ-associated complications and hospitalization, in the Canadian IC population and the general population.

RESULTS: Thirty-four articles were identified, 17 focusing on IC populations, 14 on the general population and 3 including both populations. Cumulative HZ incidence (cases per 1,000 persons) ranged between 3.2 and 12.5 in the IC population and between 0.8 and 5.9 in the general population. IC conditions with the highest cumulative HZ incidence were hematologic malignancies (12.5) and hematopoietic stem cell transplantation (11.5). HZ recurrence occurred in 0-19.5% of IC people (general population: 6.1-10.2%). The highest occurrence of postherpetic neuralgia was observed in HZ patients with hematopoietic cell transplantation (4.3-42.9%), solid organ transplantation (12.5-60.0%) and systemic lupus erythematosus (55.7%). The proportion of HZ patients hospitalized varied between 1.3-36.4% in the IC population and between 0-4.0% in the general population. Within-study comparisons showed higher HZ incidence, PHN and case fatality rates in IC populations compared with the general population.

CONCLUSIONS: Canadian HZ-related burden of disease was high, especially in the IC populations, underscoring the need for preventive strategies, including vaccination. Study results are consistent with observed burden reported in other countries. This study identified knowledge gaps concerning HZ epidemiology in several IC conditions and a scarcity of studies comparing HZ burden between IC populations and the general population.

OBJECTIVES: Herpes zoster (HZ) occurs upon reactivation of latent varicella zoster virus. Patients with an immunocompromising (IC) condition are at increased risk of HZ and its complications. This study aims to summarize the available evidence on the HZ-related burden of disease in people with IC conditions and descriptively compare it with the HZ burden in the general population in Canada.

CONCLUSIONS: NDAVM is associated with often subtle and nonspecific changes in clinical status. Few clear clinical differences exist between culture-positive and negative infections. Clinical cure without repeat infection was difficult to achieve in this cohort.

Conclusions: The Choosing Wisely Guideline from the Association of Medical Microbiology and Infectious Disease Canada suggests not repeating CD4 measurements
in patients with HIV infection if the CD4 count is above 500/μL with suppressed HIV viral loads for 2 years. A chart audit in the HIV clinic at our centre found that 67% of CD4 orders were deemed to be unnecessary based on current guidelines. Our objective was to reduce CD4 count testing per patient visit in the HIV clinic by 25%.

**METHODS:** A fishbone framework for root cause analysis revealed several potential causes underlying frequent ordering of CD4 counts. A series of Plan-Do-Study-Act (PDSA) cycles were undertaken, starting with education sessions for health care providers, followed by creation of a computerized clinical decision support (CCDS) pop up that would trigger when a CD4 count was ordered less than one year since the last one. Frequency of CD4 count testing per patient visit to our clinic was the primary outcome measure. The number of times the pop up triggered per month was the process measure. The number of patients who required a CD4 count with their routine blood work but did not get one was a balancing measure.

**RESULTS:** After implementation, there was a 52% reduction in CD4 count testing per patient visit, with no adverse outcomes for patients. The CCDS was more effective than education, consistent with previous studies. The intervention represents >$23,000 annualized savings.

**CONCLUSIONS:** We present a novel and straightforward intervention that can implemented in HIV clinics and results in substantial cost savings in addition to aligning patient care with best practices.

**P011**

**Mortality outcome of Pneumocystis jirovecii pneumonia real-time PCR assay in immunocompromised patients**

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**OBJECTIVES:** The diagnosis performance of real-time PCR respiratory isolate of PJP has been validated. Otherwise, the clinical impact of PJP load in respiratory was not assessed in immunocompromised patients.

**METHODS:** A retrospective study described the clinical impact of Pneumocystis jirovecii (PJ) PCR in immunocompromised patients at University Health Network, Toronto, Canada, between Dec 2018- 2019. Baseline characteristics, mortality at 28 days, and composite outcome; intensive care admission or mechanical ventilation, were compared in immunocompromised patients. A logistic regression was evaluated to determine the association between P. jirovecii quantitative load and PJP outcome 1000 copies/ml.

**RESULTS:** A Total of 118 patients were included in this study, with male predominant 76.0 (64.4%) and median age 65.5 [21.0, 87.0]. Stem cell transplant patients 15/ 118, hematological malignancy & Lymphoma 38/118, solid organ transplants 14/118, other 50/118. Eighty-five received P. jirovecii treatment (72%), while thirty-three (27%) were not. Mortality at day 28 and the composite outcome were more seen in not treated patients [8.00 (24.2%)/ 19.0 (16.1%), 12.0 (36.4%)/ 31.0 (26.3%), respectively. SOT patients had higher mortality and composite outcome among immunocompromised patients [4.00 (28.6%), 12.0 (36.4%) p= 0.012, p<0.001, respectively]. Furthermore, 28-day mortality and composite outcome in patients with P. jirovecii PCR load >10000 copies were [6/24 (25.0%, 9/24(37.5%) (51.6%), OR = 2.05, 1.936) respectively.

**CONCLUSIONS:** Solid organ transplanted patients had a higher mortality rate among immunocompromised patients. A low PJP PCR level has been associated with poor outcomes and mortality.

**P012**

**Effectiveness of sotrovimab for COVID-19 infection due to Omicron subvariant BA.2 versus BA.1: A retrospective multi-centre cohort study**

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OBJECTIVES: Sotrovimab was a neutralizing monoclonal antibody for mild COVID-19 infection based on RCT data demonstrating decreased hospitalization or mortality through 29 days. In April 2022, sotrovimab was removed from Canadian treatment guidelines when in vitro testing suggested decreased efficacy against the BA.2 Omicron subvariant. It is unclear whether this effect is consistent in vivo. Our study compared the clinical effectiveness of sotrovimab in patients infected with Omicron BA.2 versus BA.1.

METHODS: Setting: multicentre retrospective cohort study across several hospitals in Ontario and British Columbia between 1/Feb/2022-1/Apr/2022. Study population: patients with mild COVID-19 infection at high risk of progression to severe disease who received sotrovimab and had whole genome sequencing to identify the Omicron subvariant as either BA.2 or BA.1. Co-primary outcomes: hospitalization due to COVID-19, all-cause ICU admission, and all-cause mortality within 30 days. Analysis: matched-propensity score (1:1 ratio of BA.2 and BA.1 patients) based on logistic regression of prognostic factors including: age, sex, immunocompromise, vaccination status, and number of risk factors for progression to severe disease.

RESULTS: Eighty-five patients with COVID-19 (70 BA.1; 15 BA.2) were included. Hospitalization due to COVID-19 occurred in 8/70 (11.4%) BA.1 and 1/15 (6.7%) BA.2 patients. ICU admission occurred in 3/70 (4.3%) BA.1 and no BA.2 patients. Death occurred in 4/70 (5.7%) BA.1 and no BA.2 patients. Using matched-propensity score (14 BA.1 and 14 BA.2 patients), adjusted risk difference was -14.3% (95% CI: -39.2% to 14.2%) for hospitalization; -7.1% (95% CI: -26.3% to 13.8%) for ICU admission; and -7.1% (95% CI: -26.3% to 13.8%) for death.

CONCLUSIONS: No significant difference was demonstrated between BA.1 and BA.2 treated with sotrovimab in terms of hospitalization, ICU admission or death, though we cannot exclude clinically important differences based on the confidence intervals. Clinical data should be coupled with in vitro testing when evaluating therapeutic recommendations.

P013
Hospital COVID-19 outbreak-associated cases throughout the pandemic: A tale of declining morbidity and mortality
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OBJECTIVES: Morbidity and mortality case rates associated with COVID-19 infection have declined in the general population throughout the pandemic. The corresponding trend among hospital-associated outbreak cases is less well understood. Therefore, the objective of this observational study was to describe the morbidity and mortality due to COVID-19 hospital outbreak-associated deaths throughout the pandemic.

METHODS: Data was collected from April 2020 – October 2022 at a large tertiary academic center that included 3 acute and 3 rehabilitation sites comprising over 1500 patient beds. The total number of patients and staff attributable to outbreaks (using local public health definitions) were documented, along with subsequent patient complications. Only deaths contributed or caused by COVID-19 as stated on the death certificate were included in the mortality rate. Cases were divided into “waves” according to peaks and nadirs of local case counts that generally coincided with transitions to new dominant variants.

RESULTS: During the study period, a total of 87 outbreaks occurred involving 569 patients and 246 staff with an overall patient ICU admission rate of 3.5% and mortality rate of 5.6%. The number of patient/staff cases per outbreak was highest in Wave 1 (19) and subsequently declined to 9 by Wave 8. Average duration of outbreak also declined from 20 to 15 days during this period. ICU admission and mortality risk (14.3% and 28.6%, respectively) was highest in Wave 1 (Figure P013-1), with subsequent decline even during Wave 5, when the Omicron variant dominated and resulted in the largest number of outbreaks (21) and total patient/staff cases (242). Negative patient outcomes continued to fall despite the large volumes of patients involved in outbreaks.

CONCLUSIONS: The elevated patient risk experienced in Wave 1 occurred despite aggressive outbreak infection
control measures. Factors that contributed to subsequent improved outcomes included new treatments, immunity, vaccination, and domination of less virulent variants.

P014
The epidemiology of SARS-CoV-2 variants: A single center experience
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OBJECTIVES: The COVID-19 pandemic, caused by the SARS-CoV-2 virus, has resulted in 630 million cases and 6.6 million deaths worldwide to date. Each new variant has led to a wave of illness with slightly different epidemiology. In this study, we aimed to characterize the epidemiology of the different strains at a tertiary care center.

METHODS: This was a retrospective chart review of patients admitted with SARS-CoV-2 between March 2020 and August 2021, at the University of Alberta Hospital in Edmonton, Alberta.

RESULTS: A total of 1084 patients were included, with the majority (637) having the wild type (WT) variant, 97 with Alpha variant, 306 with Delta, 13 with Gamma, 1 with Beta and 30 were unknown/ unresolved strains. Males compromised 61.8% of the admitted patients with a mean age of 60.7 years (standard deviation 18.3 years). The infections were healthcare-associated in 10.4% of cases (primarily WT), with 32.6% of patients requiring ICU admission (primarily due to the Delta strain and unknown cases). Mortality was 18.1%, highest in the WT (19.8%) and delta (18%) strains.

CONCLUSIONS: The epidemiology of SARS-CoV-2 varied by strain, particularly with regards to healthcare-association and mortality. Continued vigilance for new strains and their epidemiological effects is important in anticipating the public health needs of the population with future waves of illness.

P015
Lessons from using wastewater-based surveillance to monitor COVID-19 outbreaks in long-term care facilities in Edmonton, Canada
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OBJECTIVES: Early detection of COVID-19 in long-term care facilities (LTCF) is critical for the protection of vulnerable individuals. During the COVID-19 pandemic, wastewater-based surveillance (WBS) of SARS-CoV-2 has been shown to be a leading indicator to clinical cases, supporting site-specific WBS as a potential early warning system for COVID-19 outbreaks. Objectives of this study are to (i) study feasibility of timely quantification of SARS-CoV-2 in site-specific wastewater samples, (ii) study lead vs lag of SARS-CoV-2 WBS to COVID-19 outbreaks in LTCF and (iii) highlight advantages and disadvantages of this approach.

METHODS: From January 2021 to June 2022, 24-hour composite wastewater samples were collected from 12 LTCF 2-3 times per week and assayed for SARS-CoV-2 using RT-qPCR. Results were reported within 24 hours to public health physicians directing LTCF outbreak investigations with outbreak management teams who collaborated with the facilities to initiate necessary protocols.

RESULTS: Of the 2027 samples tested, 485 (29%) were positive for SARS-CoV-2, with concentrations ranging from 80 to 4.2 x10^5 RNA copies/100 mL. During the study, 37 COVID-19 outbreaks were confirmed with WBS leading clinical detection of COVID-19 in 14 outbreaks, lagging clinical detection in 13 and had simultaneous clinical and WBS detection in four outbreaks; six were not detected by WBS. Of the 485 positive SARS-CoV-2 samples, 246 (51%) were not linked to any outbreaks. These discordant results can be attributed to rotating staff, incidental visitors and residents using incontinent products (i.e., not contributing to the WW system in a LTCF) as well as asymptomatic or pre-symptomatic COVID-19 cases.

CONCLUSIONS: These data demonstrate good correlations between SARS-CoV-2 WBS and clinical cases thereby supporting WBS as a sensitive, comprehensive, and non-invasive monitoring tool in LTCF. Overall, this study provides evidence that SARS-CoV-2 WBS is a practical and useful tool to monitor and prevent spread of COVID-19.

P016
Wastewater surveillance monitoring of SARS-CoV-2 variants of concern and dynamics of transmission and community burden of COVID-19

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OBJECTIVES: Wastewater-based surveillance (WBS) is a reliable tool for early detection of SARS-CoV-2 infections in communities and can be used to track variants of concern (VOC) of SARS-CoV-2. We utilized WBS to identify the emergence and levels of the Alpha, Beta, Gamma, Delta, Omicron BA.1 and Omicron BA.2 variants in wastewater over a two-year period.

METHODS: Composite influent wastewater samples collected from nine wastewater treatment plants across Alberta were concentrated by centrifugal ultrafiltration followed by RNA extraction using MagMax-96 viral RNA isolation kit. Real-time RT-qPCR using VOC-specific primers and probes was performed to target VOC circulating in the community at the time of testing. The number of days from first detection to reach a relative abundance of each VOC at 20%, 50% and 90%, which is defined as the proportion of a specific VOC among all VOC detected in a sample, was determined to gain insight into transmissibility and magnitude of infection.

RESULTS: Alpha took 38, 53, and 80 days to reach 20%, 50%, and 90% abundance, respectively. Beta was not detected in any samples, likely due to low level infection in the community that was below the detection sensitivity of the assay. Gamma took 153 days to reach 20%, and never reached a relative abundance greater than 29%, corresponding to a low transmissibility and infection burden compared to other VOC. Delta reached the specified abundance levels at 78, 104, and 111 days respectively. Omicron BA.1 and BA.2 reached 90% abundance in 35 and 62 days respectively, demonstrating their rapid spread to high magnitude of infection. The Alpha, Delta, Omicron BA.1 and Omicron BA.2 variants all reached 100% relative abundance, outcompeting the previous variants circulating in the community.

CONCLUSIONS: Tracking VOC dynamics in wastewater gives valuable insight into the emergence and spread of variants, which informs pandemic response.

P017
Diminished neutralization capacity of SARS-CoV-2 Omicron BA.1 in donor plasma collected January-March 2021

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Abstracts

CONCLUSIONS: Plasma specimens collected January-March 2021, expressed a diminished neutralizing capacity to Omicron BA.1. In an unvaccinated subgroup with evidence of prior SARS-CoV-2 infection (likely Wildtype or Alpha), Omicron BA.1 neutralization was nonexistent.

P018
Characterizing long-term antibody response of COVID-19 patients following natural infection and/or vaccination: A GENCOV Study

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OBJECTIVES: Emerging evidence suggests that plasma with an anti-SARS-CoV-2 neutralizing capability of ≥ 2 x 10^4 binding arbitrary units/ml (BAU/ml) might protect against SARS-CoV-2 Omicron BA.1 infection. Here we assessed the neutralizing capacity of donor plasma collected between January-March 2021 against SARS-CoV-2 Omicron BA.1.

METHODS: Study specimens were subsamples of a larger repeated cross-sectional design with random sampling. 63 specimens with serologic evidence of a prior SARS-CoV-2 infection (collected January-March 2021) were linked to donor vaccination histories and tested by plaque reduction neutralization 50% (PRNT₅₀): Wildtype, Alpha, Beta, Gamma, Delta, and Omicron BA.1 SARS-CoV-2. The 63 specimens plus 4390 specimens (randomly sampled regardless of serologic evidence of infection) were tested using the Abbott SARS-CoV-2 IgG II Quant assay (Anti-Spike (S), Abbott, Chicago, IL, USA; Abbott Quant assay).

RESULTS: Of the 63 specimens with serological evidence of SARS-CoV-2 infection, specimens were divided into two groups, 1) vaccinated (at least 1 dose of SARS-CoV-2 vaccine) and 2) not vaccinated. In the vaccinated group, the percentages of specimens with any measurable PRNT₅₀ vs Wildtype/VOC were Wildtype (21/25 [84%]), Alpha (19/25 [76%]), Beta (18/25 [72%]), Gamma (13/25 [52%]), Delta 19/25 (76%), and Omicron BA.1 9/25 (36%). In the unvaccinated group, the percentages of specimens with any measurable PRNT₅₀ vs Wildtype/VOC were Wildtype SARS-CoV-2 (16/39 [41%]), Alpha (16/39 [41%]), Beta (10/39 [26%]), Gamma (9/39 [23%]), Delta (16/39 [41%]), Omicron BA.1 (0/39) (Fisher’s exact tests: vaccinated vs unvaccinated for each variant, p<0.05). None of the 4453 specimens (January [n=1499], February [n=1465] and March [n=1489]) tested by the Abbott Quant assay had a neutralizing capacity of ≥ 2 x 10^4 BAU/ml.

CONCLUSIONS: Plasma specimens collected January-March 2021, expressed a diminished neutralizing capacity to Omicron BA.1. In an unvaccinated subgroup with evidence of prior SARS-CoV-2 infection (likely Wildtype or Alpha), Omicron BA.1 neutralization was nonexistent.
OBJECTIVES: The antibody response following vaccination or natural infection with SARS-CoV-2 remains to be fully elucidated. The GENCOV study aims to describe the COVID-19 serological profile and identify associations with patient factors that contribute to variability in patient outcomes. Here, we compared long-term SARS-CoV-2 antibody responses following natural infection and/or vaccination.

METHODS: Plasma samples were collected from: 1) COVID-19 participants 6 months and 12 months following a confirmed positive PCR or rapid antigen test result (n=676) and 2) SARS-CoV-2 naïve individuals 6 months following a second dose of a Health Canada approved vaccine (n= 80). COVID-19 participants were further stratified according to vaccination status: a) Vaccine-naïve (n = 70), b) breakthrough immunity (n=192, vaccinated prior to infection), and c) hybrid immunity (n=414, vaccinated after infection). Serial antibody titer levels, antigen target (including trimeric spike (S), nucleocapsid (N), and receptor-binding domain (RBD)) and viral neutralization (nABs) were assessed using an in-house developed ELISAs and the Health Canada approved Roche Elecsys® Anti-SARS-CoV-2 immunoassay.

RESULTS: At 6 months (median = 195 days) post infection or vaccination, individuals with hybrid or breakthrough immunity had significantly higher anti-S and anti-RBD IgG and IgA levels, as well as total anti-S titers compared to individuals who were vaccinated (infection naïve) or had natural infection alone. Vaccinated infection-naïve individuals also showed greater total anti-S titers compared to individuals with natural infection alone. 94.8% - 98.6% of all COVID-19 participants were positive for anti-N antibodies at 6 months. At 12 months (median = 384 days) post exposure, vaccine naïve individuals had significantly lower median anti-S and anti-RBD IgG levels and total antibody levels than those with hybrid or breakthrough immunity.

CONCLUSIONS: Understanding the long-term antibody response following vaccination and/or natural infection will help inform future health policy decision-making and vaccine development.

P019
Analysis of SARS-CoV-2 prevalence in residual antenatal serum samples in British Columbia
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OBJECTIVES: As part of the surveillance strategies used to track the progression of SARS-CoV-2 in the BC population, we are performing a sero-survey from residual antenatal serum samples. This strategy will be used as a proxy measure to track vaccination coverage and changes in the rate of infection in the general population.

METHODS: 300 samples are randomly selected on a weekly basis across different age groups and Health Authorities. Samples are tested on the Meso Scale Discovery platform for the detection of antibodies against SARS-CoV-2 Nucleocapsid, Spike and RBD. Based on the sero-positivity of the three SARS-CoV-2 antigens, we aimed to differentiate between individuals that have been vaccinated, infected or non-exposed to SARS-CoV-2.

RESULTS: An increase in infected (SP+/NC+) individuals was detected rapidly after the emergence of the Omicron variant. Rate differences in infected individuals can be seen between the Health Authorities at the beginning of 2022, but those differences disappear by March 2022. At present, no significant differences were observed between different age groups. After reaching a peak in March 2022, anti-Spike antibody levels remained constant. Lower anti-Spike levels were reported in the younger age group (16-27).

CONCLUSIONS: Residual antenatal serum samples can be used for serosurveillance monitoring, to model population infection and vaccination dynamics.

P020
Prospective, clinical comparison of self-collected throat-Bilateral Nares swabs, saline gargle and healthcare provider collected nasopharyngeal swabs among symptomatic outpatients with potential SARS-CoV-2 infection
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OBJECTIVES: Self-collected saline gargle (SG) is the only alternative to healthcare provider (HCP) collected nasopharyngeal (NP) swab in an outpatient setting to detect SARS-CoV-2 by PCR in British Columbia (B.C.). However, some individuals cannot perform a SG collection. Our study aimed to assess the performance and user acceptability of combined throat-bilateral nares (TN) swabbing as an alternative self-sampling modality among symptomatic outpatients with potential SARS-CoV-2 infection.

METHODS: Symptomatic individuals greater than 12 years of age seeking a COVID-19 PCR test at one of two COVID-19 collection centres in the Fraser Health region of Metro Vancouver were asked to participate. Consenting individuals provided three specimens, including a HCP collected NP swab, a self-collected SG, and a self-collected TN sample. All samples were tested within 48 hours after collection using PCR nucleic acid testing (NAT).

RESULTS: In total, there were 311 participants in this study. Using the NP swab result as the reference standard, SG was 99% sensitive and 98% specific and TN was 99% sensitive and 99% specific. When the final clinical test interpretation was used as the reference standard, NP was 98% sensitive and 100% specific, and both SG and TN were 99% sensitive and 100% specific. Mean cycle threshold (Ct) values for each viral target were higher in SG specimens compared to the other sample types, though this did not significantly impact the final clinical interpretation. The performance of all specimen types was comparable within the first seven days of symptom onset. There was no significant difference between observed or unobserved self-collections. SG collections were rated the most acceptable, followed by TN and then NP.

CONCLUSIONS: TN provides another less invasive sampling option for self-collection for symptomatic outpatient SARS-CoV-2 testing by PCR. Having more self-collected and less invasive sampling options can help improve testing access while reducing reliance on healthcare staff collecting samples.

PO21
Evaluation of Neat Saliva for SARS-CoV-2 detection by rRT-PCR in comparison to Nasopharyngeal Swabs (NPS)
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OBJECTIVES: We compared performance characteristics, with qualitative evaluation, of rRT-PCR for SARS-CoV-2 detection by neat saliva and nasopharyngeal swab (NPS) collection in pediatric and adult outpatients.

METHODS: Outpatients were recruited prospectively between May 19, 2021, and June 28, 2021, to provide neat saliva and a NPS when visiting COVID-19 Assessment Centres or a pediatric clinic for COVID-19 testing. Additional preparation was made on neat saliva specimens. An aliquot was mixed with phosphate buffered saline (PBS) and Spectrum buffer (SB), respectively. Neat saliva in these preparations and NPS from the same patient were tested in parallel for SARS-CoV-2 using validated rRT-PCR assays. Participants completed an online survey about their experience in providing NPS and neat saliva.

RESULTS: Twenty of the 218 patients tested positive for SARS-CoV-2. One patient tested positive only with NPS and one only with neat saliva. Compared to NPS, neat saliva has a sensitivity of 95.24% (95%CI; 76.18% - 99.88%) and specificity of 99.49% (95%CI; 97.2% - 99.99%). Compared to SARS-CoV-2 infection, that is a patient with NPS and/or neat saliva positive, the sensitivity for NPS and neat saliva was the same at 95.45% (95%CI; 77.16% - 99.88%). No performance differences were identified between neat saliva mixed with PBS or SB. The addition of PBS or SB compared to no buffer reduced amplification inhibition by 60% and 93%, respectively. VOC results (N=19) revealed 63% of the positive cases were Alpha strain. The survey results from 134 patients rated that neat saliva was easy to collect and a more comfortable collection than NPS.

CONCLUSIONS: Neat saliva is an easy and comfortable collection. Its performance in SARS-CoV-2 detection is statistically comparable to that of NPS for both children and adults. Neat saliva should be considered as an alternative to NPS for SARS-CoV-2 detection in outpatients, particularly when self-collection strategy is employed.
P022
Development and validation of real-time RT-PCR assays for the detection of sub-lineages of the SARS-CoV-2 Omicron variant

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OBJECTIVES: The Omicron variant of SARS-CoV-2 was first reported in November 2021 and has since become the predominant circulating variant worldwide. Several sub-lineages including BA.1, BA.2, BA.4 and BA.5 have caused high rates of infection, even in countries with good SARS-CoV-2 vaccination coverage attributable to enhanced immune escape and increased transmissibility.

METHODS: To detect and differentiate the BA.1, BA.2, BA.4 and BA.5 sub-lineages, we developed two real-time reverse transcriptase PCR (rRT-PCR) assays targeting four critical discriminatory nucleotide mutations responsible for the following amino acid changes: S:N501Y for all omicron sub-lineages in combination with S:214EPE insertion for BA.1, S:69/70 wild-type for BA.2, orf7b:L11F for BA.4, and M:D3N for BA.5.

RESULTS: Accuracy of the assays were determined by comparing samples with genome sequencing results to the rRT-PCR assays and ranged from 97.96% to 100% for all sub-lineages, however, BA.2 samples with the 69/70 deletion were not correctly identified. Sensitivity of the BA.1 and BA.2 assays were shown to be comparable to the previously published E gene assay. Lower sensitivity was noted for the BA.4 and BA.5 variants; these assays were modified by changing the reporter dye on the BA.4 probe from HEX to VIC and increasing the concentration of primers and probes for BA.5 in the second iteration of the assay. The intra- and inter-assay variability for all assays were less than 5% and no cross-reactivity with common respiratory pathogens was observed.

CONCLUSIONS: The use of rRT-PCR assays as a frontline screen for the surveillance of circulating lineages provides a faster turn-around-time, is amenable to large scale testing, identifies potential new variants for further characterization and is inexpensive compared to full genome sequencing. Surveillance of circulating and emerging lineages helps to determine whether specific monoclonal antibody therapies are useful for a population and aids in the development of public health guidelines.

P023
Real-world evaluation of the Lucira Check-It COVID-19 loop-mediated amplification (LAMP) test among patients and healthcare workers

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OBJECTIVES: In hospitals during the COVID-19 pandemic, laboratory testing was important to reduce SARS-CoV-2 transmissions, particularly for high-risk settings like the emergency department, pre-operative settings, and for the safe return-to-work of exposed healthcare workers (HCWs). For these applications, delayed test results from laboratory nucleic acid amplification test (NAATs) posed a barrier to maximizing efficient patient flow and minimizing staffing shortages. This quality improvement project sought to evaluate the performance of the Lucira Check-It COVID-19 Test, a rapid diagnostic test that used NAAT technology (NAAT-RDT).

METHODS: Using 10-fold serial dilutions of SARS-CoV-2, the analytical sensitivity of the NAAT-RDT was assessed against commercial NAATs used for routine diagnostic testing. Clinical performance was assessed at two Nova Scotia hospitals in 404 cases with paired swabs tested by NAAT-RDT and a laboratory-based NAATs. These represented three distinct populations: patients presenting to the emergency department (n=208), patients in the perioperative setting (n=158), and HCWs exposed to SARS-CoV-2 (n=38).

RESULTS: Analytical sensitivity of the Lucira NAAT-RDT and other laboratory NAATs was comparable. During clinical evaluation, the overall sensitivity and specificity was 92.9% and 98.3%, respectively, with little variation between settings.

CONCLUSIONS: The Lucira NAAT-RDT is a portable and self-contained device that provides an easily interpreted
result within 30 minutes following a bilateral nasal swab collection. Its performance was shown to be acceptable for use in HCW’s exposed to SARS-CoV-2 or for patients in the pre-operative or emergency department settings. To date, Lucira continues to facilitate patient flow and minimize staff shortages in these settings.

**P024**

**Operationalising Canadian SARS-CoV-2 genomic surveillance**

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**OBJECTIVES:** The COVID-19 pandemic necessitated rapid development and deployment of a national genomic surveillance program in Canada that would enable the detection and tracking of SARS-CoV-2 variants. The Public Health Agency of Canada established the CPHLN (Canadian Public Health Laboratory Network) Covid Genomics Program (CCGP), to promote collaborations between public health partners, identify opportunities to streamline operations, and spur innovations in genomic surveillance processes that would increase the efficiency of data collection and sharing across Canada.

**METHODS:** Genomics Liaison Technical Officers (GLTO) were deployed to provincial public health laboratories to build capacity and help implement a coordinated strategy for the collection and curation of genomic sequences and associated contextual metadata. Summaries of key operational metrics were generated through automated queries of a PowerBI database and visualized in HTML reports created using R shiny and R markdown. Reported results show trends over time for each partner, with jurisdictional metrics presented in context with national trends. These Genomics Operational Reports, shared with partners weekly, summarize detailed operational information on submissions of up to 40,000 SARS-CoV-2 genomic sequences per week.

**RESULTS:** The capacity provided through GLTOs and distributed Genomics Operational Reports encouraged improvements in quality, completeness, and timeliness of data sharing by highlighting metrics that influence these priorities. These prompted solutions for improved data sharing between 2021 to 2022, resulting in, for example, shorter median turnaround time for submissions to GISAID (from 88 days to 17 days), and increased completeness of the contextual data describing the purpose of sequencing (from 82% to 97%).

**CONCLUSIONS:** Monitoring operational metrics and sharing results encouraged more efficient and robust data sharing, critical to maintaining local and national situational awareness and appropriate public health responses. Solutions implemented ranged from infrastructure changes to procedural improvements and automation, which will also support genomic surveillance of other infectious diseases in Canada.

**P025**

**SARS-CoV-2 NGS can do more than identify Omicron VOC**

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**OBJECTIVES:** Breakdown the identity and prevalence of SARS-CoV-2 lineages reported as Omicron.

**METHODS:** SARS-CoV-2 genomes are sequenced by the hospital for provincial surveillance as part of the Ontario Genomic Network. The lab receives COVID-19 positive samples and performs NGS using the ARTIC-v4.1 or Midnight-1200 amplicon panels on the Illumina MiSeq or Oxford Nanopore GridION. Analysis of NGS data is performed using ncov2019-artic-nf, a Nextflow pipeline for running the ARTIC network’s field bioinformatics tools.

**RESULTS:** Since January 1, 2022, the lab has sequenced 14,896 SARS-CoV-2 genomes and reported 14,803 of them as “Omicron” (99.4%). However, NGS has actually identified 240 different SARS-CoV-2 lineages. The three lineages sequenced most frequently include BA.1.1 (n=3098, 20.9%), BA.2 (n=2022, 13.7%), and BA.5.2.1 (n= 1039, 7.0%). The BA.1.1 lineage was the major lineage in circulation in Feb. 2022 making up 76.8% of all genomes, before yielding to BA.2 which peaked in May with 58.7% of all genomes. When the BA.5 lineage evolved, it fractured into so many sub-lineages that no one lineage has never exceeded 30% of all genomes. Although BA.5.2.1 is the third most sequenced genome, its prevalence has fluctuated between 10
CONCLUSIONS: As a result of the COVID-19 pandemic, NGS has become a valuable surveillance tool for monitoring the prevalence of viral pathogens and identifying variants of concern or interest. However, current reporting protocols share very little information with their local health units and communities. Novel strategies and platforms for sharing NGS data is a critical piece missing in our current NGS surveillance.

P026
Identification and temporal clustering of SARS-CoV-2 mutations

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OBJECTIVES: Genomic surveillance of SARS-CoV-2 has been implemented across multiple regions around the world. These surveillance efforts aid in describing the emergence, spread and burden of SARS-CoV-2 variants of concern (VOC). Collected information helps to manage public health responses including targeted vaccine campaigns, testing and social restrictions. Current SARS-CoV-2 genomic surveillance rely on tracking VOCs, which are distinguished lineages assigned by dynamic nomenclature algorithms including pangolin. However, a lineage is derived from the prevalence and characteristics of a genetically distinct virus, which delays the reporting of new lineages. In addition to lagged responses, this method ignores some genetic variability within each lineage. In response, we aimed to develop a complementary approach to identify fluctuating mutations over time.

METHODS: We propose monitoring mutations above a nominal relative frequency and show monotonic trends over time. These selected mutations’ relative frequencies are used to identify groups of mutations fluctuating overtime using Euclidean-based hierarchical clustering. This approach was developed using two 9-week time windows. The first-time window encapsulated the emergence and dominance of the Delta VOC over co-circulating Alpha and Gamma VOCs, and the second time window encapsulated the subsequent emergence of the Omicron VOC, which replaced the Delta VOC.

RESULTS: Preliminary results show the displacement of 3 Gamma/Alpha VOC mutation clusters by 8 Delta VOC mutation clusters. Subsequently, 3 Delta VOC mutation clusters were supplanted by 3 Omicron VOC clusters. This approach is currently being explored in less obvious VOC transition periods to examine the robustness of our methods.

CONCLUSIONS: The detection of fluctuating mutations can help highlight mutations potentially associated with increased transmission, severity, breakthrough capability and convergent evolution. In addition, this relative frequency-based clustering approach can potentially be extended to environmental samples, which may be a heterogeneous mixture of VOC with clear groups of mutations.

P027
Development of a live-action data dashboard for monitoring SARS-COV-2 whole genome sequencing in a clinical microbiology laboratory

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OBJECTIVES: Introduction: The Infectious Disease Sequencing (IDS) Lab is a member of the Ontario COVID-19 Genomic Network (OCGN) and has been sequencing SARS-CoV-2 whole genomes (WGS) since June 2020 that includes a catchment area servicing > 1.5 million Ontarians. This surveillance program generates between 250 – 750 WGS/week and is designed to monitor the emergence of novel SARS-CoV-2 variants in real time. In collaboration with the Center for Advanced Computing (CAC), here we describe the creation, deployment, and impact of a live-data dashboard (DB) that enabled the laboratory to monitor the changing epidemiology of SARS-CoV-2, laboratory metrics and patient demographics in real-time.
METHODS: Methods: The live-data dashboard was created as a collaborative effort between IDS and The Center for Advanced Computing (CAC). The dashboard was programmed using python 3.10.8. All data transferred to the dashboard was approved by ethics and risk and privacy offices to protect patient privacy.

RESULTS: The live dashboard is updated each day at 06:00 with the latest variant and sub-variant data, and patient demographics (decade of age, biological sex, and testing location) automatically from the laboratory information system. The DB also captures and displays laboratory metrics including turn-around-time (TAT), individually displaying in hours collection time to sample receipt in the laboratory, sequencing time, analysis time and reporting duration to ensure that the laboratory can monitor TAT at each step of the WGS process. (Figure P027-1).

CONCLUSIONS: The use of automated rapid data analytics for monitoring WGS sequencing data and quality metrics ensures that laboratory data is rapidly analyzed and displayed results in real time. Continuous monitoring of laboratory metrics ensures that laboratory processes and quality are maintained to ensure the efficiency and quality of laboratory data without the need for additional human resources.

Figure P027-1: Live-action data dashboard.
P028
One Health wildlife surveillance leads to the discovery of a divergent lineage of SARS-CoV-2 in white-tailed deer with evidence of deer-to-human transmission

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OBJECTIVES: Reverse zoonotic transmission of SARS-CoV-2 can lead to the establishment of wildlife reservoirs, driving viral adaptation and potential spillback from animals to humans. In North America, there is evidence of multiple spillovers of SARS-CoV-2 from humans to white-tailed deer (Odocoileus virginianus), and consequently deer appear to have the potential to be a reservoir for SARS-CoV-2. We carried out a multidisciplinary One Health research collaboration for SARS-CoV-2 surveillance in Canadian wildlife.

METHODS: Hunter-harvested deer in Ontario were screened for SARS-CoV-2 by PCR. Whole genome sequencing and virological approaches were used to characterize SARS-CoV-2 detected from wildlife.

RESULTS: We identified a new, highly divergent lineage of SARS-CoV-2 in 6% of white-tailed deer sampled during autumn 2021. The Canadian deer SARS-CoV-2 variant has been assigned PANGO lineage B.1.641. The lineage has 76 consensus mutations including 37 previously associated with non-human animal hosts, 23 of which were not previously reported in deer. Despite a high degree of divergence relative to the closest common ancestor (49 mutations) there was no indication of recombination having given rise to this lineage. We also identified mutational signatures of adaptation to white-tailed deer with a potentially elevated mutation rate, but no indication of positive selection. Phylogenetic analysis also revealed an epidemiologically linked human case from the same geographic region and sampling period, with no evidence of forward transmission in humans. Infectious virus was isolated and replicated well in vitro. Pseudovirus neutralization assays did not demonstrate reduced neutralization by sera from previously infected or vaccinated humans. Together, our findings represent the first evidence of a highly divergent lineage of SARS-CoV-2 in white-tailed deer and of deer-to-human transmission.

CONCLUSIONS: Our findings underscore the close connections between human and wildlife health and the importance of wildlife surveillance for zoonotic pathogens through multi-disciplinary and inter-sectoral collaboration.

P029
No Time for Complacency: The CoVaRR-Net Biobank is an essential element of laboratory preparedness for infectious disease outbreaks

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OBJECTIVES: The Covid-19 pandemic highlighted the need for rapid, collaborative, and population-centric research to define and develop health impact, policies and establish diagnostic and surveillance tests. Critical for these objectives were clinical data collected in standardized fashion and large numbers of human samples pre/post viral encounter.

METHODS: Access to samples and data from infected/vaccinated individuals were needed to monitor immune durability, the possibility of increased transmissibility and virulence and vaccine protection against new and emerging VOCs.

RESULTS: Essential to the pandemic response is a strong laboratory and data research component, supported by effective biobanking and data sharing. Critically important to the speed of the research response is the rapid access to biobanked samples.

CONCLUSIONS: This paper introduces the CoVaRR-Net Biobank and defines its contribution to pandemic preparedness.
**P030**

**Increasing diversity of multidrug resistant *Streptococcus pneumoniae* serotypes in Canada: The SAVE study, 2011-2021**

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**OBJECTIVES:** The multidrug-resistant (MDR) invasive isolates of *Streptococcus pneumoniae* in Canada identified between 2011 and 2021 as part of the SAVE study were evaluated.

**METHODS:** 15,096 invasive isolates of *S. pneumoniae* were serotyped and had antimicrobial susceptibility testing performed, in accordance with CLSI guidelines (CLSI M07). Complete susceptibility profiles were available for 14,653 isolates. MDR was defined as resistance to three or more classes of antimicrobial agents (penicillin MIC ≥2 mg/L defined as resistant).

**RESULTS:** Between 2011 and 2021, 979 (6.7%) MDR *S. pneumoniae* were isolated as part of SAVE. There was no statistically significant trend in the annual rates of multidrug resistance in *S. pneumoniae* over the entire study of 2011 to 2021; however, there was a significant decrease from 8.5% (n=116) in 2011 to 5.7% (n=69) in 2015 (P<0.0001) followed by a significant increase from 3.9% (n=48) in 2016 to 8.2% (n=77) in 2021 (P<0.0001). Multidrug resistance was observed in 44 serotypes, with serotypes 19A (241, 24.6%) and 15A (219, 22.4%) predominating. A significant increase in the diversity of serotypes was observed in the MDR isolates from 2011-2021 (P<0.001). In 2011, serotype 15A and 19A represented 32.8% and 44.0% of all invasive MDR *S. pneumoniae* isolates, respectively. In 2021, serotype 15A and 19A represented 9.1% and 15.6% of all invasive MDR *S. pneumoniae* isolates, respectively. There were 6 serotypes that each represented more than 5% of the 2021 MDR isolates: 19A = 4 = 23A > 15A > 9N = 3.

**CONCLUSIONS:** The MDR isolates in the most recent years of the SAVE study included a greater diversity of serotypes than in previous years, potentially demonstrating population changes as *S. pneumoniae* continues to evolve under both vaccine and antibiotic selective pressure.

**P031**

**Comparison of PCV-10, PCV-13, PCV-15, PCV-20 and PPSV23 Vaccine Coverage of *Streptococcus pneumoniae* Serotypes in Canada over 11 years: The SAVE Study, 2011-2021**

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**OBJECTIVES:** Globally, as pneumococci continuously evolve under vaccine and antimicrobial selective pressures, it is critical to routinely track vaccine coverage of established (PCV-10, PCV-13, and PPSV23) and new PCV-15 and PCV-20 vaccine formulations. In this report, our primary objective was to compare the number and proportion of invasive pneumococcal disease (IPD) isolates from serotypes covered by PCV-10, PCV-13, PCV-15, PCV-20 and PPSV23 vaccine formulations, collected in Canada from 2011 to 2021, by demographic category and antimicrobial resistance phenotype.

**METHODS:** Between 2011-2021, the SAVE study, in collaboration with the Public Health Agency of Canada-National Microbiology Laboratory (PHAC-NML), collected 15,096 IPD isolates from Canadian provincial public health and hospital laboratories. Serotypes were determined by Quellung reaction and broth microdilution antimicrobial susceptibility testing performed following the Clinical and Laboratory Standards Institute method. MDR and XDR phenotypes were defined as resistance to ≥3 and ≥5 antimicrobial classes, respectively.

**RESULTS:** For all isolates collected from 2011 to 2021 PCV-15, PCV-20 and PPSV23 covered 43.3%, 62.4% and 71.7% of all 2011-2021 IPD isolates, respectively. PCV-13 vaccine coverage was 30.8%, with non-PCV-13 serotypes 22F and 33F (in PCV-15) adding 12.5% more coverage, and non-PCV-15 serotypes 8, 10A, 11A, 12F and 15B/C (present in PCV-20) adding 19.1% more vaccine coverage. Non-PCV-20 serotypes covered by PPSV23 (2, 9N, 17F and 20), represented 9.3% of all IPD isolates. While higher-valency vaccine formulations covered significantly more isolates by age, sex, region, antimicrobial resistance...
and MDR phenotype (p<0.0001 for all categories), serotype coverage of XDR isolates did not significantly differ between PCV-13, PCV-15 and PCV-20 formulations (p>0.05).

**CONCLUSIONS:** PCV-15 and PCV-20 provided significantly greater coverage of IPD isolates than PCV-10 and PCV-13 for all age groups, all geographic regions, and all individual antimicrobial resistance phenotypes, as well as MDR isolates.

**P032**
Genomic epidemiology of extended clusters of invasive *Streptococcus pneumoniae* in long-term care homes


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**OBJECTIVES:** *Streptococcus pneumoniae* is an important cause of pneumonia and invasive pneumococcal disease (IPD). Reductions in IPD during the pandemic have emphasized the degree to which PD may be a result of person-to-person transmission. We investigated the extent to which PD in long-term care (LTC) homes might be a result of transmission of pneumococci.

**METHODS:** Population-based surveillance of LTC home pneumococcal disease (PD) requiring hospitalization was used to identify clusters of same-serotype PD occurring in LTC homes. Epidemiologic clusters were defined as ≥3 cases of the same serotype in one home over with a rate of disease in that home higher (at P≤0.0005) than the rate of disease for the same serotype during the same time period in all other homes. Isolates were sequenced to establish whether disease in epidemiologic clusters was caused by genetically highly related isolates; <38 SNVs different was defined as highly related. Genetic relatedness of case isolates was also compared with temporally, geographically and serotype matched isolates from community-dwelling adults.

**RESULTS:** Overall, 631 episodes of PD with isolates available for serotyping occurred in residents of 103 LTC homes between 1995 and 2018. 144/631 (22.8%) isolates occurred in 29 epidemiologic clusters in 20 homes (3 – 13 isolates/cluster; clusters spanning 6 months to 22 years). Overall, 135/144 case isolates and 254/288 matched control isolates were successfully sequenced; 26 of the 29 clusters had ≥3 case isolates sequenced. Case isolates were more highly related than controls (P<0.0001). Using genomics alone, in 11/29 epidemiologic clusters all isolates were highly related, in 12/29 clusters all isolates but one were highly related, and in 6 clusters isolates were not closely related.

**CONCLUSIONS:** WGS confirmed that most epidemiologically defined clusters of PD in LTC homes were caused by genetically highly-related isolates, suggesting that undetected transmission in homes may be associated with significant burden of PD.

**P033**
Vancomycin-resistant *Enterococcus* bloodstream infections: Re-emergence of sequence type 17 among hospitalized patients in a network of Canadian acute care hospitals, 2017-2021

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**OBJECTIVES:** Sequence type (ST) 17 is a vancomycin-resistant *Enterococcus* (VRE) clone endemic in many countries. We investigated the increasing trend and epidemiology of VRE ST17 in Canada between 2017 and 2021.

**METHODS:** The Canadian Nosocomial Infection Surveillance Program (CNISP) collected data on hospitalized patients with VRE bloodstream infection (BSI) via a standardized questionnaire. Resistance profiles were determined using broth microdilution (Sensititre panel GPALL1F). Molecular characterization was completed using whole genome sequencing (WGS) data from the Illumina MiSeq platform.

**RESULTS:** From 2017 to 2021, there were 1,106 patients with VRE BSI identified from 46 of 80 hospitals participating
Abstracts

**P034**

**Characteristics of invasive and non-invasive *Haemophilus influenzae* clinical isolates collected in a hospital serving Indigenous peoples**

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**OBJECTIVES:** In the post-*Haemophilus influenzae* type b (Hib) vaccine era, invasive *H. influenzae* type a (Hia) disease emerged in North American Indigenous populations. The role of Hia in non-invasive disease is uncertain; it is unknown if non-invasive Hia infections are prevalent in populations with a high incidence of invasive disease, and whether invasive and non-invasive Hia isolates have different characteristics.

**METHODS:** We analyzed all invasive and non-invasive clinical *H. influenzae* isolates collected over 5.5 years (2013-2019) in a hospital, where 82% of the patient population are Indigenous. Serotyping, clonal analysis, and antimicrobial sensitivity testing was conducted on 233 non-invasive and 20 invasive isolates.

**RESULTS:** Most isolates were non-typeable *H. influenzae* (NTHi); only 35 were encapsulated *H. influenzae*. Most non-invasive isolates were NTHi (213/233, 91%); Hia was identified only in 7/233 cases (3%). However, Hia was the most common invasive isolate (12/20, 60%), with NTHi found in 5 cases (25%). Incidence rates of invasive *H. influenzae* disease (12.5/100,000/year) greatly exceeded average provincial data, with the highest rates found in <6-year-old children (63.9/100,000/year). The proportion of Hia among invasive isolates was 7 times larger than in the rest of the province. No difference in clonal characteristics between invasive and non-invasive Hia isolates were found. Antibiotic resistance was more common among NTHi than among encapsulated isolates, without differences between invasive and non-invasive isolates.

**CONCLUSIONS:** Considering the significance of Hia among Indigenous populations, paediatric immunization against Hia will be useful to prevent serious infections in young Indigenous children.

**P035**

**A surveillance system to monitor existing and emerging potential Transfusion-Transmissible Pathogens**

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**OBJECTIVES:** Blood-borne and emerging pathogens (EP) can threaten organizations’ mission to safeguard the blood supply, due to a risk of transmission by transfusion. Here, we present the implementation of an epidemiological surveillance system to detect and assess infectious threats for blood banking (BB) services.

**METHODS:** The Early Warning, Alert and Response (EWAR) system was adapted for implementation to our organization and field of activity. A set of criteria has been defined for the selection of health threats, based on emergence potential, pathogenicity, and detection or mitigation measures available. Event-based and indicator-based surveillance (EBS / IBS) was set up. New outbreaks, follow up on ongoing outbreaks, epidemiologic trends and relevant scientific information were searched and selected based on geographic proximity and possible impact on BB services.
Upon detection of a potential infectious threat, relevant information was transmitted to BB decision makers.

RESULTS: A dedicated organizational structure has been set up for surveillance activity. A list of 37 blood-borne and EP was made up and used for EBS and IBS. Twenty-one pathogens were identified as representing a higher concern for the blood supply in Québec. The information and data sourcing resulted in the selection of 17 sources for periodical monitoring. Between 2019 and 2021, we identified outbreaks or infection cases by 14 distinct pathogens in the most visited countries by Canadians, in each continent. Three events originated from the Québec province, resulting in the production of 1 risk analysis, and implementation of appropriated mitigation measures in our organization.

CONCLUSIONS: The systematic information generates information on potential safety threats for the blood supply, which can be transmitted to BB decision makers and leveraged to conduct risk analysis. Such system contributes to managing the risks associated with EP.

P036
The epidemiology of carbapenemase-producing Enterobacterales infections in Canadian acute-care hospitals, 2010-2021
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OBJECTIVES: Rates, patient characteristics, risk factors and outcomes among carbapenemase-producing Enterobacterales (CPE) infected inpatients in Canadian acute-care hospitals are poorly understood.

METHODS: The Canadian Nosocomial Infection Surveillance Program (CNISP) conducts surveillance for inpatients infected with CPE of all ages among 78 acute-care hospitals. Participating facilities submit eligible specimens to the National Microbiology Laboratory for detection of carbapenemase production and trained infection control professionals collect epidemiological data by chart review.

RESULTS: From 2010 to 2021, 310 CPE infections were reported by 40 hospitals across 9 provinces. The median age of patients was 63 years, and 14 infections (5%) were reported among pediatric patients. Pre-existing comorbidities were frequent (88%) and included diabetes (29%), heart disease (21%) and active cancer (19%). The most common site of infection was urine (33%) followed by blood (29%) and respiratory (16%). Nearly a quarter (24%) of patients were either in ICU at the time of positive culture or were admitted following positive culture. All-cause 30-day mortality was 17%.

The overall incidence of CPE infections increased from 0.04 per 10,000 patient-days (2010) to 0.08 per 10,000 patient-days (2021) (p=0.03), with rates highest in Western and Central Canada and few infections (n=6) reported in Eastern provinces. The incidence of healthcare-associated CPE infection in a Canadian acute-care facility increased from 0.014 per 10,000 patient-days (2016) to 0.047 per 10,000 patient-days (2021) (p=0.007). Thirty percent of patients reported international travel in the 12 months prior to positive culture and of those 90% received healthcare while abroad.

CONCLUSIONS: CPE infection rates are increasing but remain low in Canada; however, all-cause mortality is significant. National surveillance data suggest that while travel and receipt of medical care abroad remains a risk factor for acquisition, nosocomial acquisition of CPE in Canadian acute-care facilities is increasing.

P037
Continued reduction in the frequency of carbapenemase-producing Enterobacterales during COVID-19
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OBJECTIVES: Carbapenemase-producing Gram-negative Enterobacterales (CPE) are an increasing threat. Introduction of CPE is facilitated by international travel from areas of high prevalence to regions of low prevalence. International travel was dramatically reduced in 2020 and 2021 due to the COVID-19 pandemic. Correspondingly, CPE numbers in a tertiary-care clinical microbiology laboratory servicing a metropolitan urban region decreased during this time period. The goal of this study was to review changes in the frequency of CPE at this site in 2022, given an increasing amount of global flights from 2021 to 2022.

METHODS: The total number of CPE per year (all CPE per year excluding duplicates) and the total number of individual carbapenemases per year (all carbapenemases per year excluding duplicates) were graphed from 2009 through 2022. The trend from 2009 through 2019 (pre-COVID-19) was compared to that from 2019 through 2022 (COVID-19). Chi-squared test for trend was completed for each time period using GraphPad Instat.

RESULTS: 244 CPE were identified from 2009-2022 (Figure P037-01). Despite the rise in global flights from 2021-2022, there was a continued reduction in the number of CPE. From 2019 through 2022, CPE isolates declined from 29 to 22 to 20 to 16. The frequency of CPE correlated with lower amounts of all detected carbapenemases, with the exception of KPC enzymes.

CONCLUSIONS: Despite a rise in international travel, the frequency of CPE has continued to decline in 2022. However, the rise in KPC enzymes may signify more travel between regions with greater prevalence of this enzyme or higher endemic prevalence of this enzyme.

P038
Canadian Public Health Laboratory Network reporting of carbapenemase-producing Enterobacterales in Canada: 2008-2021

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Figure P037-01: Total number of Carbapenemase-producing Enterobacterales (A) and total number of carbapenemases from 2009-2022 (B). Data shows all CPE per year excluding duplicates.
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OBJECTIVES: Carbapenemase-producing Enterobacteriales (CPE) pose a threat to human health as the multi-drug resistance nature of these organisms complicates the treatment of infections. Voluntary reporting of CPEs from provincial laboratories was analysed to better understand the dynamics in Canada.

METHODS: Annual numbers of CPEs from BC, ON, and QC were reported to the National Microbiology Laboratory from the respective provincial public health laboratories. All other provinces send isolates to the NML for CPE confirmation. Duplicate isolates were removed. The data was stratified by West (BC, AB, SK, and MB), Central (ON and QC), and East (NB, NB, NS, and PE). PCR to detect CPE was conducted using in-house laboratory protocols.

RESULTS: A total of 8,148 CPE colonizations and infections were reported from 2008 to 2021. CPE rates increased from 0.01/100,000 population in 2008 to 3.8/100,000 in 2021, however rates decreased from 3.9/100,000 in 2019 to 3.3/100,000 in 2020. In 2021, rates of CPE were 2.4, 4.9, and 0.4 per 100,000 in the West, Central, and East regions, respectively. Additionally in 2021, KPC rates were 0.5, 2.7, and 0.04 per 100,000 for the West, Central, and East regions, respectively, whereas NDM rates were 1.2, 1.2 and 0.3 per 100,000 for the West, Central, and East regions, respectively, and OXA-48-like rates were 0.3, 0.7, and 0.08 per 100,000 for the West, Central, and East regions, respectively. Escherichia coli, Klebsiella spp., Citrobacter spp., and Enterobacter spp. comprised the majority of isolates (93.2%) at 30.6%, 27.9%, 18.6%, and 16.1%, respectively.

CONCLUSIONS: The West/Central regions drive the rates of CPE in Canada. Carbapenemase genes vary depending on the region of Canada which may reflect specific CPE outbreaks, international travel, or surveillance difference within these regions. Additional studies are required to better understand variation in CPE rates, genes, clonality, and species harbouring these genes.

P039 Utility of hybrid whole genome sequencing in assessing potential nosocomial VIM transmission

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OBJECTIVES: Describe how whole genome sequencing can help investigate potential carbapenemase producing organism (CPO) nosocomial transmission.

METHODS: Infection Prevention and Control (IPAC) and laboratory investigation

Patient A had a Verona integron-encoded metallo-β-lactamase (VIM) from a urine Proteus mirabilis following recent hospitalization in Greece. Patient B, without foreign travel, had recurrent admissions to hospital during the same period with a new VIM from an Enterobacter bugandensis rectal surveillance swab. Both VIMs were confirmed by PCR following phenotypic testing. Given the rarity of VIM in Canada and close time proximity, concerns arose for nosocomial transmission. IPAC investigation revealed no contact between patients or common epidemiological links. Repeat testing and audit excluded erroneous specimen contamination.

Whole Genome Sequencing (WGS) After overnight incubation, 3-5 colonies were resuspended in Tris-EDTA buffer for total nucleic and plasmid-specific extraction. Sequencing was performed on Illumina MiniSeq and Oxford Nanopore GridION at a mean 400-600x and 50-150x plasmid coverage depth, respectively. Bioinformatic analyses were performed to determine if the VIM from patient B was related, thus potentially acquired from patient A.

RESULTS: Sequencing indicated that patient A’s P. mirabilis had a blaVIM-78 located on a 51.6 kb IncQ plasmid, whereas patient B’s E. bugandensis had a blaVIM-4 located on a 61.5 kb IncP plasmid. WGS also identified other plasmid and chromosomal beta-lactamases. Sequencing coverage of plasmids was similar regardless of extraction method.

Given two different VIM phenotypes and differences in the associated plasmids and integrons, the cases are suspected to be unrelated. No outbreak was declared based on the sequencing results and lack of epidemiologic link from IPAC investigation.
CONCLUSIONS: WGS can characterize uncommon CPOs to support IPAC investigations. Results help guide decision making in determining potential transmissions and outbreaks, in conjunction with epidemiological tracing. Developing standardized methods, analysis, and reporting is needed so clinical laboratories and IPAC teams can optimally utilize WGS.

P040
Earliest report of the tetracycline destrucase tet(X3) in an Acinetobacter junii from Israel from 2004

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OBJECTIVES: Carbapenem-resistant Acinetobacter baumannii (CRAB) is a World Health Organization critical priority pathogen. Therapeutic options for CRAB are usually limited to tigecycline and colistin. CRAB are increasingly resistant to these antibiotics due to acquisition of antibiotic-resistant genes (ARGs) such as tet(X) and mcr variants respectively. tet(X3), the predominant tet(X) variant among Acinetobacter spp., was initially reported in 2019 in an A. baumannii isolated in China in 2017. Retrospective analyses have since highlighted the role of non-baumannii Acinetobacter (nbA) in the spread of tet(X3), with the earliest evidence being in nbA from 2010. We report an Acinetobacter junii strain (IL_130) harbouring tet(X3), isolated from a human blood culture in 2004 in Israel.

METHODS: IL_130 underwent whole-genome sequencing (Illumina and Oxford Nanopore) and computational analyses: assembly (Unicycler), annotation (Prokka), taxonomic classification (Kraken2), and search for ARGs using ResFinder and BLDB. Antibiotic susceptibility testing (AST) was carried out using the VITEK2 N801 card and Sensititre CAN1MSTF plate.

RESULTS: IL_130 was resistant to gentamicin, tobramycin, tetracycline and trimethoprim/sulfamethoxazole. It was sensitive to other antibiotics tested, including beta-lactams and tigecycline. Search for ARGs revealed both tet(X3) and the blaOXA-58 carbapenemase co-located on a 367 kb plasmid.

CONCLUSIONS: We report the earliest evidence of tet(X3), in an Acinetobacter junii from 2004. This gene is capable of conferring resistance to most members of the tetracycline family of antibiotics, including tigecycline. Despite this, IL_130 was sensitive to tigecycline (resistant to tetracycline). This report further supports the role of nbA in the initial dissemination of tet(X3) towards CRAB. Whereas tigecycline use has been linked to the emergence of tet(X) variants, this study demonstrates that tet(X3) predated its commercialization in 2005. Finally, we highlight the limitations of relying on AST as a means of retrospectively tracking the origins and spread of ARGs.

P041
Molecular characterization carbapenemase-producing Enterobacterales from the Atlantic provinces, 2011-2021

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OBJECTIVES: Carbapenemase-producing Enterobacterales (CPE) is a concern due to the increasing resistance to multiple classes of antimicrobials. This study examines the genes, molecular strain types, and epidemiologic data associated with CPE in the Atlantic provinces.

METHODS: Presumptive CPE isolates were identified using in-house methodologies from 2011 to 2021 and voluntarily submitted to the National Microbiology Laboratory for additional characterization. Whole genome sequencing (WGS) was conducted using the Illumina platform. AMR prediction and sequence type was determined using StarAMR. Phylogenetic analysis was conducted using the SNVyl pipeline.

RESULTS: 80 non-duplicate isolates were collected from 77 patients with 3 patients harbouring more than one species of CPE. A total of 20 colonizations and 39 infections were reported with infections as follows: urine (n=29; 74.4%), wound (n=4; 10.3%), blood (n=5; 12.8%), and respiratory (n=1; 2.6%). Carbapenemases identified included NDM (n=45), OXA (n=18), SME (n=11), KPC (n=9), IMI (n=4), IMP (n=3); and VIM (n=1) with 11 isolates harbouring 2 carbapenemases. The most common species harbouring CPEs were as follows: Enterobacter cloacae complex (n=24; 30.0%); Klebsiella pneumoniae (n=21; 26.3%); Escherichia coli (n=17; 21.3%); Serratia marcescens (n=13; 16.3%) and
others (n=5; 6.3%). One Salmonella Enteritidis carrying an OXA-48 was identified which is the first Salmonella carbapenemase-producing isolate in Canada. There were 13 different sequence types among the E. cloacae complex with STs 171, 177, 190, and 499 representing the most common (n=3), respectively. There were 13 K. pneumoniae STs with 101 being the most common (n=7), and 13 E. coli STs with 405 (NDM-5, n=3) representing the most common. No large outbreaks (>3 cases) were observed at any site.

CONCLUSIONS: Although numbers of CPE remain low in the Atlantic provinces, there are differences observed compared to the rest of Canada. For example, SME is the 3rd most common carbapenemase, and nosocomial transmission is rare.

P042 Molecular investigation of Carbapenemase-producing Enterobacteriales infections in Canadian Acute-Care Hospitals, 2010-2021

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OBJECTIVES: Global increase of carbapenem producing Enterobacteriales (CPE) raises concern over availability of treatment options. Occurrence and molecular mechanisms of CPE from infections are discussed.

METHODS: The Canadian Nosocomial Infection Surveillance Program (CNISP) conducts surveillance for CPE infected patients of all ages among 78 acute-care hospitals. Participating facilities submit specimens for confirmation of carbapenemase by PCR followed by whole genome sequencing.

RESULTS: Between 2010 and 2021, 330 isolates were collected from 316 infections. The majority of isolates were identified from urine (34%), blood (27%) and respiratory (14%) samples. Common carbapenemase genes detected were KPC (38%), NDM (30%) and OXA-48 (18%). Species harbouring OXA-48 were almost exclusively Klebsiella pneumoniae (Kp; 52%) or Escherichia coli (Ec; 38%). NDM was distributed among Ec (35%), Kp (27%) and Enterobacter cloacae (Ecl) (23%), KPC was associated with Kp (40%), Ec (26%) and Citrobacter freundii (Cf) (12%). Sequence typing showed 48% of Ec were among 4 sequence types (ST167, 38, 405 and 410), all were high risk clones and all but one harboured NDM and or OXA-48. Alternatively, 56% of Kp were among 7 sequence types (ST 11, 14-16, 147, 258/512). All ST258/512 were exclusively associated with KPC whereas the remaining ST were more commonly observed in NDM and or OXA-48. 83% of isolates with linked travel data harboured NDM and or OXA-48. Of these 56% were from India or Pakistan. XDRO was observed in 65% of isolates. Among the dominant species, Ec, Eclo, Kp and Cf, extensive drug resistance (XDR) was observed in 65%, 65%, 78% and 81% of isolates, respectively.

CONCLUSIONS: Certain carbapenemases are associated with bacterial species (OXA-48 and Ec/Kp), whereas others are found in more diverse bacterial collections (KPC and NDM). Ec carbapenemase infections, specifically NDM and OXA-48, are concerning as they are associated with global high-risk clones and international travel.

P043 Sub-lethal antimicrobial peptide challenge selectively induces AMP-resistance in multi-drug resistant E. coli

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OBJECTIVES: The widespread use of antibiotics has accelerated the emergence of multi-drug resistant (MDR) bacteria, known as “superbugs”. We employ computational and microbiology techniques to discover novel AMPs from amphibian and insect transcriptomes. A panel of MDR
bacteria, including carbapenem- and colistin-resistant *Escherichia coli* are used to validate AMP activity. Highly active AMPs are further examined for their propensity to stimulate resistance.

**METHODS:** Antimicrobial susceptibility testing (AST): AMPs are synthesized and serially diluted from 128 to 0.25 μg/mL in a 96-well format before being combined with a standardized bacterial inoculum. Minimum inhibitory concentration (MIC) values are reported at the concentration in which provide no visible growth following overnight incubation.

Resistance: Induction: Experiments: Surviving *E. coli* present in the ½ MIC well are passaged for 10 consecutive days in a repeat AST experiment. AMPs are tested alongside amikacin, penicillin, ciprofloxacin, and colistin antibiotics. Bacteria are prepared into a new AST experiment each day, with the MIC-drift being recorded for each antimicrobial condition; bacteria are glycerol preserved for downstream electron microscopy analysis.

**RESULTS:** We present novel AMPs with considerable (MIC < 4 μg/ml) activity against MDR bacteria. Three AMPs from insects (TeBi1, TeRu4, PaVa1) and one from amphibians (PeNi4) were found potent against *E. coli* (MIC = 1-2 μg/ml). Of these, PaVa1 was observed to rapidly induce resistance in vitro, resulting in a steep increase (128X) to this AMP’s MIC. The other three AMPs provided no notable shift in MIC over the 10-day experiment. Electron microscopy images show a thickening of the outer membrane following repeat treatment with PaVa1.

**CONCLUSIONS:** An AMP can rapidly induce resistance upon sub-lethal challenge in vitro. Experimental PaVa1*E. coli* show thickening of the outer cell wall, implicating the role of membrane synthesis for this AMP’s mechanism of action. This challenges the assumption that AMPs will not produce resistance at the same rate as conventional antibiotics.

**P044**
Diagnostic accuracy and limit of detection study for the Seegene Allplex™ GI-Parasite Assay using sodium acetate/acetic acid/formalin-preserved stool

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**OBJECTIVES:** The Seegene Allplex™ GI-Parasite Assay (GIPA) is a multiplex polymerase chain reaction (PCR) assay detecting Blastocystis hominis, Cryptosporidium spp., Cyclospora cayetanensis, Dientamoeba fragilis, Entamoeba histolytica, and Giardia duodenalis in fecal samples suspended in modified Cary-Blair (CB) medium. It is unclear whether using sodium acetate/acetic acid/formalin (SAF)-preserved stool affects the GIPA’s performance characteristics. Our study’s primary objective was to determine the performance characteristics of the GIPA assay in SAF-preserved stool specimens.

**METHODS:** SAF-preserved clinical stool samples submitted for stool ova and parasite examination at LifeLabs Ontario from March to September 2019 were prospectively assessed by GIPA assay after performing microscopic detection using standard procedures established in the laboratory. Samples were subjected to nucleic acid extraction using the Seegene STARlet system, and amplification on the CFX96 system. Analytical sensitivity of GIPA assay in SAF versus CB medium was assessed using spiked plasmids harboring amplification targets for each of the parasitic pathogens at final concentrations 1 – 10,000 copies/mL. We used descriptive statistics to analyze data; statistical testing was two-sided, with p<0.05.

**RESULTS:** Of 163 patient samples, 115 had parasites identified by standard microscopy, while 48 were negative. When compared to microscopy, the GIPA using SAF-preserved stool was 98.1% sensitive (95% CI: 93.2-99.8%) and 94.7% specific (95% CI: 85.4-98.9%); the diagnostic odds ratio was 918.00 (95% CI: 148.83-5662.05). Using target plasmids, the limit of detection of the assay in SAF was 10 copies/mL, which was one log higher than that in CB medium.

**CONCLUSIONS:** The GIPA using SAF-preserved clinical specimens had acceptable performance characteristics compared to microscopy. Analytical sensitivity with plasmids spiked in SAF was lower than that of CB, likely because of DNA degradation or crosslinking; however, this was still within the detection limits established by the manufacturer. These results support the use of the GIPA with SAF-preserved stool specimens.

**P045**
Validation of a multiplex qPCR assay to quantify antibiotic resistance genes in wastewater

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OBJECTIVES: blaNDM, blaKPC, blaOXA-48 are 3 clinically important antibiotic resistant genes (ARG) associated with carbapenamase-producing organisms (CPOs). MCR-1, a gene associated with colistin resistance, is reported in 57 countries including Canada. Here we present the validation of a multiplex qPCR assay to detect and quantify OXA-48, NDM, KPC, MCR-1 in municipal wastewater (WW).

METHODS: WW from five wastewater treatment plants (WWTPs) were spiked with bacterial isolates (positive for OXA-48, NDM, KPC), concentrated, then spiked with MCR-1 oligonucleotides. ARG-spiked WW was extracted, then tested in singleplex and multiplex. Singleplex and multiplex cycle thresholds (Ct) for each target were compared using ANOVA tests, Coefficient of Variation (CoV), and standard deviation (SD). Follow-up tests compared Cts of mixed ARG concentrations (one high, three low) against low ARG concentrations (all low). External standard curves were generated for every ARG to determine the limits of quantification (LOQ). The assay evaluated 38 samples from September 2021 to December 2021.

RESULTS: 15 spiked WW samples (three samples per WWTP) tested in singleplex and multiplex produced similar Cts for every ARG. ARGs at equimolar low concentrations produced comparable Cts to three low concentration ARGs mixed with a high concentration ARG. External standard curves defined the assays limit of quantification as 10 copies/μl for OXA-48, NDM, KPC, and 5 copies/μl for KPC. Between September to December 2021 at all five WWTPs, OXA-48 and KPC were consistently detected at 102 to 103 copies/ml, while NDM and MCR-1 detection was comparatively sporadic and low.

CONCLUSIONS: Validation findings and ongoing tests using the multiplex assay on current and archived samples demonstrate robustness and sensitivity at detecting all four ARGs of concern in WW.

P046
Molecular subtyping and macrolide resistance surveillance of Treponema pallidum in British Columbia

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OBJECTIVES: The increase of syphilis cases and widespread macrolide resistance in Treponema pallidum, have become a health concern in many countries. We applied CDC typing schemes and point mutation detection for macrolide resistance to monitor the trends of the circulating Treponema pallidum isolates in British Columbia.

METHODS: Real time polymerase chain reaction, targeting polA and tpp47, were used as a preliminary screening assay. Selected reaction-positive specimens were included in the subtyping and drug resistant study. Molecular subtyping was performed using the CDC typing method. This included examining the number of 60-bp repeats in the acidic repeat protein (arp) gene, T. pallidum repeat (tpr) polymorphism, and tpp0548 gene sequence typing. Macrolide resistance was assessed by point mutation detection in the 23S rRNA gene using restriction fragment length polymorphism.

RESULTS: Circulating T. pallidum strains were resolved around 30 subtypes, among which, subtype 14d/g was predominant, followed by subtype 14d/d. Point mutations in the 23S rRNA, which is associated with macrolide resistance, were detected in the majority of cases. The mutation A2058G was detected most frequently followed by A2059G.

CONCLUSIONS: Our study suggests that the typing resolution might not be high enough to distinguish between outbreaks but provided useful information for monitoring trends. While the 14d/g subtype was the predominant strain of T. pallidum in this study, we also observed evidence of other subtypes emerging as well as fluctuating between years. High frequency of macrolide resistant associated point mutants indicates that macrolide antibiotics, such as azithromycin and clarithromycin should be avoided as a treatment option.

P047
Concurrent sexually transmitted and blood borne infections (STBBIs) among people living with HIV in Manitoba 2018-2022

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OBJECTIVES: Our objective is to describe the frequency and type of sexually transmitted and blood borne infections (STBBIs) amongst people living with HIV (PLHIV) in Manitoba prior to their HIV diagnosis, at entry into HIV care, and during follow-up, disaggregated by sex at birth, gender, drug use, and unstable housing.

METHODS: A retrospective cohort study was completed. Clinical charts of all people ≥18 years old newly diagnosed with HIV in Manitoba, Canada between January 1st, 2018 and December 31st, 2021 were reviewed. We collected sociodemographic data such as sex at birth, gender, and age, as well as information regarding housing status, prior or current drug use, including use of injection drugs, past and current STBBIs.

RESULTS: 90% of females and 83.3% of males newly living with HIV in 2021, presented with at least one STBBI prior to their HIV diagnosis. At time of HIV diagnosis 88.9% of females and 86.3% of males had a concurrent STBBI. Between 2018-2021, 25-40% of newly diagnosed PLHIV experienced houselessness and had higher proportions of multiple concurrent STBBIs compared to those with stable housing. People who inject drugs had higher numbers of concurrent STBBIs at time of HIV diagnosis, and the number of STBBIs among PWID increased from 2018-2021. Rates of syphilis, hepatitis C virus, Chlamydia and Gonorrhea all increased from 2018-2021. In 2021 56% of newly diagnosed PLHIV had a syphilis infection and 42% had a hepatitis C virus infection at time of diagnosis.

CONCLUSIONS: The significant burden of additional STBBIs prior to HIV diagnosis, and during HIV follow up support the need for comprehensive STBBI testing, point-of-care testing and treatment and greater resources to prevent STBBI transmission, particularly among at-risk groups.

P048

Early observations on the impact of the COVID-19 pandemic on tuberculosis epidemiology in Ontario: A preliminary laboratory data analysis

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OBJECTIVES: The World Health Organization’s 2022 Global Tuberculosis (TB) Report described a rise in active TB cases, deaths, and burden of drug-resistant TB between 2020 and 2021 – the first time in almost two decades that these global data trends have been found to increase. These findings have been attributed to TB service disruptions during the pandemic. In 2021, Stop TB Canada conducted a survey to assess COVID-19 related disruptions on TB services in Canada. TB program staff reported diagnostic delays, more advanced disease, and large-scale diversions of TB staff to COVID-19 work leading to significant disruptions in contact tracing and latent TB infection management. To build an understanding of the impact of the pandemic on provincial TB epidemiology, we conducted an analysis based on laboratory data.

METHODS: Laboratory data were extracted from the provincial laboratory information system for the January 1st, 2017 and December 31st, 2022 date range. The impact of the pandemic on number of laboratory-confirmed TB cases, disease severity and drug resistance were determined by comparing differences in proportions between 2017-2019 and 2020-2022.

RESULTS: Annual submission of specimens to the mycobacteriology laboratory was significantly reduced compared to pre-pandemic years. However, percent positivity of cultures isolating Mycobacterium tuberculosis complex were significantly elevated each year from 2020-2022, and also corresponded to an increase in laboratory-confirmed cases of TB. Disease severity, based on smear grade of initial culture-positive specimens, was not found to differ across the 6 years evaluated. Similarly, no differences were observed in rates of resistance to first- or second-line therapy drugs.

CONCLUSIONS: These analyses begin to unravel the potential impacts of the early phases of the COVID-19 pandemic on TB in Ontario. Continuous monitoring of cases, disease severity and drug resistance throughout Canada is needed to further characterize and address the pandemic’s impacts on TB prevention and care.

P049

The resurgence of Influenza A to pre-pandemic levels as non-medical COVID-19 interventions ease

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¹¹¹
OBJECTIVES: The introduction of non-medical interventions such as masking, lockdowns, and expanded testing at the onset of SARS-CoV-2 pandemic in 2020 had a significant impact on SARS-CoV-2 and other respiratory viruses. Here we present incidence of influenza A (FluA) in periods with and without such interventions.

METHODS: The clinical microbiology laboratory performs respiratory virus detection by real-time PCR (qPCR) for the hospital and several of its regional partners, serving a combined population of ~500,000. FluA, influenza B (FluB) and respiratory syncytial virus (RSV) were interrogated in a multiplexed qPCR (INFAB) prior to Feb 2020. In subsequent years, SARS-CoV-2 (COVID) was tested either as a stand-alone qPCR (COVID) or incorporated into INFAB (RESP1).

RESULTS: COVID testing increased respiratory PCR testing volume by 16,000% (~1300 vs. 209,000 test per year). The pre-COVID seasonal FluA positivity waves, peaking at ~30%, were absent in the 2019/2020 and 2020/2021 seasons. There was a spike in FluA cases (n=634, 3.3%) in early 2021 that was not observed elsewhere in the province. However, within the first six weeks of testing (Oct 27 – Dec 7, 2022), FluA activity (n=672, 34.3%) has surpassed that from the entire 2020/2021 season and the positivity rate has returned to pre-pandemic levels.

CONCLUSIONS: Non-medical interventions during the first two years of the SARS-CoV-2 pandemic (2020 – 2022) coincided with the virtual absence of FluA. A resurgence of FluA activity is observed since the easing of these interventions.

P050
Laboratory-based surveillance for high pathogenicity avian influenza (HPAI) in exposed human patients
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OBJECTIVES: A Canada-wide outbreak of high pathogenicity avian influenza (HPAI) caused by H5N1 has been ongoing since February 2022. Detection of possible spillover of H5N1 from birds to humans is a high priority. Appropriate testing strategies are necessary to detect H5N1 in persons with exposure to infected poultry premises that have respiratory symptoms. We develop a testing strategy for suspect avian influenza cases and carried out this testing strategy during a time period (Fall 2022) where there was a high number of HPAI infected premises and high rate of respiratory infection in human community cases.

METHODS: The testing algorithm implemented was as follows: Suspect avian influenza cases are flagged by public health to the microbiology lab. Samples are tested for influenza A by tests targeting the matrix gene. Samples positive for influenza A are reflexed to an H1/H3 subtyping qPCR; if negative for H1/H3, samples are reflexed to an H5 subtyping qPCR. Samples negative for influenza A are tested by qPCR and/or respiratory panels to determine a respiratory diagnosis. Testing for suspect cases is captured in the laboratory information system with a specific comment code.

RESULTS: Ten suspect avian influenza cases were flagged by public health by Dec 8, 2022; none were positive for HPAI. Two cases were positive for SARS-CoV-2, 2 cases were positive for influenza A and subtyped as H3N2, 5 cases were negative for respiratory viruses and 1 sample was not forwarded for additional testing according to the process.

CONCLUSIONS: Spillover events of infectious diseases between animal and human populations are rare but can have significant impacts. Laboratory testing algorithms need to be able to rapidly detect avian influenza in humans to manage public health risk.

P051
Respiratory virus co-infections: increased prevalence or increased testing?
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OBJECTIVES: Monitor incidence and prevalence of respiratory virus co-infections by qPCR multiplex testing of hospital samples.

METHODS: Data from all qPCR multiplex tests conducted by the hospital from Nov. 1, 2017 – Dec. 7 2022 was obtained from the hospital information system. The tests include INFAB (targets: Influenza A (FLUA), Influenza B
Abstracts

A total of 1098 influent samples from five wastewater treatment plants (WWTPs) could be used to understand norovirus activity in the community.

RESULTS: The number of qPCR multiplex tests has increased from 49.4 tests per week pre-pandemic, peaked at 4614.0 tests per week during the pandemic, and settled around 933 tests per week post-pandemic. Since Nov. 2017, there have been 11,078 samples that tested positive for at least one virus, and 80 samples that tested positive for two or more viruses (0.72%). The percent positivity for co-infections was 0.36% from INFAB (n=3, total infections =828), 0.52% from RESP1 (n=51, total infections =9842), and 6.37% from RESP2 (n=26, total infections =108). Combinations of FLUA, COVID-19, and RSV account for 70% of the co-infections, where the other 30% of co-infections are attributed to viral targets in RESP2 (range: 1.3 – 3.8%). Finally, the percent positivity for co-infections is highest in children between the ages of 0-10 years (1.0%) and 10-19 years (0.72%) compared with all other age groups (range: 0.15-0.31%)

CONCLUSIONS: The emergence of novel pathogens (SARS-CoV-2) and increased testing (number of targets) impact the number of co-infections that are identified. Detecting respiratory virus co-infections are important in susceptible populations and to identify patients who may have different responses to vaccines, biologics and antiviral therapy.

P052 Monitoring norovirus in the community using wastewater-based epidemiology
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OBJECTIVES: Norovirus is a gastrointestinal pathogen of global importance, which causes frequent global outbreaks, and has a significant burden on global healthcare systems. Despite this, norovirus is frequently under-reported, and asymptomatic cases are missed from healthcare recording systems, meaning that norovirus transmission and sources are elusive. Wastewater-based epidemiology has

been employed throughout the COVID-19 pandemic for monitoring of SARS-CoV-2 within communities, and has helped to pre-empt local outbreaks and identify new variants. The objective of this study was to understand the utility of wastewater surveillance for norovirus. We studied the correlation between norovirus outbreak data and norovirus levels in wastewater to see if monitoring of norovirus in influent from wastewater treatment plants (WWTPs) could

METHODS: A total of 1098 influent samples from five WWTPs were collected from January 2021 to November 2022. The samples were processed through a viral concentration and extraction protocol and tested using real-time qRT-PCR for quantification of norovirus GI and GII. Correlations were assessed using Kendall’s Tau and the differences in outbreak and wastewater data were assessed using the Wilcoxon Rank-Sum test.

RESULTS: Clinical outbreak data from 2021-2022 was significantly correlated to GII norovirus levels in wastewater (p< 0.001, tau = 0.44). Norovirus outbreaks were found to be significantly higher in the first half of 2022 compared to the first half of 2021 (p= 0.013). Norovirus levels in wastewater during these same periods were also significantly higher in 2022 than 2021 (p= 0.0039). Changes in COVID-19 counter-measures in 2022 may explain the higher norovirus levels and outbreaks that year.

CONCLUSIONS: The clear correlations between outbreak and wastewater data presented in this study suggest that, in the absence or under-reporting of clinical norovirus cases, wastewater-based epidemiology can be used to identify the occurrence of norovirus outbreaks within the community.

P053 Genomic analysis suggests transmission of fluconazole non-susceptible Candida parapsilosis within two hospital networks
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OBJECTIVES: Candida parapsilosis infections are a common cause of non-albicans invasive candidemia. It is increasingly recognized that C. parapsilosis has the potential to cause serious healthcare associated illness, as well as the potential to be transmitted in a healthcare setting and to develop drug resistance to commonly used antifungal agents. Here, we use whole genome sequence (WGS) analysis to retrospectively investigate fluconazole non-susceptible isolates collected from patients of two Ontario acute care hospital networks from 2016 to 2022 in order to determine genetic relatedness and potential in-hospital spread.

METHODS: Phylogenetic analysis was conducted using WGS data of all 20 fluconazole resistant (MIC ≥ 8 μg/mL), 8 suscepible-dose dependent (SDD) (MIC = 4 μg/mL) isolates during 2016 and 2022 from the 2 hospital networks, as well as 13 fluconazole susceptible (MIC ≤ 2 μg/mL) C. parapsilosis isolates from the same facilities (n=39 blood; n=1 synovial fluid, and n=1 ascitic fluid). An additional 20 blood isolates from Ontario patients not related to the investigation were also analysed.

RESULTS: Twenty-seven of 28 fluconazole non-susceptible isolates and 2 susceptible isolates from the 2 hospital networks formed a phylogenetic cluster. Two isolates from other healthcare institutions were also part of the cluster. Cluster isolates were genetically highly similar and distinct from non-cluster isolates. The results suggest the presence of a persistent strain of fluconazole non-susceptible C. parapsilosis causing infections in patients of the hospital networks over a period of 6.5 years. Twenty-eight of 29 fluconazole non-susceptible cluster isolates had a K143R mutation in the lanosterol 14-a-demethylase (ERG11) gene, a mutation associated with azole resistance.

CONCLUSIONS: The findings underscore the importance of monitoring local antimicrobial resistance trends and demonstrates the value WGS analysis to detect and characterize clusters and outbreaks. Timely access to this type of information can inform targeted infection control measures.

P054
A reduction in Candida parapsilosis susceptibility to fluconazole between 2019 and 2021

Ceylon Simon¹, Susan M Poutanen¹²

OBJECTIVES: Antimicrobial resistance continues to be a concern for bacterial and fungal species. An academic hospital microbiology laboratory in a metropolitan urban region was recently alerted to concerns of rising numbers of fluconazole-non-susceptible Candida parapsilosis in an ICU. The aim of this work was to compare C. parapsilosis susceptibility to fluconazole over time across multiple hospitals served by the academic hospital laboratory.

METHODS: Consecutive C. parapsilosis blood isolates from four tertiary-care hospitals, one patient per year, from 2016 through 2021 were reviewed. The proportion of isolates that were fluconazole susceptible (defined as susceptible or susceptible dose-dependent) were graphed with 95% confidence intervals calculated using GraphPad QuickCalcs. Trends were compared across sites.

RESULTS: A total of 213 C. parapsilosis blood isolates were identified from four hospitals (ranging from 20 to 105 blood isolates per hospital) from 2016 through 2021. A reduction in fluconazole susceptibility was noted in all hospitals from 2019 to 2020 to 2021 from a weighted average percent susceptibility of 100% to 85% to 76%, respectively. Among the index ICU ward, percent susceptibility to fluconazole among blood C. parapsilosis isolates dropped from 100% to 58% to 29% over the same time period (Figure P054-1).

CONCLUSIONS: A reduction in fluconazole susceptibility in C. parapsilosis was noted across four different hospital sites with a dramatic drop noted in susceptibility in ICU isolates at one hospital between 2019 and 2021. Molecular typing and epidemiological analysis are ongoing to determine relatedness of isolates and possible nosocomial transmission. Trending data over time and by hospital ward in real-time would have allowed an earlier detection of this concerning reduction in fluconazole susceptibility in C. parapsilosis.

P055
Isolation of an emerging Trichophyton species, in an Ontario community laboratory

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OBJECTIVES: Recently there have been reports of the global spread of an emerging trichophyton species which was first described from the Indian subcontinent in 2019. This new species was named Trichophyton indotineae (*T. indotineae*) and it belongs to genotype VIII of *Trichophyton mentagrophytes*. *T. indotineae* differs from *T. mentagrophytes* / *T. interdigitale* complex by being positive for urease test and Hair Perforation Test (HPT). It has point mutations in the squalene epoxidase gene and is reported to cause extensive dermatophyte infection of the skin which is resistant to treatment with terbinafine.

This study aimed to determine the presence of this novel trichophyton species, *T. indotineae*, in skin specimens submitted to a large community laboratory.

METHODS: Between April 1 and August 31, 2022, we prospectively investigated skin specimens submitted to the mycology laboratory for the presence of *T. indotineae*.

Figure P054-1: Percent fluconazole susceptible or susceptible dose-dependent *C. parapsilosis* blood isolates from 2016-2021 at Index Hospital and Index Hospital-ICU.
**P056**

**WITHDRAWN**

**P057**

**Screening practices for antimicrobial-resistant organisms in a network of Canadian acute care hospitals**

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**OBJECTIVES:** To understand variations in antimicrobial-resistant organism (ARO) incidence, we describe the different screening practices of acute care hospitals in the Canadian Nosocomial Infection Surveillance Program (CNISP) network in 2021.

**METHODS:** CNISP – a hospital-based surveillance system – annually collects data on methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* (VRE), carbapenemase-producing *Enterobacterales* (CPE) and *Candida auris* screening practices, and number of screening tests via a standardized questionnaire.

**RESULTS:** In 2021, of 89 acute care hospitals participating in CNISP surveillance, 40 (45%) provided data regarding MRSA, VRE, CPE and *C. auris* screening practices. Hospitals were distributed across central (20/40, 50%), western (18/40, 45%), eastern (1/40, 2.5%) and northern (1/40, 2.5%) Canada, the median number of beds was 358 (interquartile range: 214 to 480), and almost three-quarters were teaching hospitals (n=29, 72%). Almost all screened for MRSA (41% universal admission screening (UAS), 56% targeted screening (TS) and 3% no screening (NS)) and CPE (23% UAS, 72% TS and 5% NS). Two-thirds screened for VRE (15% UAS, 51% TS and 33% NS). Approximately one-quarter screened for *C. auris* (28%) – all of which screened for *C. auris* in patients hospitalized outside of Canada in the past 12 months. Among screening hospitals, all screened for MRSA, VRE and CPE in patients during hospitalization. Hospitals more commonly screened for VRE than MRSA and CPE in intensive care, hematology/oncology, and transplant patients. The number of screening tests per 100 admissions was highest for MRSA (90), followed by VRE (40) and CPE (28).

**CONCLUSIONS:** Universal admission screening was most common for MRSA, followed by CPE and VRE. The majority of hospitals performed targeted screening for CPE and did not screen for *C. auris*. Despite responders representing a subset of Canadian acute care hospitals, these data help quantify differences in ARO screening practices. ARO rates should be evaluated in the context of these differences.

**P058**

**Prevention of infections in cardiac surgery study (PICS): a pragmatic cluster-randomized factorial crossover vanguard study**

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**OBJECTIVES:** There is a wide range of prophylactic antibiologic regimens used for patients undergoing open-heart cardiac surgery. We present a vanguard cluster cross-over factorial trial comparing cephalazolin monoprophylaxis to a combination with vancomycin, and short versus prolonged administration.

**METHODS:** We randomized four cardiac surgical institutions to 1:4 different orders of the four study arms. Ethic boards approved a waiver of individual informed consent with a patient opt-out option. Data collection was based on chart review and a phone call on or after postoperative day 90 to eligible patients who underwent cardiac surgery. In
Clinical justification for urine cultures may reduce unnecessary testing and therefore improve antibiotic stewardship and more relevant microbiology results. We sought to determine the impact of mandatory clinical justification for urine cultures on urine culture volumes and laborato

RESULTS: We enrolled four study sites in a staggered manner and enrolled 5,992 patients with complete data to date. The proportion of patients not receiving pre-, intra- and post-operative antibiotics according to the study protocol was 2.8%, 2.5%, and 3.0%, respectively. Deep/organ-space infections occurred in n=64 (1.1%) and superficial infections in n=100 (1.7%) cases. Agreement by the three outcome adjudicators was 100% and 92%. Based on the intra-class correlation of 0.0028 and the overall event rate of 1.1% from the vanguard phase, we require an additional 15 study sites with 31,000 patients to achieve 80% power to detect a difference in the relative risk of 30% for the two study questions in hierarchical order at a significance level of 5%.

CONCLUSIONS: The cluster-randomized factorial crossover design is feasible and highly efficient to address two study questions in one study. We successfully enrolled 4 sites with 6,000 patients and are working towards conducting the full trial powered for clinical outcomes.

P059
Mandatory clinical justification for urine cultures does not impact Long-term culture volumes or culture positivity

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OBJECTIVES: Clinical justification for urine cultures may result in improved utilization of urine cultures, improved antibiotic stewardship and more relevant microbiology results. We sought to determine the impact of mandatory clinical justification for urine cultures on urine culture volumes and positive test proportion.

METHODS: On June 1, 2021, Manitoba hospital microbiology laboratories implemented a strict requirement for clinical justification of urine cultures through a standardized requisition. Appropriate justification included lower urinary tract infection symptoms, suspected pyelonephritis, suspected sepsis, NICU admission, culture for asymptomatic bacteriuria in pregnancy or prior to an invasive urological procedure, and culture for bacteriuria after recent renal transplant. Samples without justification were rejected with the opportunity for clinical staff to provide the clinical justification by contacting the laboratory. In this study, we compared total urine culture volumes in the pre-intervention (January-May 2021), immediate post-intervention (June 2021) and late post-intervention period (July-December 2021) at three urban hospital laboratories to determine any significant impact on total cultures and laboratory workload. In addition, we compared the positive culture proportion between these three periods as a surrogate for inappropriate culture requests.

RESULTS: In the pre-intervention period, the average total volume of urine cultures was 7,904 per month at the three hospital laboratory sites. This abruptly declined in the immediate post-intervention period to 6,982 (-11.7%) but rose again to pre-intervention volumes in the late-post-intervention period (8,004 specimens per month, +1.3%). The positive proportion of urine cultures changed very marginally from 54.8% to 56.7% between the pre- and post-intervention periods (+1.9%, p=0.0419) and was 55.6% during the immediate post-intervention period.

CONCLUSIONS: Implementation of a strict justification requirement with a standardized requisition for urine cultures did not reduce volumes in the long term. As a surrogate for more appropriate use of urine cultures, positive culture proportion increased slightly in the long-term, by only 1.9%.

P060
Seal or no seal? The effect of sealant on respirator particulate filtration efficiency testing

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OBJECTIVES: Our confidence in respirators to provide protection is due to the rigorous certification process by the National Institute for Occupational Safety and Health (NIOSH). As part of certification, respirators undergo particulate filtration efficiency (PFE) testing, which measures the proportion of particles intercepted by the filtration material. To ensure particles travel through, not around, the
filtration material, respirators are sealed to metal plates. NIOSH PFE guidelines, while comprehensive, do not clarify how to make this seal. Consequently, a variety of sealants are used, which may affect the accuracy of testing. This variability could mean that respirators fail when they are meant to pass or vice versa. Our lab assessed an assortment of sealants to identify the best one for PFE testing.

**METHODS:** N95-respirators (3M-Model-8210; St. Paul, USA) were sealed in triplicate to metal plates using one of six sealants (silicone, polyvinyl acetate, cyanoacrylate, ethylene-vinyl acetate [hot-melt], epoxy, and polyurethane). Beeswax, the unofficial industry-standard, was used as the control. Sealant effectiveness was assessed by ease of application (“difficult” if sealant reapplication required), sealant-curing time (evaluated continuously via visual inspection), and PFE (tested at 0, 30, 60, 300, and 600mins post-sealant application using NIOSH protocol [TEB-APR-0059]). Results were reported as mean %PFE±SD (Excel).

**RESULTS:** Beeswax, hot-melt, polyvinyl acetate, polyurethane, and silicone were applied easily, and beeswax and hot-melt cured quickly (Table P060-1). PFE was >95% for all respirators after one hour, except those sealed with cyanoacrylate. There were no significant changes in PFE at 5 and 10 hours except for cyanoacrylate, which increased to 99.2%±0.255 and 99.1%±0.273, respectively.

**CONCLUSIONS:** PFE remained >95% for six of the seven sealants throughout testing. Of those six, four were unusable due to long cure times and difficult application. We found beeswax and hot-melt performed the best. As beeswax is renewable, we recommend it for N95 PFE testing.

**P061**

**Performance evaluation of insignificant urine culture growth categorization by WASPLab PhenoMATRIX**

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Dynacare Laboratories, Brampton, ON, Canada

**OBJECTIVES:** Artificial intelligence-based software and automation offer clinical microbiology laboratories a way to perform repetitive tasks and presumptively identify cultures with minimal involvement from Medical Laboratory Technologists (MLT). The objective of this study was to evaluate the performance of WASPLab™ PhenoMATRIX™ (COPAN Diagnostics, Murrieta, California) digital analysis compared to manual interpretation of urine cultures demonstrating no growth (NG) or no significant growth (NSG).

**METHODS:** Urine cultures were processed on Brilliance™ UTI Clarity™ (Themo Fisher Scientific, Waltham, Massachusetts) in WASPLab using a 1 ul inoculation loop and 16-hour 37 °C incubation. A 27-megapixel plate image was produced at 0 and 16 hours and used by PhenoMATRIX to segregate cultures based on user defined thresholds for NG and NSG. Manual interpretation by two blinded MLTs was performed. If results differed, interpretation by a third blinded MLT was performed. Interpretations were considered in agreement if PhenoMATRIX and two manual readings agreed. Reproducibility was assessed by re-culturing samples identified as NG or NSG in replicates of twenty.

**RESULTS:** Of 1010 and 1032 cultures identified by the PhenoMATRIX as NG and NSG, 879 (87.0%) and 827 (80.1%) agreed with manual readings, respectively. Post-adjusted agreements of 94.4% (953) and 85.3% (880) were obtained with inclusion of a third manual interpretation. Post-adjusted agreements for reproducibility of NSG were 90% (18), 95% (19), and 65% (13). The post-adjusted agreement for a re-cultured NG sample was 95% (19).

**CONCLUSIONS:** Results showed WaspLab PhenoMATRIX interpreted cultures without growth with greater agreement than cultures with NSG. Agreement increased when a third manual interpretation was performed and was highest in reproduced cultures containing pure or no bacterial growth and lowest in a culture containing multiple organisms. These data demonstrate that automated digital analysis can be used to segregate and presumptively identify urine cultures that obtain NG or NSG with similar agreement to that of an MLT.

<table>
<thead>
<tr>
<th>Sealant</th>
<th>Ease of Application</th>
<th>Sealant curing time</th>
<th>%PFE±SD after 1h</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beeswax control</td>
<td>Easy</td>
<td>&lt;5 mins</td>
<td>99.5%±0.113</td>
</tr>
<tr>
<td>Hot-melt</td>
<td>Easy</td>
<td>&lt;5 mins</td>
<td>99.0%±0.643</td>
</tr>
<tr>
<td>Epoxy</td>
<td>Difficult</td>
<td>&lt;5 mins</td>
<td>99.6%±0.087</td>
</tr>
<tr>
<td>Polyvinyl acetate</td>
<td>Easy</td>
<td>&gt;24 hours</td>
<td>99.6%±0.063</td>
</tr>
<tr>
<td>Polyurethane</td>
<td>Easy</td>
<td>&gt;24 hours</td>
<td>99.3%±0.236</td>
</tr>
<tr>
<td>Silicone</td>
<td>Easy</td>
<td>&gt;24 hours</td>
<td>99.4%±0.085</td>
</tr>
<tr>
<td>Cyanoacrylate</td>
<td>Difficult</td>
<td>&lt;5 mins to &gt;1 hour</td>
<td>92.2%±8.94</td>
</tr>
</tbody>
</table>

Table P060-1: Measures of sealant effectiveness.
**P062**

**Performance of BD Kiestra™ Urine Culture Application for automated digital image identification of pure or presumptive *E. coli* and automated release of negative urine cultures**

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**OBJECTIVES:** Evaluate accuracy of BD Kiestra™ Urine Culture Application (UCA) to segregate Pure or Predominant Presumptive *E. coli* (PPEC) compared to manual review (MR). Validate automated release (AR) of No Growth (NG) and No Significant Growth (NSG) urines by UCA.

**METHODS:** Over 25000 sequential hospital urine cultures on BD CHROMagar™ Orientation Medium from May - November 2022 were segregated by UCA and MR by technologists into 5 categories ([Figure P062-1](#)). Urines segregated as NG were AR while all others required technologist MR resulting. Results were retrospectively analysed with discords independently arbitrated. Complete agreement was defined when UCA and MR matched, tolerable discrepancy if UCA and MR were discordant but was corrected by MR, and intolerable discrepancy if UCA led to incorrect results not corrected by MR in those automated released.

**RESULTS:** Of ~14000 NG and NSG urines, only 6 resulted as intolerable discrepancy with remainder in complete agreement or tolerable discrepancy if AR. No intolerable discrepancies occurred within ~ 9000 NG urines that were AR. All 6 intolerable discrepancies were *Aerococcus urinae* with hazy growth, segregated as NSG by UCA and resulted as CG upon MR. 36 *A. urinae* isolates with good growth were correctly segregated by UCA. UCA correctly segregated 92.9% of ~2500 urines as PPEC. UCA called 7.0% as CG whereas MR identified as PPEC. UCA incorrectly segregated 3 specimens as PPEC that MR identified as *Citrobacter* spp. displaying purple instead of blue.

**CONCLUSIONS:** UCA demonstrated accurate AR of NG urines, saving resources and time. Only proportion of *A. urinae* with hazy growth may be missed if AR of NSG is implemented. UCA accurately segregated over 90% of PPEC, which can be designed to initiate further workup like identification and susceptibility testing, prior to technologist

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Segregation Category</th>
<th>Definition</th>
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</thead>
<tbody>
<tr>
<td>NG</td>
<td>No Growth</td>
<td>No Growth Detected</td>
</tr>
<tr>
<td>NSG</td>
<td>No Significant Growth</td>
<td>Quantity of Growth Detected &lt; 10^4 CFU/ml</td>
</tr>
<tr>
<td>CG</td>
<td>Complex Growth</td>
<td>Quantity of Growth &gt; 10^4 CFU/ml</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Mixed purity with 2 or more isolate types not classified as Pure or Predominant</td>
</tr>
<tr>
<td>PPRR</td>
<td>Pure or Predominant non-<em>E. coli</em> Requiring Review</td>
<td>Quantity of Growth &gt; 10^4 CFU/ml</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pure: ≥99% of growth of one isolate type</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Predominant: 90-99% of growth as one isolate type, where total 2 or more isolate types exist</td>
</tr>
<tr>
<td>PPEC</td>
<td>Pure or Predominant Presumptive <em>E. coli</em></td>
<td>Quantity of Growth &gt; 10^4 CFU/ml</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rose coloured colony that is:</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pure: ≥99% of growth of one isolate type</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Predominant: 90-99% of growth as one isolate type, where total 2 or more isolate types exist</td>
</tr>
</tbody>
</table>

[Figure P062-1](#): Sequential hospital urine cultures on BD CHROMagar™ Orientation Medium from May - November 2022.
review. Urine segregation allows focus on complex and positive cultures while saving time on NG and NSG urines with AR.

**P064 Laboratory detection of infant botulinum neurotoxin serotype B by mouse neutralization bioassay**

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**OBJECTIVES:** A previously healthy infant was admitted with clinically diagnosed infant botulism and an enema fluid from the infant was tested using the reference laboratory method for botulinum neurotoxin (BoNT): the mouse neutralization bioassay. From 1979-2021, laboratory-confirmed cases of infant botulism were predominantly BoNT serotype A. Here we describe a less common occurrence of laboratory-confirmed infant botulism attributed to BoNT serotype B.

**METHODS:** The enema fluid was processed for direct and culture testing using the mouse neutralization bioassay (intraperitoneal injections (IP) into female CD-1 mice) according to the laboratory-developed method and Health Compendium MFHPB-16 (published by Health Canada). Direct testing required injections including: neat (no antitoxin), with anti-ABE (trivalent) antitoxin, and with monoclonal anti-A, anti-B and anti-E antitoxins. Inoculated mice were observed for mouse toxicity, before euthanization. To confirm the presence of BoNT-producing *Clostridium botulinum*, primary enrichment cultures (unheated and heated) were prepared. A further trypsinized enrichment culture was prepared from presumptive *C. botulinum* isolated from primary enrichments. All enrichments were subjected to a similar injection schema to confirm BoNT through the mouse neutralization bioassay.

**RESULTS:** The direct testing showed mouse toxicity consistent with BoNT in neat, Anti-A, and Anti-E antitoxin injections. Anti-ABE and Anti-B injections neutralized toxicity, indicating BoNT serotype B detection. Injections from the primary enrichments did not detect BoNT, since no mouse toxicity was observed. In contrast, presumptive *C. botulinum* isolated from the primary unheated enrichment, (inoculated to the trypsinized enrichment), confirmed serotype B BoNT in the mouse toxicity test.

**CONCLUSIONS:** Both the direct sample and enrichment cultures prepared for the mouse neutralization bioassay are important for confirming infant botulism in the laboratory setting. Additionally, typing using an assortment of antisera can help confirm less common causes for infant botulism, such as BoNT serotype B presented here.

**P065 Evaluation of COPAN FecalSwab and ESwab Media for use in the BD Max Clostridioides difficile Assay**

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**OBJECTIVES:** *Clostridioides difficile* is responsible for nosocomial infections characterized by severe diarrhea. Clinical *C. difficile* assays typically use bulk stool as a specimen type, which presents challenges for transport and stability beyond 24 hours. The goal of this study was to evaluate the use of stool swabs collected into COPAN FecalSwab and ESwab media and tested in the BD Max *C. difficile* PCR assay.

**METHODS:** Swabs of bulk stool were collected and placed into FecalSwab and ESwab media. To determine the volume of each media to use in the BD Max assay, varying volumes of both medias from two separate *C. difficile* positive stools were compared to bulk stool. To evaluate stability, aliquots of FecalSwab and ESwab media from one positive stool were stored at 4 °C, room temperature, and 35 °C, then tested on the BD Max at 24, 48, and 72 hours and 7 and 14 days. To evaluate repeatability, 70 clinical specimens were tested by a lab-developed LAMP
assay using bulk stool, and the BD Max using bulk stool, FecalSwab, and ESwar.

RESULTS: Compared to unpreserved stool, 100 μl of both FecalSwab and ESwar media had a comparable crossing threshold and characteristic amplification curves. Crossing thresholds had a difference of <1.5 cycles across all storage periods, for each storage temperature, except for ESwar which was not reproducible at day 7 and 14 at room temperature and 35 °C. Among the clinical specimens, FecalSwab and ESwar had 100% positive/negative agreement compared to bulk stool when tested in the BD Max.

CONCLUSIONS: Stool swabs collected into FecalSwab and ESwar media are comparable to bulk stool for the detection of C. difficile using the BD Max C. difficile assay. Both medium were stable at 4 °C for 14 days but FecalSwabs were also stable at room temperature and 35 °C for 14 days.

P066
WITHDRAWN

P067
Comparison of two lateral flow assays and CIM in detection of carbapenemase in Enterobacterales

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OBJECTIVES: We evaluated the performance of two lateral flow assays to detect carbapenemase production in clinical and reference isolates of Enterobacterales, in comparison to the Carbapenem Inactivation Method (CIM).

METHODS: Fifty-nine clinical isolates were included in this retrospective study of carbapenemase detection in Enterobacterales using the NG-Test® CARBA-5, K.N.I.V.O. Detection K-Set, and CIM. The two lateral flow assays are designed to detect KPC, NDM, VIM, IMP and OXA-48-like carbapenemases from a bacterial colony within 15 minutes. Forty-nine isolates harbored one or two molecularly confirmed carbapenemase genes including KPC (10), NDM (9), VIM (8), IMP (3), OXA-48-like (14), OXA-48-like+NDM (3), IMI (1) and SME (1). Ten isolates carried only ESBL or de-repressed AmpC resistance. For CIM testing, a 10ul-loop was used to generate the inoculum. A meropenem disk was then immersed in the suspension of the isolate for 2 or 4 hours.

RESULTS: The accuracy of both lateral flow assays was 98%. False positive results were observed in one KPC isolate tested on the K-Set assay, which displayed weak lines for both NDM and OXA-48-like. One mucoid non-carbapenemase-producing Klebsiella isolate produced an invalid result on the CARBA-5 assay. The intensity of the ‘test lines’ were comparable for both lateral flow assays and background signal was not observed. CIM provided a sensitivity of 79% and 76% with 2 and 4 hours of incubation, respectively. It was particularly poor at detecting OXA-48-like strains. The specificity of CIM was 40% and 70% at 2 and 4 hours of incubation, respectively.

CONCLUSIONS: The two lateral flow assays provide excellent performance for the detection of carbapenemases, with minimal hands-on-time, easy interpretation, and rapid results. In contrast the CIM test provides sub-optimal performance, is laborious, slow, and challenging to interpret. Our findings also revealed that the two lateral flow tests are superior to CIM for precision, 100% agreement vs. 67% agreement.

P068
Evaluation of 16S rDNA PCR and sequencing results from clinical specimens for diagnostic purposes from a large reference laboratory

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OBJECTIVES: 16S rDNA PCR and sequence analysis is an attractive option to aid in diagnosis when routine bacterial cultures are negative, yet bacterial infection is suspected. Here we present a large data set on specimen characteristics and 16S rDNA PCR results including bacteria identified. This information can help inform on appropriate specimens for testing and interpretation of results.

METHODS: We performed a retrospective review of all clinical specimens submitted to PHO’s Laboratory for direct 16S rDNA testing between 2013 and 2021. Information was collected on Gram stain findings, culture results and if patient had received antibiotics prior to specimen collection. 16S rDNA testing included an end-point PCR followed by Sanger sequencing and analysis. Specimen data were extracted from a secure database.

RESULTS: A total of 1410 clinical specimens were evaluated. The average percent positivity was 14.4%. The most
common specimen types submitted for 16S rDNA testing were tissue (N=610; 43.3%), CSF (N=365; 25.9%) and other sterile fluids (N=348; 24.7%). A total of 198 clinical specimens (14.0%) were 16S rDNA PCR positive. Percent positivity was highest in tissue (N=77; 5.5%), fluid (N=73; 5.2%) and CSF (N=36; 2.6%). Cardiac tissue (N=40; 2.8%) and fluid from CNS (N=19; 1.3%) and pleura (N=15; 1.1%) was most frequently positive. Organisms were seen on Gram stain in 30.6% (N=52) of specimens that were 16S rDNA PCR positive and 10.8% (N=111) that were PCR negative. Antibiotics were used in 81.8% (N=130) of PCR positive and 72.7% (N=738) of PCR negative specimens. A total of 44 different genera were identified. *Streptococcus* spp. (N=71; 35.9%), *Fusobacterium* spp. (N=13; 6.6%) and *Staphylococcus* spp. (N=13; 6.6%) were detected most frequently.

**CONCLUSIONS:** 16S rDNA PCR and sequencing can be useful for some infections where cultures have been negative, in particular cardiovascular infections. 16S rDNA PCR positive specimens were more likely to have organisms seen on Gram smear.

**P069**

Assessing metagenomic stool extraction kits for use with Nanopore sequencing

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**OBJECTIVES:** Oxford Nanopore sequencing offers several benefits over Illumina for clinical metagenomics. These benefits include speed, low upfront cost, scalability, and long-reads. Long-reads facilitate genome assembly but to generate long-reads, long DNA fragments must remain after extraction. Further, the choice of extraction method impacts community composition and while many studies have examined this impact with Illumina, no studies have explored the impact using Nanopore.

**METHODS:** Among 25 commercially available extraction methods screened, we selected five for comparison: Qiagen DNeasy Blood and Tissue, Norgen stool DNA Isolation, QIAamp Fast DNA Stool Mini, MN NucleoMag DNA Microbiome, and ZymoBIOMICS DNA Mini Prep. The main selection criteria were frequency of use for metagenomics, variation in method type, availability, cost, and time. Methods were tested using ZymoBIOMICS Microbial Community Standard and evaluated using the Qubit, TapeStation, and MinION or PromethION.

**RESULTS:** DNA concentrations ranged from 4.8 to 25.8 ng/μL; DNA fragment peaks ranged from 18.7 to >60 kb; and read length N50s ranged from 5.9 to 12.2 kb. NucleoMag generated long fragments (56.6 kb) and read length N50 (12.2 kb) as expected from this magnetic bead method. ZymoBIOMICS maintained a community composition closest to the theoretical; all other methods had community compositions skewed towards gram-negative bacteria. ZymoBIOMICS had the highest concentration (25.6 ng/μL), shortest fragments (18.7 kb), and shortest read length N50s (5.9 kb). Given ZymoBIOMICS’ extensive bead beating (40 min) compared to the other methods (<10 min), short fragments/reads and accurate community composition are not surprising.

**CONCLUSIONS:** Our study will assist laboratories to select an appropriate extraction method for Nanopore metagenomics. Laboratories can choose their priority, community composition or read length to fit their purpose. If maintaining community composition is crucial, we recommend ZymoBIOMICS knowing shorter reads may affect downstream applications. This method may also best support pathogen detection with its high DNA concentrations.

**P070**

Are molecular methods changing how we diagnose enteric infections?

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**OBJECTIVES:** Molecular methods for infectious disease diagnostics have an important and expanding role in the microbiology laboratory. One area of focus has been for the detection of enteric pathogens. A survey of clinical microbiology laboratories in Canada was conducted to assess the current state of diagnostic methods used to detect enteric pathogens from stool specimens.

**METHODS:** Medical laboratory directors were sent an email in November 2019, requesting completion of the online survey facilitated by REDCap. Data was evaluated and summarized.
RESULTS: In total, 28 of 72 laboratories (39%) of laboratories responded. These include Ontario (N=14;50%), British Columbia (N=4;14%), Nova Scotia (N=2;7%), Newfoundland (N=2;7%), Alberta, Saskatchewan, Manitoba, Quebec, New Brunswick, and Prince Edward Island each had one laboratory respond (4%). Laboratories self-identified as a primary hospital (N=16), tertiary hospital (N=13), community diagnostic (N=4) or public health (N=2) laboratory, with the option to select multiple categories. Any method of enteric testing (i.e., molecular or culture) was performed for bacteria (N=27;96%), *Clostridium difficile* (N=26;93%), parasites (N=10;36%) and viruses (N=9;32%). Of laboratories that perform enteric testing, molecular testing was most frequently implemented for parasites (N=6;60%), viruses (N=5;56%) and *C. difficile* (N=14;54%). Molecular testing was least commonly performed for the detection of bacteria (N=6;22%). The uptake of molecular testing was low for any organism except *C. difficile*. Overall, the introduction of molecular methods changed laboratory testing criteria for bacteria (N=3;50%), *C. difficile* (N=2;14%), parasites (N=3; 50%) and viruses (N=1;20%).

CONCLUSIONS: The incorporation of molecular diagnostics in the microbiology laboratory has been increasing. We anticipate continued uptake of molecular methods for the diagnosis of enteric infections.

**P072**

**Assessment of the Seegene Allplex™ Respiratory Panels using repurposed capital equipment from COVID-19 pandemic testing**

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**OBJECTIVES:** The repurposing of capital equipment purchased during the pandemic for SARS-CoV-2 workflows using semi-automated instrumentation, was assessed in the verification of the Seegene Allplex™ Respiratory Panel Assays (RP1A, RP2 and RP3).

**METHODS:** Accuracy, precision, and analytical sensitivity were performed. To perform this validation, an economically lean workflow was assessed, which was not validated, or Health Canada approved by the manufacturer.

RESULTS: Using a combination of manual pipetting, and semi-automated extraction on the Roche MagNA Pure 96, we demonstrate 100% accuracy, excellent precision and lower limit-of-detection compared to our reference. The manual workflow and repurposing of SARS-CoV-2 extraction equipment was successful in demonstrating the higher performance of the Seegene Allplex™ respiratory panels compared to the current in-house lab-developed test. Repurposing of existing laboratory infrastructure used for SARS-CoV-2 testing, negated additional capital costs.

CONCLUSIONS: The use of a semi-automated workflow that included repurposing SARS-CoV-2 capital equipment was demonstrated for validation of the Seegene Allplex™ respiratory panels and highlighted the opportunities for cost-savings that other diagnostic testing labs can implement.

Next, we will look to repurpose and incorporate the Tecan Fluent® 1080 to replace manual pipetting, to improve workflow, and reduce the chances of errors and hands-on time. We will then directly compare our modified workflow with the manufacturer validated workflow.

**P072**

**Simultaneous detection and quantification of SARS-CoV-2, influenza A, influenza B, and respiratory syncytial virus from wastewater as a population-level surveillance tool**

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**OBJECTIVES:** Wastewater testing has been demonstrated to be an important surveillance tool during the COVID-19 pandemic. This study aimed to evaluate the feasibility of monitoring wastewater for multiple respiratory viruses using a single assay. We adapted and optimized a clinical assay for the detection of SARS-CoV-2, influenza A, influenza B, and respiratory syncytial virus (RSV) for use in wastewater testing. After validation, the assay was then applied retrospectively to archived wastewater samples.
METHODS: To adapt the clinical assay for use in wastewater testing, two targets were removed, probe dyes were reassigned, a passive reference dye was added, and external standard curves were generated. Primer and probe concentrations were optimized, and assay suitability was examined by: (1) determining the lower limits of quantification, (2) assessing potential competition between multiplexed targets, and (3) evaluating trends between wastewater results and clinical data from September 2021 to June 2022.

RESULTS: (1) SARS-CoV-2, influenza A, and RSV were all consistently detected (≥90%) at 20 copies/reaction. Influenza B was consistently detected (100%) at 5 copies/reaction. (2) The presence of a highly concentrated target (2000x-4000x) did not significantly affect the Ct values of weaker targets. The coefficients of variation of Ct values between weak targets with and without the presence of a highly concentrated competing target were, on average, below 3.5%, and were considered negligible. Importantly, (3) preliminary analyses indicated that wastewater quantifications of influenza A, influenza B, and RSV from September 2021 to June 2022 trended with clinical data.

CONCLUSIONS: The molecular multiplex assay developed in this study was able to reliably detect and quantify SARS-CoV-2, influenza A, influenza B, and RSV in wastewater. Monitoring multiple respiratory viruses within a single assay maximizes wastewater testing capacity and provides public health officials with unbiased and consistent population-level data on the incidence of SARS-CoV-2, influenza, and RSV within local communities.

P073
Testing the limits of multiplex respiratory virus assays at high cycle threshold values: Comparative performance of cobas 6800/8800 SARS-CoV-2 & Influenza A/B, Xpert Xpress SARS-CoV-2/Flu/RSV, and cobas Liat SARS-CoV-2 & Influenza A/B
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OBJECTIVES: Multiplex real-time RT-PCR assays for the detection of respiratory pathogens have emerged as valuable tools to optimize laboratory workflow and turnaround time during the COVID-19 pandemic. This study evaluates the detection of low viral loads of SARS-CoV-2 by four multiplex molecular assays: Roche cobas 6800/8800 SARS-CoV-2 & Influenza A/B Test, Cepheid Xpert Xpress SARS-CoV-2/Flu/RSV, cobas Liat SARS-CoV-2 & Influenza A/B, and a laboratory-developed test (LDT).

METHODS: Retrospective upper respiratory tract specimens at a range of cycle threshold (Ct) values (19 to 40) for various respiratory pathogens were tested by the four multiplex assays. Validated reference methods (for SARS-CoV-2: LightMix ModularDx SARS-CoV E-gene assay [TIB Molbiol] and for influenza A/B and RSV: Xpert Xpress Flu A/B/RSV test [Cepheid]) were used to analyze positive and negative percent agreement (PPA and NPA).

RESULTS: A total of 82 samples were assessed, with discordant results observed in a portion of the samples (10/82, 12.2%) where Ct values were >33. The majority of the discordant results (6/10, 60%) were false negatives. Overall, PPA was 100% (58/58) for cobas 6800, 97.4% (38/39) for GeneXpert, 100% (17/17) for Liat, and 90.5% (57/63) for the LDT. PPA for the LDT increased to 92.1% after manual review of amplification curves.

CONCLUSIONS: Commercial multiplex respiratory virus assays have good performance for samples with medium to high viral loads (Ct values <33). Laboratories should consider appropriate test result review and confirmation protocols to optimize sensitivity/specificity and may consider reporting samples with additional interpretive comments when low viral loads are detected.

P074
Automating a lab-developed respiratory virus panel using Hamilton MicroLab STAR, CFX and instrument manager
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OBJECTIVES: Laboratory developed (LD) assays, such as 12-target respiratory virus panel (RVP), require set-up of multiple PCR reactions and are complex to perform and interpret. Here we describe a method using MicroLab Star automated liquid handler (Hamilton), CFX96 Touch Real-Time PCR detection system (Biorad, CFX) and Instrument Manager (Data Innovations, IM) to automate extraction,
PCR set-up, result interpretation and result entry into the laboratory information system (LIS).

**METHODS:** Specimens, organized into single (32 specimens) or double (two sets of 32 specimens) runs were loaded directly onto the STAR to perform extraction and PCR plate set-up in a single process. The RVP assay requires set-up of three multiplex PCR reactions per sample and were prepared in a single 96-well PCR reaction plate (PCRrp) divided into three sections: A1:H4, A5:H8 and A9:H12. Real-time PCR of each plate was performed using an assay-specific plate template. Following verification of quality control metrics, run results were exported to IM and interpreted using an algorithm of logic statements incorporating acceptance criteria for internal control and interpretive criteria based on the cycle threshold (Ct) each target. The interpreted result for each target and Ct were subsequently deposited into LIS. Specimens with valid negative results were auto-final verified and those with any positive target, indeterminate or invalid result were flagged for technologist review before final verification.

**RESULTS:** The total instrument time, from loading specimens to a result deposited in LIS is 210 minutes for 32 specimens and 240 minutes for 64 specimens. Result interpretation by IM logic is highly accurate.

**CONCLUSIONS:** LD assays are often a cost-effective option for molecular testing, however, can be viewed as cumbersome to perform. This method describes a fully automated end to end processing of a multi-tube multiplex LD RVP assay that enables quick turnaround-time, high throughput, minimal hands-on time, standardized result interpretation and minimizes transcription errors.

**P076 WITHDRAWN**

**P077**

Analytical performance characteristics of commercial versus laboratory-developed assays for quantification of Epstein-Barr virus and BK virus DNA in plasma

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**OBJECTIVES:** Interpretation and comparison of plasma viral loads post-transplantation can be challenging, particularly for Epstein-Barr virus (EBV) and BK virus (BKV) due to a lack of standardized units and wide variety of in-house assays and molecular targets used. In this study, analytical performance characteristics of our laboratory-developed tests for EBV and BK viral load (“EBV LDT” and “BKV LDT”) were compared to new commercial assays (Roche cobas EBV and BKV quantitative nucleic acid tests).

**METHODS:** Retrospective clinical specimens previously characterized by the EBV or BKV LDT were tested in duplicate on cobas EBV or BKV and analyzed using linear regression and Bland-Altman plots. To assess precision, positive controls were tested in 20 replicates and the coefficient of variation (CV) of each assay was compared.

**RESULTS:** For cobas EBV, positive percent agreement (PPA) with EBV LDT was 90.9% (90/99), and negative percent agreement (NPA) was 100% (10/10). Of positive samples within the reportable range (n=77), Pearson’s correlation coefficient was 0.918. Bland-Altman demonstrated a systematic bias of -0.433log10 (cobas EBV running 2.7-fold lower). When samples with sufficient volume were re-tested in tandem on EBV LDT and cobas EBV (n=29), Pearson’s improved to 0.967 and systematic bias shifted to -0.006log10 (assays essentially equal), cobas EBV demonstrated improved precision with a CV of 13.5% (vs 19.4%).

For cobas BKV, PPA with BKV LDT was 100% (20/20), and NPA was 81.8% (9/11). Of positive samples within the reportable range (n=16), Pearson’s correlation coefficient was 0.957. Bland-Altman demonstrated a difference of +0.033log10 (cobas BKV running marginally higher). cobas BKV demonstrated improved precision with a CV of 11.2% (vs 13.4%).

**CONCLUSIONS:** Commercial assays (cobas EBV and BKV) demonstrated similar quantitative results and improved precision over LDT methods. When comparing assays using frozen banked specimens, samples should be tested in tandem to overcome potential bias from repeated freeze/thaw cycles.

**P077**

Evaluation of performance and workflow achieved by coupling a high-throughput automation instrument with a laboratory developed BK virus quantitative PCR assay

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**OBJECTIVES:** Interpretation and comparison of plasma viral loads post-transplantation can be challenging, particularly for Epstein-Barr virus (EBV) and BK virus (BKV) due to a lack of standardized units and wide variety of in-house assays and molecular targets used. In this study, analytical performance characteristics of our laboratory-developed tests for EBV and BK viral load (“EBV LDT” and “BKV LDT”) were compared to new commercial assays (Roche cobas EBV and BKV quantitative nucleic acid tests).

**METHODS:** Retrospective clinical specimens previously characterized by the EBV or BKV LDT were tested in duplicate on cobas EBV or BKV and analyzed using linear regression and Bland-Altman plots. To assess precision, positive controls were tested in 20 replicates and the coefficient of variation (CV) of each assay was compared.

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For cobas BKV, PPA with BKV LDT was 100% (20/20), and NPA was 81.8% (9/11). Of positive samples within the reportable range (n=16), Pearson’s correlation coefficient was 0.957. Bland-Altman demonstrated a difference of +0.033log10 (cobas BKV running marginally higher). cobas BKV demonstrated improved precision with a CV of 11.2% (vs 13.4%).

**CONCLUSIONS:** Commercial assays (cobas EBV and BKV) demonstrated similar quantitative results and improved precision over LDT methods. When comparing assays using frozen banked specimens, samples should be tested in tandem to overcome potential bias from repeated freeze/thaw cycles.
OBJECTIVES: BK virus (BKV) test volumes have increased 300%, to >3600 annually, since 2018 due to a growing renal transplant program at our hospital. Currently, BKV DNA extraction is performed using a mid-throughput (24 samples/run) semi-automated instrument, requiring multiple rounds of DNA extraction per weekly PCR run. Decreasing SARS-CoV-2 testing volumes has afforded the opportunity to re-purpose high-throughput SARS-CoV-2 testing instruments to support routine molecular microbiology testing. Thus, we evaluated the performance, hands-on time, and cost of a testing workflow that coupled the AltoStar® AM16 Automation System with a PCR-based laboratory developed test (LDT) for the detection and quantitation of BKV in plasma.

METHODS: Previously tested BKV positive (n=118; <2.0x10² IU/ml to 4.4x10⁶ IU/ml) and negative (n=75) clinical plasma samples were extracted on the AM16, and BKV detection and quantitation was performed using a PCR LDT. Limit of detection (LOD), linearity (5.0x10²–1.0x10⁶ IU/ml), and precision (at 2.5x10³ IU/ml and 2.5x10⁵ IU/ml) were evaluated using the WHO BKV international standard spiked into human plasma.

RESULTS: Sensitivity and specificity were 100% and 95.6% respectively, when compared to results from the existing BKV testing workflow. Linearity of the AM16-LDT workflow was found to extend over the entire tested range (R² > 0.99). LOD was estimated to be 1.65x10² IU/ml based on probit analysis. Precision (expressed as %CV) was 21.8% at 2.5x10⁵ IU/ml and 38.5% at 2.5x10³ IU/ml. Bland-Altman analysis showed that the accuracy of the viral load measurements obtained by the AM16-LDT workflow did not differ compared to the in-use commercial testing workflow. The AM16-LDT workflow reduced technologist hands-on-time and cost per test by approximately 65% and >60%, respectively.

CONCLUSIONS: Utilization of high-throughput automation instruments such as the AM16, in conjunction with LDTs, can yield robust quantitative molecular tests with considerably improved testing efficiencies and reduced costs.

P078
Enterovirus D68 PCR performance investigation against contemporary strains and establishment of a surveillance testing strategy in response to virus re-emergence in 2022
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OBJECTIVES: Enterovirus D68 (EV-D68) can cause severe respiratory illness and neurologic complications, particularly in children. Objectives: Following reports of EV-D68 re-emergence in 2022, we aimed to evaluate an EV-D68 specific PCR based on the VP1 region that was designed during the 2014 outbreak against current circulating strains and develop a surveillance strategy involving add-on testing for certain populations.

METHODS: 2014 EV-D68 specific PCR primer/probe sequences were compared to the same regions of recent EV-D68 strains, and PCR performance was evaluated by VP1 amplicon sequencing and comparison of PCR results from the original assay to a newly designed assay that corrected for observed primer/probe mismatches. A surveillance strategy was designed to add-on EV-D68 specific PCR to respiratory samples positive for rhino/enterovirus from paediatric cases (<19 years old) across the province during the EV-D68 season (August to December).

RESULTS: Primers/probes of the 2014 EV-D68 specific PCR observed mismatches against circulating strains from NCBI/Nextstrain in 2022: 2 bases in forward primers and 1 base in reverse primer. However, use of the 2014 PCR on rhino/enterovirus positive samples from 2022 detected positives and sequencing of the VP1 amplicon confirmed EV-D68. A new EV-D68 specific PCR was designed to address the mismatches to current circulating strains; performance was 100% in accordance with an average delta cycle threshold of 1.18 compared to the original assay, confirming that the original test was unaffected by the observed mismatches. In total, 364/1601 (23%) samples tested by add-on PCR in 2022 were positive for EV-D68. Typing results were not reported to ordering physicians unless the test was specifically requested. The positivity rate was highest in October (43%) and in children aged <6 (88% of positive cases).

CONCLUSIONS: Detection of EV-D68 requires evaluation of typing tests against current circulating strains and development of a surveillance strategy.

P079
Validation of a Real-Time PCR assay for the detection of Monkeypox Virus DNA
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OBJECTIVES: Monkeypox virus (MPXV) is an enveloped double-stranded DNA virus that belongs to the Orthopoxvirus genus of the Poxviridae family. There are two distinct genetic clades of the MPXV: Clade I (previously Central African Congo Basin clade) and Clade II (previously West African clade). Monkeypox is a viral zoonosis where the symptoms are similar to smallpox, with less clinical severity. Monkeypox virus has emerged as an orthopoxvirus of public health importance with multiple cases being identified in several non-endemic countries including Canada in May 2022 necessitating the need for a sensitive, specific, and rapid detection protocol for case identification.

METHODS: Previously published real-time PCR assays targeting the G2R region of the tumor necrosis factor receptor (TNFr) gene from monkeypox virus was validated for use at the Provincial Public Health Lab in Alberta, Canada. Performance of this assay was compared to the results obtained using a commercial kit detecting orthopoxviruses from Altona Diagnostics.

RESULTS: The 95% LOD was determined to be less than 3 copies/reaction using probit analysis on results from quantitated plasmid DNA. Assay reproducibility for positive samples with a high and low viral load tested in triplicate on three independent runs showed that the %CV ranged from 0.12% to 1.00%. Linear amplification of target was noted over seven logs of template concentration. Accuracy comparison with the commercial assay from Altona Diagnostics using urine, CSF, blood and lesion, skin, mouth, genital and nasopharyngeal swabs showed an overall sensitivity of 93.62% and specificity of 97.67%. A total of 868 specimens from 496 patients were tested between May and November, 2022 for MPXV and 117 specimens from 45 patients tested positive.

CONCLUSIONS: Assay performance was comparable to the commercial assay available. Local testing improves the turn-around-time for case identification and facilitates timely diagnosis to control the spread of contagious preventable infectious diseases.

P080
Hunting for Monkeypox mimickers: Use of the BioFire meningitis/encephalitis panel on lesion swabs to support alternative viral diagnoses

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OBJECTIVES: Monkeypox (MPX) is an emerging zoonotic disease of public health concern that presents as a rash mimicking other common viral exanthems. Unlike traditional testing algorithms relying on several assays, the BioFire FilmArray meningitis/encephalitis (ME) panel simultaneously detects common viral etiologies causing rashes; however, Biofire ME is only licensed for testing on cerebral spinal fluid. This study evaluated use of the BioFire ME panel for detection and discrimination of herpes simplex virus types 1 and 2 (HSV-1 and HSV-2), varicella zoster virus (VZV), human herpesviruses type 6 (HHV-6), enteroviruses (EVs), and human paroviruses (HPeVs) from a dermal or mucocutaneous swabs collected in universal transport media (UTM).

METHODS: Results of the BioFire ME panel were compared against methods used during clinical testing. Ten-fold serial dilutions in UTM of cultured viruses were used to compare analytical sensitivity, and analytical specificity was assessed using panels of microorganisms in UTM. Clinical sensitivity and specificity were assessed using 20 positive specimens each for HHV-1, HHV-2, HHV-6, VZV, EVs, and HPeV, as well as 35 known negative specimens that included 15 MPX-positive specimens.

RESULTS: BioFire ME was as sensitive as comparator methods, and correctly discriminated all HSV-1, HSV-2, VZV, HHV-6, EVs, and HPeVs from MPX and MPX-mimickers. Cross-reaction between EV and rhinoviruses A, B, and C were noted in the specificity panel.
CONCLUSIONS: Swabs in UTM collected for MPX testing are suitable for use on the BioFire ME panel, allowing more streamlined diagnostic testing for viral exanthems in patients under investigation for MPX infection.

P081
Evaluation of four real-time PCR assays for the detection of monkeypox virus

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OBJECTIVES: Mpox disease spread rapidly in the spring/summer of 2022 to over 100 countries including Canada. As a result, there was an urgent need to rapidly expand availability of diagnostic testing. Several commercial and lab developed tests (LDTs) were produced. Here we evaluated the performance characteristics of four different PCR assays for the detection of monkeypox virus.

METHODS: A total of 62 known positive, clinical, samples (one/patient) and 15 negative samples (positive for other viral targets e.g., HSV) were tested. Positives included lesion, nasopharyngeal, throat, and rectal swabs. Samples were extracted on the NucliSENS easyMag (bioMérieux). Extracted nucleic acid was run in parallel on 4 PCR assays: Altona RealStar Orthopoxvirus PCR kit (ARO), Altona FlexStar monkeypox virus PCR kit (AFM), Seegene Novaplex™ MPXV assay (SNM), and an LDT with both pan-non-variola orthopoxvirus and monkeypox virus-specific gene targets. Most assays (AFM/SNM/LDT) included a sampling control gene target. Results were compared to those of the Provincial reference laboratory.

RESULTS: Sensitivity and specificity, as well as average ΔCt (relative to ARO), of the 4 assays were: ARO 98.4% [61/62], 100%, ΔCt=n/a; AFM 96.8% [60/62], 100%; ΔCt=+1.0; SNM 93.5% [58/62], 100%, ΔCt=+3.8; and LDT 98.4% [61/62], 100%, ΔCt=+3.4. Five known positive samples were missed by one or more assays; all of these had a Ct value >32. PCR run times varied from 60 to >100 minutes. Detection of TNF Receptor Gene Deletion strains was not investigated. SNM and AFM assays were compatible with vendor-specific high throughput DNA extraction and automated PCR setup, with SNM also offering automated analysis.

CONCLUSIONS: All evaluated assays displayed excellent sensitivity and specificity. Each of these assays could pair with existing laboratory extraction workflows enabling rapid deployment. Implementing diagnostics in a timely manner during a public health crisis has proven critical for patient care and outbreak containment.

P082
WITHDRAWN

P083
Targeted amplification based whole genome sequencing of Monkeypox virus in clinical specimens

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OBJECTIVES: The 2022 mpox outbreak has led to more than 81,000 cases in 110 countries. Whole genome sequencing (WGS) has been at the forefront of surveillance and outbreak investigations for different pathogens of public health significance. Most institutions performing WGS on Monkeypox virus (MPXV) use a metagenomic approach, which is resource intensive. Thus, we designed a targeted amplification based WGS method to optimise the sequencing process of MPXV.

METHODS: We designed 43 pairs of primers (amplicons ~5 kb) with PrimalScheme to cover the ~200 kb genome and then added 12 primers to optimize the amplification step. We extracted nucleic acids from 130 clinical specimens (lesions, genital area and nasopharyngeal swabs). Nucleic acid amplification of two primer pools was performed with the Q5 Hot Start High-Quality DNA Polymerase with a modified thermocycling program. We used Nextera XT DNA Library preparation kit for library preparation followed by sequencing on the MiniSeq platform. Reads were mapped to a reference genome to produce a consensus sequence.

RESULTS: Consensus sequences had a mean depth of ≥350x for specimens with PCR cycle threshold of ≤28 with our targeted amplification WGS method. The targeted amplification method provided high virus reads, genome coverage (average 99.6%, 95% CI 99.3-99.8%) and mean depth (average 1409, 95% CI 1290-1520).

CONCLUSIONS: Targeted amplification enrichment is an efficient method for MPXV WGS. It increases genome
coverage and throughput, reduces turn-around time and cost, and can benefit public health surveillance and outbreak management. Our amplification approach with long amplifiers could be used for other viruses with large genomes.

**P084**

**Automatic surveillance and reflex PCR testing in response to Mpox emergence in Canada**

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**OBJECTIVES:** Mpox caused outbreaks globally in 2022, including in Canada. In response to the spread of Mpox outside of endemic regions, we developed a surveillance strategy for testing and reflex testing to ensure emerging and evolving strains were detected.

**METHODS:** A surveillance strategy was designed to add-on Mpox virus PCR to skin/mucosal lesion swab samples that were submitted for HSV testing from high-risk STI clinics and a subset of the general population from June to October 2022. Following reports of Mpox variants with deletions that could affect the sensitivity of our Mpox virus PCR, based on a widely used CDC protocol, all Mpox virus PCR negative samples were reflexed for testing by an Altona pan-orthopoxvirus PCR.

**RESULTS:** Results: In total, 3869 persons were tested by Mpox PCR between June and October 2022: 1290 by request and 2579 by add-on testing. The median age and sex distribution of cases tested by request and add-on testing were 33 years/71% male and 34 years/39% male, respectively. The percent positivity was 19% by requested testing and 0.4% by add-on testing. The demographics and risk factors of all 4 cases identified with add-on testing matched the known outbreak epidemiology. Reflex PCR testing to a pan-orthopoxvirus assay on Mpox virus PCR negative samples was performed on 431 cases collected between September and December 2022; all Mpox PCR negative samples were also negative by pan-orthopoxvirus PCR.

**CONCLUSIONS:** Conclusions: Laboratory response to an emerging pathogen such as Mpox virus should involve a broad diagnostic strategy, including implementation of testing for surveillance and to ensure all variants are detected.

**P085**

WITHDRAWN

**P086**

**PEP-in-Pocket (PIP): Long-term follow up of on-demand HIV post-exposure prophylaxis**

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**OBJECTIVES:** Pre-exposure prophylaxis (PrEP) and post-exposure prophylaxis (PEP) are established methods of HIV prevention. However, the suitability of these tools for individuals with infrequent, higher-risk HIV exposures might be limited due to cost, high pill burden and/or barriers to care. PEP-in-pocket (PIP) involves prospectively identifying such individuals and proactively prescribing them 28 days of PEP medication, along with instructions on when to initiate medications and how to follow up with care. We present long-term follow-up of a cohort of patients provided with PIP for HIV prevention.

**METHODS:** We conducted a retrospective evaluation of the clinical characteristics and outcomes of patients who used PIP for HIV prevention. Patients referred for PrEP or PEP care were offered PIP if they reported a low frequency (0-4 per year) of high-risk HIV exposures of any type. HIV prevention method was chosen based on shared decision-making between patients and clinicians and was outside the realm of this study. Patients were followed at regular 4-6 months intervals.

**RESULTS:** We followed 109 patients aged 20-69 for a total of 168 patient-years. 106 (97.2%) patients were assigned male at birth. Thirty-three (30.3%) patients self-initiated a total of 59 courses of PIP during the observation period. Patients fluidly transitioned between HIV prevention modalities as circumstances warranted: 34 (31.2%) changed from PIP to PrEP, and 32 (29.4%) changed from PrEP to PIP. There were 14 episodes of bacterial sexually transmitted infections in 9 individuals (8.3%) using PIP. No HIV seroconversions were detected.

**CONCLUSIONS:** PIP is an innovative and useful HIV prevention strategy for individuals with a low frequency of
higher-risk exposures, and provides patients with autonomy and agency over their care. Patients may transition between PIP and PrEP based on evolving risk. PIP should be included with PEP and PrEP as a biomedical HIV prevention option for individuals at risk for infection.

**P087**

**Applying a quality-framework to National Genomic Surveillance of a Pathogen: Lessons learned from the SARS-CoV-2 pandemic**

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**OBJECTIVES:** In response to the arrival of SARS-CoV-2 in Canada, the Public Health Agency of Canada, and the Canadian Public Health Laboratory Network (CPHLN), rapidly scaled up whole genome sequencing (WGS) of the virus to enable pathogen surveillance. To date, nearly 550,000 sequences are included in the Canadian SARS-CoV-2 database. Sequencing on such a scale has required implementing a distributed model whereby Canadian health partners contribute towards sequencing and analysis efforts. This scale-up requires coordination and quality control to ensure consistency across sites. Prior to the pandemic, WGS-based analyses were used primarily for research purposes, and therefore were performed with little consideration for accreditation-level quality management. To ensure high-quality analyses for public health action, quality standards and routine monitoring of analytical parameters have been implemented for operationalized genomic processes.

**METHODS:** This project required review of international standards of practice for genomic analysis, and implementation for the operationalization of SARS-CoV-2 sequencing and analysis.

**RESULTS:** Minimum quality standards have been established, and wet lab and analytical protocols are shared among partners. Operational bioinformatics workflows are available to partners through the PHAC-NML GitHub site (https://github.com/phac-nml/SARS-CoV-2-resources). Software development best practices and version control are documented per the git framework, and specialized tools for the evaluation of version updates have been developed. Documented procedures govern method changes and updates, and validations are shared via test summary packages. Test datasets for Illumina and Nanopore bioinformatic pipelines were developed for proficiency testing purposes, and wet-lab proficiency was conducted through a bi-annual external quality assurance program. Finally, all data are deposited and reanalyzed in a central database, enhancing uniformity for National-level surveillance activities.

**CONCLUSIONS:** This work represents our progress towards establishing a general quality-management framework to facilitate the operationalization of National genomic surveillance. Implementation and expansion of these activities are critical to ensure the broad-based utility of pathogen-based genomics can be realized.

**P088**

WITHDRAWN

**P089**

**The design and implementation of a patient and procedure-specific surgical antimicrobial prophylaxis computerized decision support tool: An OPTIMIZing surgical PROphylaxis (OPTIMIS PRO) project**

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**OBJECTIVES:** Although surgical antimicrobial prophylaxis (SAP) is a mainstay of surgical site infection prevention, its selection is often improvisational and suboptimal. In this study, we aimed to both assess barriers to evidence-based prophylaxis decision-making and develop a tool to improve appropriate prophylaxis selection for each patient and procedure.
METHODS: We conducted audits of SAP from 2018-2019 at a tertiary academic hospital based on guideline concordance (appropriate dosing/re-dosing; selection of agent for operation, etc.). Audit results were subsequently used to inform the creation of a decision support tool installed within the hospital information system to support patient-specific SAP recommendations in 2022.

RESULTS: SAP audits (n=200) showed that 39% of all procedures were guideline discordant, most often due to inappropriate dosing (56%) and initial antibiotic selection (17%). A computerized decision support tool was therefore subsequently created to provide specific, tailored, and guideline supported SAP recommendations that incorporated the patient’s procedure, allergy status, MRSA status, and weight (Figure P089-1). To determine the safety of using cefazolin in the pre-operative setting among patients with self-reported beta-lactam allergy, an evidence-based simplified two-item questionnaire was included (modACCEPt). To provide procedure-specific SAP recommendations for 3046 unique operations, international guidelines, recent literature, and input from 14 surgical divisions at our institution was sought. The novel support tool was designed as a best practice advisory that informed anesthesiologists of the recommended therapy at the moment of SAP decision making, and before administration. The prompt also provided an opportunity for potential modification and discussion with surgical colleagues. The tool was successfully installed, and the alert fired more than 16 000 times since implementation.

CONCLUSIONS: Surgical antimicrobial prophylaxis is often discordant with guidelines. Optimization is feasible using a novel patient- and procedure-specific computerized decision support tool.

P090
Impact of core lab critical calling elevated vancomycin trough levels
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OBJECTIVES: Delays in acting on supratherapeutic vancomycin levels can harm patients. We aimed to evaluate the impact of the core lab immediately calling vancomycin trough levels ≥30 mg/L.

METHODS: Quasi-experimental study of a random sample (n=105) of inpatients across two adult hospital sites with vancomycin trough levels ≥30 mg/L PRE- (2017 calendar year) and POST- (2019 calendar year) implementation of a critical call policy.

RESULTS: Overall, the mean age was 62.2 years and 56/105 (53%) of patients were females. The mean vancomycin level called was 38.4 PRE and 39.9 POST, respectively. On average, it took 559 minutes to change a vancomycin order PRE, vs 194 in the POST group (p<0.001 mean difference 365 minutes (mean difference 365.3, 95% CI 220.9 to 509.6). There was a similar number of patients PRE (21/50, 42%) vs. POST (26/55, 47%) who had their creatinine increased 1.5x from baseline within 7 days (p=0.59, OR 1.24, 95% CI 0.57 to 2.68). However, a larger proportion required dialysis in the PRE (9/45, 20%) than in the POST group (3/54, 5.6%; p=0.03, OR 0.24 95% CI 0.06 to 0.93). Similarly, more patient in the PRE group (4/49, 8%) required permanent hemodialysis than in the POST group (0/55, 0%; p=0.03; OR 0.92, 95%
CI 0.85 to 0.998). Numerically smaller proportions required ICU admission (6/32 (19%) PRE vs. 1/36 (3%) POST; p=0.06, OR 0.12 95% CI 0.01 to 1.09) and similar proportions died within 30 days (14/50 (28%) vs 11/55 (20%); p=0.34, OR 0.64 95% CI 0.26 to 1.59).

**CONCLUSIONS:** Our experience highlights the important role that the core lab can play in patient care: by initiating the critical call to address supratherapeutic vancomycin trough levels resulted in earlier dose adjustments, and the data suggests potential better patient outcomes.

**P091**

**Antibiograms: Value of trend analysis**

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**OBJECTIVES:** Annual antibiograms serve as a guide for empirical therapy. However, susceptibility is presented as an average percent susceptible, providing only a single static interpretation of susceptibility. To detect emerging antimicrobial resistance, especially those that are subtle, graphing susceptibility over time can visualize trends. The purpose of this study was to analyze susceptibility trends in the most prevalent organisms in a single tertiary-care academic hospital over time.

**METHODS:** Antibiotic susceptibility of bacterial isolates of blood and urine samples from 2013 to 2021 of a tertiary-care academic hospital was obtained from annual antibiograms created following the Clinical and Laboratory Standards Institute (CLSI) M39 document. Updated CLSI M100 breakpoints were used for all antibiograms throughout the study period. Trends were shown using Excel.

**RESULTS:** *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most prevalent Gram-negative organisms from blood and urine cultures. Susceptibility trends for *E. coli* and *K. pneumoniae* are shown in Figure P091-1. *E. coli* displayed a subtle trend in decreasing susceptibility for ceftriaxone, and a similar trend is seen for ceftriaxone, trimethoprim-sulfamethoxazole and tobramycin in *K. pneumoniae*. From 2019, urine isolates show a notable reduction of 38% in tobramycin susceptibility in *E. coli* and 78% reduction in *K. pneumoniae*. Not shown in Figure P091-1, blood and urine *P. aeruginosa* and blood and urine *Staphylococcus aureus* and enterococci, the

![Figure P091-1: Trends of antibiotic susceptibility of bacterial isolates of blood and urine samples from 2013 to 2021.](https://jammi.utpjournals.press/doi/pdf/10.3138/jammi.8.s1.abst - Thursday, November 16, 2023 11:39:45 AM - IP Address:174.116.52.24)
most prevalent Gram-positive organisms, showed relative stability in susceptibility.

CONCLUSIONS: Reporting antimicrobial susceptibility over time for bacterial isolates, as opposed to only reviewing static data at a single point of time, is valuable for detecting emerging resistance. Subtle trends, such as those seen for ceftriaxone from blood Gram-negative isolates, and dramatic trends, such as those seen with tobramycin from urine Gram-negative isolates, can go unnoticed by review of mass data sets presented in separate disconnected annual antibiograms.

P092
An analysis of the value added of subgroup stratification of antibiograms

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OBJECTIVES: The Infectious Disease Society of America and Clinical and Laboratory Standards Institute recommend the use of stratified antibiograms to guide empiric clinical treatment. Generating annual unit- and specimen-specific susceptibility reports is a laborious task involving large datasets and data manipulation. This stratification is often limited to academic hospital-based laboratories due to resource allocation challenges. This study compares differences in antibiotic susceptibility between an accumulative hospital-wide, all-specimen antibiogram and stratified antibiograms in order to identify the value added of subgroup stratification of antibiograms.

METHODS: Antibiotic susceptibility of bacterial isolates from 2021 at a tertiary-care academic hospital was obtained from published accumulative and unit- and specimen-specific stratified antibiograms. Differences in percent susceptibility by organism and drug between the accumulative and stratified antibiograms were calculated. A weighted proportion antibiogram percent susceptibility (WPAPS) was calculated for the accumulative and each stratified antibiogram. Heat maps representing differences in WPAPS were created and differences in WPAPS were compared for significance using Chi-squared Test. Excel and R Statistical Software were used for graph generation. GraphPad QuickCalcs was used for statistics.

RESULTS: Antibiograms from emergency department (ED) samples had significantly higher susceptibility measured by WPAPS whereas intensive care unit (ICU) and transplant (TR) show reduced susceptibility (Figure P092-01). Blood isolates and urine isolates were significantly less susceptible compared to hospital-wide isolates. In subgroup analysis, blood samples showed significantly higher susceptibility in the ED and significantly reduced susceptibility in the ICU. Urine shows higher susceptibility in ED and lower susceptibility in TR. Respiratory samples in TR showed a large reduction in susceptibility.

CONCLUSIONS: There are unit- and specimen-specific differences in susceptibility compared to accumulative hospital-wide antibiogram susceptibilities suggesting the need for unit- and specimen-specific antibiograms for optimal empiric antimicrobial management.

P093
Implementation of a Clinical Decision Support System for antimicrobial stewardship designed for Malagasy prescribers

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OBJECTIVES: Antimicrobial resistance (AMR) is a leading cause of death worldwide, with the highest burden in low-and middle-income countries (LMIC), making it a top public health priority. In the field of antimicrobial stewardship (AMS), clinical decision support systems (CDSS) can improve antimicrobial prescription. In LMIC, CDSS are scarce, their introduction for antibiotic prescribing could have a measurable impact: assisting prescribers with up-to-date information, broadly diffusing national guidelines, and informing the prescriber on the local epidemiology and resistance patterns.

To describe the first implementation and use of a CDSS for antimicrobial stewardship in Madagascar, a LMIC, Antibiotika Tsara (Smartbiotic). A first analysis of queries made on the CDSS, freely available on Android since September 2022, by healthcare prescribers.

METHODS: Madagascar has 28,427,000 inhabitants, with about 5,150 prescribers, there are about 0.18 medical doctors/1000 inhabitants. Antibiotika Tsara is a knowledge based CDSS, available with an offline mode, designed for and with Malagasy microbiologists, medical doctors, and epidemiologists. It was launched on the 7th of September 2022 and broadcasted through social network. It combines 55 pathologies described in the Malagasy national infectious guidelines produced by the Société de Pathologie Infectieuse Malgache, prescription tools and confronts them to the local epidemiology and bacterial resistance patterns issued from local reports. Anonymized utilization data was extracted via Google analytics.

RESULTS: Antibiotika Tsara was downloaded by 846 users in 20/22 regions of Madagascar in 3 months. 23,177 queries were observed during the last nine weeks. The most frequent queries were: genital discharge, urinary tract infections, acute infectious diarrhea and erythematous angina.

CONCLUSIONS: Antibiotika Tsara has been adopted and is widely used by health prescribers in Madagascar. CDSS in LMIC tailored to the local ecology are needed in order to address bacterial resistance and provide guidance in under-resourced territories. The burden of AMR is worldwide: this CDSS could also support AMS in Canada.

P094

Antimicrobial resistance of urinary tract pathogens isolated from non-hospitalized pregnant patients as determined by the Novel Weighted-Incidence Syndromic Combination Antibiogram (WISCA) Resistance (WISCA-R) profiling method

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OBJECTIVES: The weighted-incidence syndromic combination antibiogram (WISCA) is a recently described novel approach, used to inform empiric therapy decision-making. It displays antimicrobial susceptibilities per drug regimen for a given syndrome, rather than per organism as in traditional antibiograms. Asymptomatic bacteriuria during pregnancy can lead to urinary tract infection (UTI) which if left untreated can progress to serious complications, such as acute pyelonephritis, bacteremia, and fetal loss. We sought to construct a WISCA resistance (R) profile (WISCA-R) per oral agent used in the treatment of UTIs in pregnant patients, to identify agents with low resistance.

METHODS: Isolates were identified by conventional methods from urine cultures over a 2-year period ending November 2022 and were tested by disk diffusion or the Vitek-2 system (bioMérieux), according to CLSI guidelines, against amoxicillin-clavulanic acid (AMC), ampicillin (AM), cefazolin (KZ), cefixime (CEF), nitrofurantoin (FM), and trimethoprim/sulfamethoxazole (SXT). WISCA-R was constructed by multiplying the weighted incidence by the corresponding probability of resistance to the studied drug, including intrinsic resistance/imputed susceptibility, followed by the sum of obtained probabilities, to determine the WISCA-R rate for that drug.

RESULTS: Of 170,747 urine specimens processed over 2 years, a total of 318 isolates were recovered from prenatal cultures that yielded $\geq 10^6$ CFU/L, including Escherichia coli ($n = 178$), Streptococcus agalactiae (66), Enterococcus (23), Klebsiella (22), Proteus (13), Citrobacter (7), Enterobacter (2), and Staphylococcus (7) species. WISCA-R rates for AMC, FM, CEF, KZ, AM, and SXT were 4.4%, 10.3%, 12.6%, 18.6%, 35.8%, and 43.1%, respectively.
Abstracts

CONCLUSIONS: Of the oral agents commonly used to treat UTIs in pregnancy reported in this study, AMC and FM had the lowest WISCA-R rates among community urinary isolates. These results provide support for AMC and FM as useful agents with low likelihood of resistance, for the empiric treatment of UTIs in non-hospitalized pregnant patients.

P095
Antimicrobial use among adult inpatients in northern Canada
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OBJECTIVES: Antimicrobial resistance threatens our ability to prevent and treat infections. There are well-documented links between antimicrobial use (AMU) and emergence of resistance. AMU data from northern Canada are limited. Here we present benchmark AMU rates for adult inpatient populations in the territories and Statistics Canada’s provincial north.

METHODS: Participating acute-care hospitals submitted annual AMU data on all systemic antimicrobials from 2019 to 2021. Data were analyzed using defined daily doses per 1000 inpatient days (DDD/1000pd). Friedman tests were used to detect differences across years. Antimicrobials were categorized using the World Health Organization’s access/reserve (AWaRe) classification.

RESULTS: Between 2019 and 2021, 42–45 hospitals participated each year; all with <200 beds. More than 90% of participating hospitals were in Alberta or British Columbia. There was large variation in AMU between hospitals; the interquartile range for overall AMU ranged from 429 to 779 DDD/1000pd in 2021.

From 2019 to 2021, there was an overall 43% relative increase in use from 442 to 633 DDD/1000pd (p=.17). Third- and first-generation cephalosporins increased by 66% and 67% respectively and accounted for 39% of the overall increase in AMU.

The six most frequently used antimicrobials in 2021 were ceftriaxone (116 DDD/1000pd), cefazolin (68 DDD/1000pd), azithromycin (63 DDD/1000pd), piperacillin-tazobactam (42 DDD/1000pd), cefuroxime (32 DDD/1000pd) and ciprofloxacin (31 DDD/1000pd).

Among the AWaRe reserve antimicrobials, there was an increase in daptomycin from 1 to 6 DDD/1000pd (2019 to 2021, p=.04).

CONCLUSIONS: This study represents the largest collection of AMU data among inpatients in northern Canada to date. There was a 192 DDD/1000pd increase in AMU from 2019 to 2021, primarily driven by increases in third- and first-generation cephalosporins. A significant increase in daptomycin was found but contributed to only a small amount of total AMU. Ongoing surveillance is crucial for establishing benchmarks and antimicrobial stewardship guidelines.

P096
Adverse drug effects during community-based intravenous antimicrobial therapy
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OBJECTIVES: Although outpatient parenteral antimicrobial therapy (OPAT) reduces hospital stay and cost while improving patient satisfaction, an estimated 20% of patients experience an adverse drug effect (ADE). Given the lack of Canadian data, the objective was to characterize ADEs in a regional OPAT program over 3 years between 2019-2021.

METHODS: A search was conducted to identify ADEs (excluding mild gastrointestinal) during OPAT with vancomycin, daptomycin, or ertapenem. Electronic charts were reviewed to confirm ADEs and collect patient- and infection-related information. For each ADE, signs/symptoms, associated antibiotic(s), causality (Naranjo-score), severity (WHO-classification), timing, and outcome were detailed.
RESULTS: Overall, 147 ADEs were characterized: 68 vancomycin-associated, 40 daptomycin-associated, 20 ertapenem-associated, and 19 possibly associated with multiple agents. Causality was certain/probable in 76.5% (vancomycin), 62.5% (daptomycin), and 60% (ertapenem) of cases. In 67.6% (vancomycin), 82.5% (daptomycin), and 75% (ertapenem) of cases, the ADE was moderate/severe. The most common vancomycin ADEs were infusion-related reactions (39.7%), acute kidney injury (AKI, 22.1%) presenting at 18 days (median, [IQR 9–26]), non-anaphylactic allergies (16.2%, 6 days [2–11]), and neutropenia (14.7%, 16 days [13–22]). Vancomycin ADEs required emergency/urgent care assessment or hospitalization in 11.8% of cases, and vancomycin was changed to an alternative in 19.1%. Most daptomycin ADEs (87.5%) were elevated CPKs/myalgias (14 days [11–25]). Daptomycin ADEs required emergency/urgent care assessment or hospitalization in 7.5% of cases, and daptomycin was changed to an alternative in 17.5%. The most likely ertapenem ADEs were CNS effects (35%) presenting at 12 days [4–13] and Clostridioides difficile infection (20%). Ertapenem ADEs required emergency/urgent care assessment or hospitalization in 20% of cases, and ertapenem was changed to an alternative in 25%.

CONCLUSIONS: These data will be used to support OPAT practice guidelines including multidisciplinary approaches to monitoring and managing patient response including unintended ADEs.

P097 Antibiotic utilization at a tertiary care children’s hospital: Prospective audit and feedback during the viral surge

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OBJECTIVES: Surging occupancy of children’s hospitals due to viral and bacterial infections have posed challenges to antimicrobial stewardship efforts across the country. Little is known about institutional patterns of antibiotic utilization during this unique period. Our objective is to describe the results of hospital-wide prospective audit and feedback (PAF) of antibiotic use during the viral surge at a free-standing children’s hospital.

METHODS: PAF of all intravenous and enteral antimicrobial orders for patients admitted to medical, surgical, and intensive care units was conducted daily for three weeks. Inpatient units operated consistently above 100% capacity during the period. Recommendations were categorized by type and if they were implemented. Descriptive statistics were used to characterize antibiotic use, and linear regression was used to evaluate changes in the proportion of recommendations made and implemented over the audit period.

RESULTS: 1092 antibiotic-days were provided to 130 distinct patients. Most were prescribed by pediatric medicine (PM) (384; 35.2%), followed by Oncology (205; 18.8%) and critical care medicine (CCM) (136; 12.5%). The most common antibiotic prescribed was ceftriaxone (162 antibiotic-days; 14.8%). Respiratory tract infections were the most common indication (51.6%), accounting for 97.7% and 65.5% of antibiotic-days given by CCM and PM respectively. 147 recommendations were made for 79 distinct patients, with an average of 13 per day – an increase from 2 per day during the same month in 2021. The most common recommendations were to stop (71/147; 48.3%) or narrow therapy (32/147; 21.8%) antimicrobials. Overall, the rate of implementation was 53.4% (78/147). Over the audited period, the proportion of patients reviewed yielding recommendations decreased (p=0.03), and the proportion of recommendations accepted significantly increased (p=0.02).

CONCLUSIONS: Antibiotic utilization concentrated within PM and CCM for upper respiratory tract infections during the audit period. Syndrome- or specialty-based PAF strategies could be considered by resource-limited antimicrobial stewardship programs to maximize impact and resource-efficiency.

P098 Reduced susceptibility in Candida species: Value of Candida antibiograms and trend analysis

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OBJECTIVES: The emergence of antimicrobial-resistant organisms poses an ongoing challenge. Emerging resistance is largely focused on bacteria with hospital data presented typically in single-time-point formats. Reduced fluconazole susceptibility in Candida parapsilosis was recently identified as a concern by antimicrobial stewardship at an urban academic hospital. This study investigates the value in creating
Analyses of Antifungal prescribing in critical care: A retrospective descriptive chart review

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METHODS: A retrospective descriptive chart review was conducted in adult ICUs from August 1, 2020, to July 31, 2021. Data collected was reported using descriptive statistics.

OBJECTIVES: To describe patients who were prescribed antifungal therapy in terms of patient demographics, risk factors, pathogens cultured, sites of fungal growth, duration of antifungal therapy, and to determine if antifungal therapy was tailored to culture results.

RESULTS: 334 charts were analyzed. The majority of patients were admitted into the ICU for a medical indication (70.4%), were male (59.6%), and had a median age of 61 years. Common risk factors and considerations for IFI included fever, leukocytosis, neutrophilia, and documented severe sepsis. Only 23.4% of patients had documented multifocal colonization with a fungal pathogen, while 42.8% had only one site of growth and 33.8% having no documented growth. Oropharyngeal colonization with a Candida species was the most common fungal growth cultured (30.8%) and Candida albicans was the most common pathogen (33.6%). Antifungal spectrum was narrowed and broadened in the same proportion of patients (13.2%). The median duration of antifungal therapy was 9 days.

CONCLUSIONS: Antifungals may be overprescribed in the critical care setting and there is potential for antimicrobial stewardship efforts. Clinical decisions regarding not treating non-infectious colonization, and tailoring therapy when appropriate are opportunities for improved prescribing practices.

P100 What are the medico-legal risks of infectious disease physicians in Canada

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OBJECTIVES: The medico-legal risk of Infectious Disease specialists in Canada is unknown. The objective of this study was to identify the causes of these medico-legal risks with the goal of improving patient safety and outcomes.

METHODS: A 10-year retrospective review of Canadian Medical Protective Association (CMPA) closed medico-legal cases from 2012-21 was performed. Cases included civil-legal, regulatory college and hospital complaints against Infectious Disease physicians (TOW-52). Peer expert criticism was used to identify causes at the practitioner, team or system level using the CMPA contributing factors framework and was contrasted with the patient complaint.

RESULTS: Over 95% of Canadian physicians are members of the CMPA. At the end of 2021, there were 571 ID physician members of the CMPA (0.5%). In the 10-year period, there were 96 patient complaints: 45 college, 40 legal and 11 hospital. Both patient complaints and the peer experts identified deficient assessment and diagnostic error as key issues.

CONCLUSIONS: Antifungals may be overprescribed and the medico-legal risk of Infectious Disease physicians in Canada is unknown. The objective of this study was to identify the causes of these medico-legal risks with the goal of improving patient safety and outcomes.
10 cases were associated with severe harm including death. The rate of complaints during this time period was lower among ID clinicians compared to the rate of all physician members. As well the unfavourable medico-legal outcome was 26%. Although ID college complaints were much lower (17 vs 48 per 1000 members), this rate was increasing faster over the time period compared to all CMPA members.

CONCLUSIONS: The medico-legal risk of ID physicians is lower than the average Canadian physician. However, the rate of regulatory college complaints is rising. Attention to follow-up of test results and focus on clear patient communication may help mitigate or reduce patient harms and medico-legal complaints.

**P101**

**Design and uptake of a web-based, trivia-themed, medical education serious game in infectious diseases**

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**OBJECTIVES:** We applied gamification theory to create and design a daily, web-based, trivia game themed around infectious diseases, and measure its use.

**METHODS:** A web-based platform named Microbial Pursuit (https://firstline.org/microbial-pursuit) was created using a popular JavaScript framework called React. Puzzles were developed and validated by a community of practice including infectious disease physicians and pharmacists. The content of each puzzle incorporated history, etymology, epidemiology, microbiological characteristics, diagnostics, treatment and prevention strategies, spectrum of activity, or other unique facts. A unique puzzle was released daily following the launch of Microbial Pursuit on July 5, 2022, each with a series of four clues detailing information about the corresponding pathogen or antimicrobial. Players earned points based upon the number of clues needed to solve puzzles; the more clues a player used; the fewer points potentially earned. Puzzles from previous days remained accessible to players. Microbial Pursuit was free to play and was promoted through social media platforms, mobile apps, newsletters, and website forums.

**RESULTS:** 149 puzzles were produced and featured in Microbial Pursuit from July 5 to November 30, 2022. Microbial Pursuit was accessed a total of 12,956 times and played in 90 countries. Microbial Pursuit was played by a total of 5,004 users. A mean of 87.0 games were played daily and mean gameplay duration was one minute and fourteen seconds. 63% of Microbial Pursuit accessions were from a mobile device whereas 37% of accessions were from a desktop or laptop computer.

**CONCLUSIONS:** Microbial Pursuit demonstrated high uptake globally and accessions were quick with built-in gamification elements and incentives such as earning points. Additional features including cumulative points, streak records, and leaderboards might enhance our serious game. There is also potential to further study the user experience of Microbial Pursuit and its learning potential.

**P102**

**Introducing students to careers in laboratory medicine through a structured undergraduate course**

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**OBJECTIVES:** Staffing challenges are affecting laboratories across Canada. We are asked to do more with less and this is leading to recruitment difficulties, retention challenges and early retirements. Calls to action from the Canadian Society for Medical Laboratory Science (CSMLS) and provincial organizations have recommended promoting medical laboratory sciences as career options to high school and university students. The Laboratory Medicine entry-route Harmonization Task Force made similar recommendations in their report earlier this year. Our response to this was the development of a second-year undergraduate course entitled “Introduction of Medical Laboratory Sciences”.

**METHODS:** A course was designed to give students exposure to the breadth of laboratory medicine careers and specialties. The curriculum covered a wide range of disciplines with teaching workload shared across departments. Lectures covered: an introduction to the specialty, types of jobs and training required for these, a day in the life of a laboratory professional and how the lab has helped patients. Additional sessions covered Artificial Intelligence and Machine learning, Careers in Laboratory Medicine and the Future of Laboratory Medicine. Anonym ous course evaluations were sent out by the Bachelor of
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Health Science program and a survey was distributed by the course coordinator.

RESULTS: Informal feedback from students was overwhelmingly positive. Most reported that they will recommend this course to their peers and an informal survey showed that all respondents agreed that the course increased their awareness of careers in Laboratory Medicine, and they may consider pursuing a career in Laboratory Medicine as a result of completing the course.

CONCLUSIONS: Staffing shortages will continue unless we promote our specialty to the next generation of learners. This undergraduate course was an effective strategy to promote laboratory medicine. Similar educational initiatives are needed at other centers.

P103
The SAVE study, 2011-2021: Antimicrobial susceptibility profiles of invasive Streptococcus pneumoniae isolates reveals a changing epidemiology in Canada

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OBJECTIVES: To assess the antimicrobial susceptibility profiles of 14,138 invasive Streptococcus pneumoniae isolates collected in Canada between 2011 and 2021.

METHODS: Antimicrobial susceptibility testing was performed using the broth microdilution reference method (CLSI M07). Susceptibility was determined by comparing minimal inhibitory concentrations (MICs) to established breakpoints (CLSI M100).

RESULTS: In 2021, 89.8% of invasive pneumococci were susceptible to penicillin, according to the most stringent (meningitis IV) breakpoint. Additionally, 96.3% of isolates were susceptible to ceftriaxone, according to the most stringent breakpoint, whereas 100% of isolates were susceptible to levofloxacin. Across the 11-year study period, small but significant differences (P<0.05) in the percent of isolates that were susceptible to chloramphenicol (-2.1%), trimethoprim-sulfamethoxazole (-5.4%), penicillin (IV, non-meningitis breakpoint only, +1.6%), or ceftriaxone (+1.0%) were observed. During the same period, susceptibility to penicillin (IV, meningitis and oral breakpoints) and all other agents was not significantly different. The percentage of isolates that exhibited multi-drug resistance (MDR; resistance to three or more antimicrobials from different classes) in 2011 (8.5%) and 2020 (8.2%) was not significantly different, though there was a significant interim decrease observed between 2011 and 2015 (P<0.001) followed by a significant increase between 2016 and 2021 (P<0.001). Generally, resistance rates to antimicrobial agents included in MDR analysis were significantly associated with patient age, specimen source, geographic location in Canada, or concurrent resistance to penicillin or clarithromycin, but not biological sex of patients.

CONCLUSIONS: Invasive pneumococcal isolates exhibited similar in vitro susceptibilities to commonly tested antimicrobial agents between 2011 and 2021, though small differences emphasized the importance of continued surveillance as pneumococcal conjugate vaccines continue to change the epidemiology of S. pneumoniae in Canada.

P104
Manitoba’s HIV syndemic: Identifying the intersection of substance use disorder, houselessness, and other comorbidities in people living with HIV

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OBJECTIVES:
1. To describe the Manitoba HIV syndemic with a focus on substance use, houselessness, and previously diagnosed comorbidities in PLHIV in Manitoba.
2. To highlight the importance of a syndemic approach in providing patient centred care to PLHIV.
3. To describe the growing number of women living with HIV and the unique challenges they face.
METHODS: A retrospective cohort study was completed. Clinical charts of all people newly diagnosed with HIV in Manitoba, Canada between January 1st, 2018, and December 31st, 2021, were reviewed. Basic sociodemographic data, substance use history, STBBI and other comorbidities were collected. Further information on linkage to the Manitoba HIV program, and adherence to anti-retrovirals (ARVs) during follow up was collected.

RESULTS: We reviewed 517 individuals referred to MB HIV program, 415 were newly diagnosed in Manitoba. The main self-reported modes of transmission were heterosexual sex and injection drug use. Greater than 60% of women and 40% of men reported injection drug use, with methamphetamine as the primary substance. Of the new diagnoses, 42.4% were female sex. The reported sexual orientation of new diagnoses was: 75.6% heterosexual, 18.8% gay, 5.1% bisexual, 0.5% lesbian. Pre-existing medical conditions was reported by 81.7%, with mental health and sexually transmitted infections the most common. Houselessness was reported by 31%.

CONCLUSIONS: Manitoba is experiencing a syndemic of houselessness, injection drug use and mental health comorbidities among people with newly diagnosed HIV, as well as increasing representation of females who experience higher burden of houselessness and injection drug use. A multipronged approach addressing underlying social determinants of health, structural barriers, substance use disorder, housing, and mental health supports is needed to help diagnose, link to care and provide antiretroviral therapy to people living with HIV in Manitoba.

STUDENT POSTER PRESENTATIONS

SP001
Effects of oral iron supplementation on gut bacterial composition in Cambodian women of reproductive age: A randomized controlled trial
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OBJECTIVES: In countries where anemia prevalence is more than 40%, such as Cambodia, the World Health Organization recommends untargeted oral iron supplementation for all women of reproductive age (WRA). Most of the common iron supplements, however, have poor bioavailability. As such, the majority of iron remains unabsorbed in the colon where it can potentially confer a competitive advantage to iron-dependent enteropathogens. We aimed to examine the effects of two iron supplements with differing bioavailability on the gut microbiomes of Cambodian WRA. We hypothesized that women who consumed ferrous sulfate (lower bioavailability) would have a higher relative abundance of enteropathogens compared to ferrous bisglycinate.

METHODS: This study is a secondary analysis of a double-blind, randomized controlled trial of oral iron supplementation among 480 Cambodian WRA. Participants received 60 mg iron as ferrous sulfate, 18 mg iron as ferrous bisglycinate, or placebo daily for 12 weeks. Blood and stool specimens at baseline and 12 weeks were collected. Stool specimens from a subset of participants (n=172) were randomly selected for microbial analysis by 16S rRNA sequencing and targeted real-time PCR (qPCR).

RESULTS: At baseline, 1% of women had iron-deficiency anemia (hemoglobin <120 g/L and ferritin <15 mcg/L). Amongst the sampled subset, the most abundant phyla were Bacteroidota (45.7%) and Firmicutes (42.1%). Alpha and beta diversity were not significantly altered after either iron supplement. Ferrous bisglycinate appeared to increase the relative abundance of Escherichia-Shigella, but this was not replicated using other analytical tools. Nevertheless, qPCR detected a small, but significant increase in the enteropathogenic Escherichia coli virulence gene, bfpA, in the group that received ferrous sulfate.

CONCLUSIONS: We found that 12-weeks of ferrous sulfate and bisglycinate did not significantly alter the gut microbial composition in our study population. Furthermore, to our knowledge, this is the first study to characterize the gut microbiome in Cambodian WRA.

SP002
SARS-CoV-2 variants of concern show differential replicative fitness in primary human respiratory tract cells and transmission in Syrian golden hamsters
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SP003 Immunogenicity of COVID-19 vaccines: Initial findings from a prospective longitudinal cohort study

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OBJECTIVES: Many questions remain regarding the immunogenicity of novel SARS-CoV-2 vaccines. "Stop the Spread Ottawa" is a 34-month-long prospective longitudinal cohort study for which over 1,000 participants were recruited starting in September of 2020 and was created to study novel SARS-CoV-2 vaccines. The objectives of these analyses are to describe the SSO cohort after 10 months of follow-up in terms of SARS-CoV-2 vaccination, immunocompromised status, the number, timing, and types of vaccines received, and determine the impact of these factors, and additional covariates, on humoral vaccine response.

METHODS: IgG titres against SARS-CoV-2 spike, nucleocapsid and receptor binding domain proteins were quantified in monthly blood samples. Participant characteristics were described according to prior infection at baseline, dose 1 type, and vaccine type combinations for dose 1 and dose 2. Predictors of immunogenicity were investigated through univariate and multivariable quantile regression for participants without a prior infection based on self-report and serum testing.

RESULTS: Of 1,034 participants, 316 individuals had a compromised immune system at baseline and 952 were vaccinated at the time of analysis. 259, 562, and 119 individuals had received 2, 3, or 4 doses, respectively. Most participants received a Moderna or Pfizer-BioNTech vaccine for their first and second doses (n=833 and n=932). 117 people received Oxford-AstraZeneca for dose 1 and 11 for dose 2. The median time between dose 1 and 2 was 58 days (IQR: 35-76). Age and immunocompromised status were significant predictors of median IgG response 3 months (±1 month) post dose 2 in univariate quantile regression and multivariable quantile regression (while adjusting for sex,
race, BMI, smoking history, dose 1 and 2 type combinations, and the time between dose 1 and 2).

CONCLUSIONS: Immunogenicity of SARS-CoV-2 vaccines is significantly reduced as age increases and in those with a compromised immune system compared to immunocompetent individuals.

SP004
Characterizing the acute SARS-CoV-2 antibody response: Serological profiling of participants enrolled in the GENCOV study
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OBJECTIVES: Characteristics of the SARS-CoV-2 antibody response associated with COVID-19 severity and protective immunity remain unclear. The GENCOV study aims to link serological profiles and participant characteristics (e.g., demographics, disease severity) to identify factors contributing to variability in COVID-19 outcomes. We assessed the acute SARS-CoV-2 antibody responses of GENCOV participants to identify differences following COVID-19 diagnosis and/or vaccination.

METHODS: Plasma specimens were collected from 1) COVID-19 participants 1-month following a positive PCR result (n=848) and 2) SARS-CoV-2-naïve individuals 1-month following a second dose of a Health Canada-approved vaccine (n=67). COVID-19 participants were stratified by vaccination status: 1) unvaccinated (n=539), 2) breakthrough infections (n=219, vaccinated pre-infection), and 3) hybrid immunity (n=90, vaccinated post-infection). Antibody levels, antigen targets (including trimeric spike (S), nucleocapsid (N), and receptor-binding domain (RBD)) and viral neutralization (nAbs) were assessed using in-house-developed ELISAs and the Health Canada approved Roche Elecsys® Anti-SARS-CoV-2 immunoassay.

RESULTS: 1-month post-diagnosis (median: 37 days), vaccinated COVID-19 participants (hybrid or breakthrough) had significantly higher levels of total anti-S (including anti-S/RBD IgG and IgA) and nAbs compared to unvaccinated participants. Individuals with a breakthrough infection had higher levels of anti-S/RBD IgG and IgA compared to those with hybrid immunity and had anti-S/RBD IgG levels comparable to infection-naïve individuals’ post-vaccination. Infection-naïve individuals mounted significantly weaker IgA and IgM responses compared to COVID-19 participants. After 1-month, 92.2–97.2% of COVID-19 participant groups were positive for anti-N antibodies. However, breakthrough infections had lower anti-N and IgM antibodies compared to other COVID-19 groups. Multiple quantile regression identified that greater unvaccinated participant age and COVID-19 severity (based on hospitalization) were independently associated with higher total anti-S antibodies.

CONCLUSIONS: Understanding the basis for the variability in the acute antibody response and how this variability is associated with participant characteristics will aid in improving future vaccine development and roll out plans.
**SP005**

**Evaluation of the Abbott ID NOW™ COVID-19 assay with nasopharyngeal swab viral transport media and saline gargle samples from symptomatic adults and children**

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**OBJECTIVES:** The rapid Abbott ID NOW™ COVID-19 assay is intended for direct testing of swabs, which leaves no residual sample if follow-up testing is required. We sought to evaluate diagnostic performance of this assay for detecting SARS-CoV-2 in nasopharyngeal (NP) swabs in viral transport media (VTM) and saline gargle (SG) samples previously collected from symptomatic adults and children who presented for RT-PCR COVID-19 testing.

**METHODS:** Sensitivity and specificity of this assay with these sample types was evaluated through testing of previously collected RT-PCR positive and negative samples. 0.2 mL of thawed NP swab VTM or SG sample was pipetted into the ID NOW™ instrument sample receiver, instead of direct swab elution. Testing was carried out via rapid, automated, isothermal amplification of SARS-CoV-2 nucleic acid until a qualitative result was reported within 5-13 minutes. ID NOW™ reported results were compared to matched RT-PCR results from clinically validated laboratory developed tests targeting E/RdRp or Spike/Orf8 genes.

**RESULTS:** 83 RT-PCR positive and 20 negative samples were tested. Sensitivity of the ID NOW™ overall was found to be 90.4% (95% Confidence Interval 82.1-95.0) and comparable across sample types. There were no false positives, and 8 false negatives reported. 7 of these false negatives had RT-PCR cycle threshold (Ct) values of ≥ 33.

**CONCLUSIONS:** The overall performance of the Abbott ID NOW™ COVID-19 assay approaches clinical RT-PCR testing for both SG and NP swab VTM samples, demonstrating relatively high sensitivity and specificity. This assay has potential to serve as triage for RT-PCR in point-of-care settings, allowing for rapid detection to assist with therapeutic decision making, patient isolation, and outbreak identification, with the added benefit of having residual sample that can be forwarded for testing for other viruses, confirmatory testing, and/or sequencing.

**SP006**

**Using a novel genomic algorithm to reconstruct networks of SARS-CoV-2 transmission in an acute care facility outbreak**

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**OBJECTIVES:** Infection control and outbreak investigation in health care settings is increasingly supported by genomic sequencing. Genetic similarity between pathogens in specimens are being used to infer epidemiological connections between cases. These analyses are dominated by phylogenetic trees. Phylogenetic trees have two important limitations. First, they do not depict directional relationships, so chains of transmission are not readily apparent. Second, they do not inherently partition cases into separate clusters of transmission. Subjective distance-based cut-offs are applied to the tree after the fact, introducing bias into epidemiological interpretations. We created an alternative to phylogenetic trees called GenomeTracer. It applies a novel genomic algorithm to sequencing data to reconstruct chains of transmission and partition cases into clusters. Outbreaks are visualized as interactive network diagrams, with nodes representing cases connected by arrows showing directional transmission events. We evaluated GenomeTracer on an outbreak of SARS-CoV-2 infections at an acute care facility in British Columbia, Canada.

**METHODS:** An epidemiologically well-defined outbreak of 180 COVID-19 cases was identified at an acute care facility in British Columbia and samples were sequenced at the British Columbia Centre for Disease Control Public Health Laboratory. 143 high-quality genomes were analyzed with GenomeTracer. Case metadata was provided by the Health Authority where the facility is located, who conducted an in-depth, independent investigation using traditional epidemiological methods.

**RESULTS:** GenomeTracer identified 7 transmission clusters, ranging in size from 2 to 78 cases. These transmission clusters all formed monophyletic clades on a conventional phylogenetic tree, and conventional SARS-CoV-2 lineages...
Temporal dynamics and genomic surveillance of SARS-CoV-2 variants in COVID-19 patients from Toronto, Canada

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OBJECTIVES: Rapid transmission and worldwide spread of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) led to the emergence of various viral lineages, impacting disease severity, clinical presentations, and transmissibility. We sought to temporally track variant dynamics and investigate viral genomic diversity in a subset of coronavirus disease 2019 (COVID-19) inpatients and outpatients.

METHODS: A multi-centred cohort of COVID-19 patients from 7 hospitals in the greater Toronto area were recruited from March 2020 to April 2022. RNA from nasal swabs were subjected to whole genome sequencing with a minimum of 100 times read depth and 75% genome completeness. The Phylogenetic Assignment of Named Global Outbreak LINEages (PANGOLIN) tool was used for SARS-CoV-2 lineages assignments. Nextclade was used for mutation analyses.

RESULTS: In 951 patients with available lineage data, we observed 90 unique lineages (including sublineages). Thirty-nine percent (374/951) of cases were variants of concern (VOCs); 14% (138/951) Delta, 10% (92/951) Omicron, 7% (69/951) Gamma, 6% (65/951) Alpha, and 1% (10/951) Beta. SARS-CoV-2 whole genomes and mutation profiles from 629 patients were further investigated. Forty-eight percent (301/629) of patients were hospitalized. The B.1 lineage was the most prevalent in both inpatients and outpatients. Sixteen percent (47/301) of inpatients and 24% (80/328) of outpatients with whole genome sequences had VOC cases. A total of 4222 amino acid substitutions were detected in inpatients and 5042 in outpatients. Transition/transversion ratios were compared; 2.5 for outpatients and 2.69 for inpatients. We detected 665 and 503 total deletions in the inpatient and outpatient groups respectively.

CONCLUSIONS: We observed a dynamic distribution of SARS-CoV-2 lineages throughout the first six waves of COVID-19 within a 25-month period. There were minimal differences in the whole genomes of SARS-CoV-2 samples from hospitalized patients versus outpatients other than differences characteristic of known variants. Our work emphasizes the importance of ongoing genomic SARS-CoV-2 surveillance.
Abstracts

OBJECTIVES: Across the world, people living with HIV (PLWH) have faced unique challenges during the COVID-19 pandemic including pandemic-related loss of income and employment, worsened mental health, and decreased access to necessary medical care. PLWH may also have difficulty placing trust in the health care system, making it difficult to advocate for preventative behaviours in this population. There is a paucity of people living with HIV (PLWH)-specific data examining demographic factors and preventative behaviour practices with respect to COVID-19.

METHODS: Using data from the CIHR Canadian HIV Trials Network prospective observational cohort study (CTN 328) of PLWH and Canadian Immunity Task Force questionnaire responses, we examined the relationships between participant characteristics and behavioural practices intended to prevent COVID-19 infection.

RESULTS: Among 375 participants, mean age was 52.0 years (SD 13.3 years) and median duration of HIV infection was 17.0 years (interquartile range 7.0-24.0 years). Forty-nine participants had COVID-19 infection before study enrolment and 78 contracted COVID-19 during the study. The proportion of participants reporting preventative behaviours included 87% masking, 79% physical distancing, 70% limiting social gatherings, 65% limiting contact with at-risk individuals, 33% self-isolating due to symptoms, and 26% self-quarantining due to possible exposure. Participants with known prior COVID-19 infection (n=25) were more likely to self-quarantine when thought to have been exposed to COVID-19 but were asymptomatic (65.0% vs 23.4%, p<0.001). Participants with multiple comorbidities were more likely to endorse physical distancing (85.7% vs 75.5%, p=0.044).

CONCLUSIONS: PLWH in this cohort endorsed high rates of preventative behaviours. PLWH with prior COVID-19 infection and multimorbidity endorsed higher rates of preventative behaviours than PLWH without prior COVID-19 infection and multimorbidity.

SP009

Surveillance of SARS-CoV-2 amongst the homeless population

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OBJECTIVES: The homeless population is at high risk for SARS-CoV-2 infection and outbreaks. A surveillance program was established to facilitate early identification and isolation of SARS-CoV-2 infected individuals in the homeless population in an effort to reduce transmission and the extent of outbreaks. The surveillance program allows for observation of trends throughout the various stages of the pandemic that can inform public health decisions on infection control and prevention in these at-risk communities.

METHODS: From January 1 to December 31, 2021, asymptomatic clients and staff from 54 facilities serving the homeless population voluntarily participated in self-swabbing once weekly, using oral-nares swabs. Swabs were collected into McMaster Molecular Media and tested using a laboratory-developed PCR multiplex. A turnaround time of 6 hours from specimen arrival at the lab was maintained throughout the study.

RESULTS: The SARS-CoV-2 positivity at any time during the year was 9.2% and 6.4% for staff. Positivity rates for each facility type were as follows; 0.9% for both emergency shelters and supportive housing, and 2.1% for drop-in sites. Testing of staff in isolation centres and offices found a positivity rate of 4.3% and 0%, respectively. A total of 52 outbreaks (2 or more unique positive tests within 14 days) occurred in 23 out of the 54 facilities. The median (interquartile range) for size and duration (days) of outbreaks was, 4 (2,8) and 8 (3,14), respectively. Nine outbreaks had 10 people or more. Emergency shelters and supportive housing programs
experienced the majority of outbreaks, each accounting for 23 outbreaks. Drop-in centres accounted for 5 outbreaks and an isolation centre experienced 1 outbreak.

CONCLUSIONS: Our SARS-CoV-2 surveillance program successfully demonstrated that a large-scale surveillance program with a rapid turnaround time is feasible and proves to be a promising intervention in effectively isolating cases and limiting transmission in this population.

SP010
WITHDRAWN

SP011
Characterization of provincial and global invasive pneumococcal serogroup 20 isolates
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OBJECTIVES: Invasive disease due to Streptococcus pneumoniae is a global healthcare burden. In Alberta, invasive S. pneumoniae serogroup 20, comprised of serotypes 20A/20B, has been increasing since 2007. The objectives of this study were to characterize provincial invasive serogroup 20 isolates collected from 1993–2019 and compare them to invasive and non-invasive isolates from the Global Pneumococcal Sequencing (GPS) Project collected between 1998–2015.

METHODS: Alberta isolates of invasive serogroup 20 were sequenced, and GPS sequences were obtained from the NCBI Sequence Read Archive. Trends in descriptive clinical data and antimicrobial susceptibility results were evaluated, and genomes were subjected to molecular sequence typing, virulence and antimicrobial resistance gene identification, phylogenetic analysis, and pan-genome calculation.

RESULTS: Of the 284 serogroup 20 isolates collected in Alberta, 274 were sequenced and analyzed. Most Alberta serogroup 20 isolates were identified after 2007 in primarily middle-aged adults. The isolates typed predominantly as serotype 20B and ST235, a sequence type that was rare among GPS isolates (2/95). All Alberta and GPS genomes carried molecular resistance determinants implicated in fluoroquinolone and macrolide resistance, with a few Alberta isolates exhibiting phenotypic resistance to azithromycin, clindamycin, erythromycin, tetracycline, and trimethoprim-sulfamethoxazole, as well as non-susceptibility to tigecycline. Additionally, all isolates carried multiple virulence factors including those involved in adherence and immune modulation, as well as exotoxins and exoenzymes. Phylogenetically, Alberta serogroup 20 isolates clustered primarily with invasive GPS isolates from the USA, Israel, Brazil, and Nepal. The pangenome for all Alberta and GPS isolates was comprised of 1396 core genes, 1353 accessory genes, and 436 singleton genes.

CONCLUSIONS: In Alberta, invasive disease due to serogroup 20 has been increasing over the past 15 years, represented predominantly by ST235. Characterization of this serogroup and continued surveillance can contribute to outbreak prevention and help provide epidemiological information in the era of serotype-based pneumococcal vaccines.

SP012
The impact of COVID-19 pandemic on the rate and severity of bacteremias presenting to the emergency department
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OBJECTIVES: We conducted a large retrospective cohort study (n = 86 470) to determine the incidence and severity of community-acquired bacteremia among patients presenting to the emergency department (ED) during the first year of the COVID-19 pandemic compared to the year immediately prior.

METHODS: All patients aged 18 or older who presented to the ED with positive blood cultures drawn within 48 hours of hospital admission were included. The primary outcome was the incidence of bacteremia in each group. Multivariable Poisson regression was used to obtain the rate ratio adjusted for age, sex and comorbidity. Secondary outcomes were multiple and included measuring severity of bacteremia among cases using the qSOFA score. Multivariable Poisson regression was used to obtain the relative rate for a 1-unit increase in qSOFA score, adjusted for age, sex and comorbidity.

RESULTS: In the pandemic cohort, the incidence rate was 7.38 (95% CI: 6.51 to 8.25) bacteremias per 1000 ED visits. In the pre-pandemic cohort, the incidence rate was 5.15 (95% CI: 4.52 to 5.78) bacteremias per 1000 ED visits. The unadjusted relative rate of bacteremia comparing the
The genomes of 37 previously identified naturalized Escherichia coli strains were isolated from wastewater treatment and meat processing plants. Using validated administrative data from International Classification of Diseases-10th revision in Canada codes, patients who developed a complex infection within one year of the index procedure were identified. Demographic characteristics of patients were summarized. Logistic regression models were used to analyze device type, comorbidities, and demographics associated with infection rates and mortality.

RESULTS: There were 27,830 CIED implants resulting in 205 infections (0.74%). Factors associated with infection were younger age (OR 0.73, 95% CI 0.66-0.82, p<0.001), and having two or more comorbidities. Generator replacement procedures (OR 0.55, 95% CI 0.34-0.84, p=0.008) and index procedure after 2014 were protective. Comparing the infected to uninfected groups, hospitalizations were 2.63 compared to 0.69, and mortality 10.73% compared to 3.49%, respectively (p<0.001). Common comorbidities were risk factors, including congestive heart failure (OR 2.37 95% CI 1.78-3.18, p<0.001), hypertension (OR 3.62 95% CI 1.63-6.95, p<0.001) and diabetes (OR 1.5, 95% CI 1.11-2.02, p=0.008). Factors not associated with infection included Elixhauser Index, material, or social deprivation index, and urban or rural residence.

CONCLUSIONS: There is a slightly lower overall rate of CIED infections in our province compared to previously described epidemiology. Implants after 2014, and generator replacements showed a decreased burden of infection. Patients with younger age, and two or more comorbidities are at greatest risk of CIED infection. The burden of hospitalization and mortality is substantially higher in infected patients.

OBJECTIVES: Although E. coli is commonly known as a commensal gut microbe, select strains have evolved to survive in non-host, natural environments. Recently, such naturalized strains have been identified in ‘industrial’ environments, where they may act as reservoirs for clinically important genes. We sought to characterize the resistome, virulome and mobiome of naturalized E. coli strains isolated from wastewater treatment and meat processing plants.

METHODS: The genomes of 37 previously identified naturalized wastewater and meat plant E. coli strains were
downloaded from NCBI. Alongside 61 representative commensal, intestinal pathogenic and extraintestinal pathogenic strains, all genomes were screened for antibiotic resistance genes against the Comprehensive Antibiotic Resistance Database and virulence genes against the Virulence Factor Database. Additionally, plasmids were characterized using PLASMIDFINDER and pMLST.

**RESULTS:** On average, the naturalized wastewater (32.85 ± 5.50) and meat plant (29.35 ± 0.49) strains possessed significantly fewer virulence genes than their commensal (61.14 ± 21.77), intestinal pathogenic (95.04 ± 30.76), and extraintestinal pathogenic (96.91 ± 17.19) counterparts (p < 1E-5; ANOVA). In contrast, all groups possessed comparable numbers of antibiotic resistance genes (39.94–43.24), with select naturalized strains harboring resistance genes against aminoglycosides (ANT(2’)-Ia), quinolones (qnrA1), sulfonamides (sul1, sul2), tetracyclines (tet(A)), and beta-lactams (blaFOX-5, blaKPC-2, blaTEM-1). Interestingly, all naturalized strains possessed the beta-lactamase blaEC-15, which was only variably present across the other groups analyzed. Most naturalized strains also possessed a unique ‘F100:A-B-’ type IncFII plasmid.

**CONCLUSIONS:** With a diminished virulence gene repertoire, the naturalized strains do not appear to represent a direct pathogenic risk to human health. Despite this, many wastewater and meat plant strains possessed various key antibiotic resistance genes and the plasmids to mobilize them to other, clinically relevant microbes. These findings suggest that naturalized *E. coli* populations may serve as reservoirs for clinically important antibiotic resistance genes within wastewater treatment and meat processing plants.

**SP015**

**Changing Trends of Antimicrobial Resistance among Shigella species in British Columbia: A call for change in empiric management**

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**OBJECTIVES:** Shigella species are a leading cause of bacterial diarrheal illness. In the last decade, a rise in multi-drug resistant and extensively-drug resistant Shigella species has been reported from around the globe, resulting in a significant impact on treatment and public health. We aim to assess the susceptibility profile of Shigella species among the community in the province of British Columbia, Canada.

**METHODS:** We retrospectively reviewed the susceptibility profile of Shigella species from clinical isolates collected by LifeLabs a large outpatient community laboratory serving Metro Vancouver, Fraser Valley, and Vancouver Island from 2016 to 2021.

**RESULTS:** A total of 477 isolates were analyzed during the study period. Samples were most commonly obtained from males (60.4%) and young adults between the ages of 20 - 40 years (36.2%). The two most common species were Shigella sonnei (62.7%) and Shigella flexneri (30%). The overall resistance to Ciprofloxacin was 44.8%, with an increasing resistance rate over the study period from 23.6% in 2016 to 91.7% in 2021. Resistance to Trimethoprim/Sulfamethoxazole was 84% in all isolates, with a declining resistance rate over the initial study period and an increase over the last year to 90% in 2021. Cefixime resistance was 9.7% in all isolates, with a resistance rate remaining under 10% in the study period except for one year, when it reached 18.6% in 2019. Shigella sonnei had a higher resistance rate compared to Shigella flexneri in this study period.

**CONCLUSIONS:** There has been a significant rise in antimicrobial resistance among Shigella species in British Columbia, limiting therapeutic options to third-generation cephalosporins. This change in resistance pattern calls for a review of the current recommended management of Shigella infections in terms of performance of susceptibility testing and empiric first-line management.

**SP016**

**WITHDRAWN**

**SP017**

**Population-level provider compliance with provincial treatment guidelines for the management of gonorrhea in infants, children and adolescents in Alberta, Canada, 2000-2019**

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OBJECTIVES: Gonococcal infections are a rising public health concern in Canada with increasing rates among infants, children, and adolescents. Appropriate antimicrobial therapy is one of the essential strategies in the global control of gonorrhea. We sought to determine provider compliance with Alberta treatment guidelines for gonococcal infections in the age group <16 years.

METHODS: Retrospective population-based analysis of gonorrhea treatment January 1, 2000 to December 31, 2019 using data extracted from the communicable disease outbreak database. Bivariate analyses were used. Prevalence ratios were calculated for provider compliance to treatment guidelines by patient, infection and treating provider characteristics.

RESULTS: There were 896 cases in youth <16 years. The majority (84.2%; n=754) were female of which 27 (9%) were pregnant. First Nations make up 6.5% of the general population but accounted for 55.3% of cases (ethnicity missing for 12.3%). 95% were aged 11-16 years. Cases were treated by family physicians (47.6%), STI clinics (16.9%) and youth center (8.6%). Provider compliance with treatment guidelines was 90.2% and was highest when the treatment was provided by a youth offender center, family physicians, and STI clinic (100%, 96% and 94.5% respectively). Provider compliance was the lowest when treating males (13.2%), age group 0-5 years (15.3%), individuals of “unknown race/ethnicity” (17.9%), and those treated in emergency department (27.3%).

CONCLUSIONS: Delivery of STI care at youth offender centres, by family physicians and by nurse-led models at STI clinics led to almost perfect compliance with treatment guidelines. Targeted interventions are needed to improve compliance for the provision of treatment in children 0-5 years and in emergency departments.

SP018
Cases of PCR-Positive Blood for Anaplasma phagocytophilum in Nova Scotia: A Review from May – September 2022

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OBJECTIVES: Anaplasmosis is an infectious disease caused by the bacterium Anaplasma phagocytophilum, primarily transmitted to humans through the bite of black-legged ticks, which are endemic in Nova Scotia. Its clinical presentation can range from a mild flu-like illness to multi-organ failure and death. Since the first case of anaplasmosis in NS in 2017, there have been very few reported in subsequent years. The summer of 2022 demonstrated a significant increase in cases, suggesting emergence of this tick-borne pathogen. The purpose of this study is to identify trends in the geographic distribution, clinical presentation, and laboratory findings of patients with Anaplasma PCR-positive blood.

METHODS: This study is a retrospective chart review. All patients in Nova Scotia with PCR+ blood for Anaplasma phagocytophilum from May 1st to September 30th 2022 were included. Anaplasma PCR testing had either been ordered specifically by the treating clinician or had been added reflexively by the microbiology lab to samples submitted for Lyme testing. Patient data from PCR+ samples was collected using local and provincial electronic medical records.

RESULTS: Of the 116 cases reviewed to date, the majority (87.9%) of samples were collected from patients with postal codes in the Western Zone of the province, an area encompassing Lunenburg to Digby. Median age was 66, and 57.8% of patients were male. 64.1% had blood smears consistent with Anaplasma. Fever was the predominant presenting symptom. Laboratory abnormalities included anemia, lymphopenia, thrombocytopenia, and elevated liver enzymes.

CONCLUSIONS: The vast majority patients presenting to care with PCR+ blood for Anaplasma phagocytophilum in this review reside in the Western Zone of the province. Clinical presentation commonly included fever, cytopenias, and elevated liver enzymes. These findings may help clinicians identify those patients at high risk of anaplasmosis and lead to timely testing and treatment decisions for this emerging disease in Nova Scotia.
**SP019**

**Global burden of non-tuberculous mycobacteria in the cystic fibrosis population: A systematic review and meta-analysis**

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**OBJECTIVES:** People living with cystic fibrosis have an increased risk of lung infection with non-tuberculous mycobacteria (NTM), which is reportedly increasing. We conducted a systematic review of the literature to estimate the burden (prevalence and incidence) of nontuberculous mycobacteria in the cystic fibrosis population.

**METHODS:** Electronic databases, registries, and grey literature sources were searched for cohort and cross-sectional studies reporting epidemiological measures (incidence and prevalence) of NTM infection or NTM pulmonary disease (NTM-PD) in cystic fibrosis. The last search was conducted in September 2021; we included reports since database creation and registry reports published since 2010. The methodological quality of studies was appraised with the Joanna Briggs Institute tool. A random effects meta-analysis was conducted to summarize the prevalence of NTM infection, and the remaining results are presented in a narrative synthesis.

**RESULTS:** Ninety-five studies were included in this review. All 95 studies reported on NTM infection, and 14 of these also reported on NTM-PD. The pooled estimate for the point prevalence of NTM infection was 7.9% (CI 95%, 5.1 – 12.0%). In meta-regression, sample size and geographical location of the study modified the estimate. Longitudinal analysis of registry reports showed an increasing trend in NTM infection prevalence between 2010 and 2019.

**CONCLUSIONS:** The overall prevalence of NTM infection in CF is 7.9% and is increasing over time based on international registry reports. Future studies should report screening frequency, microbial identification methods, and incidence rates of progression from NTM infection to pulmonary disease.

**SP020**

**Wastewater surveillance of Respiratory Syncytial Virus (RSV) as environmental predictor of RSV epidemics**

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**OBJECTIVES:** Recurrent epidemics of respiratory syncytial virus (RSV) disproportionately impact infants and young children. Environmental surveillance of RSV in wastewater may provide a minimal-resource opportunity to predict pediatric RSV epidemics in near-real time.

**METHODS:** We conducted a retrospective study examining city-wide wastewater samples and pediatric RSV-related hospitalizations in Ottawa over an 18-week period between August 16 and December 7, 2022. Daily twenty-four-hour composite samples of primary clarified sludge were collected from the City of Ottawa’s sole water resource recovery facilities and screened for RSV by RT-qPCR using methods adapted from SARS-CoV-2 wastewater monitoring. Clinical data were restricted to Ottawa residents, as identified by their household postal codes; patients admitted from other jurisdictions were assumed to have minimal contributions to wastewater signals and were excluded from analyses. The primary outcome was the presence of an RSV community outbreak. We evaluated the 7-day midpoint average of RSV wastewater measurements against numbers of pediatric RSV-related hospitalizations using Pearson’s Rank correlation analysis to determine the degree of concordance. A time-step analysis was performed by offsetting wastewater measurements forward in time by a period of 1–25 days to determine the presence of a lag time, measured in days.

**RESULTS:** RSV was detected in 89 of the 101 wastewater samples collected during the study period (88%). The first detection of RSV in wastewater samples occurred on August 18, 2022. The strongest Pearson’s R correlation of 0.727 was observed when offsetting wastewater measurements forward with pediatric hospitalization data by 11 days (Figure SP020-1).

**CONCLUSIONS:** By quantifying, typing, and subtyping RSV in municipal wastewater prior to and during a community outbreak, we were able to forecast a surge in
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Wastewater-based surveillance of human influenza and respiratory syncytial virus

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OBJECTIVES: The circulation of respiratory viruses changed dramatically since the COVID-19 pandemic. Wastewater-based surveillance (WBS) has been widely used to monitor COVID-19 burden at a community level but WBS of other respiratory viruses is limited. The main objective of the present study is to monitor the presence and temporal trend of influenza A, influenza B and respiratory syncytial virus (RSV) in wastewater samples collected from two wastewater treatment plants serving Edmonton and surrounding regions in Alberta.

METHODS: We measured concentrations of influenza A and B, and RSV RNA in post-grit raw influent wastewater samples (500 ml of 24-hour composite sample) with three samples collected per week since January 2022. Viruses were concentrated from 100 ml WW followed by viral RNA extraction. Detection and quantification were performed by RT-qPCR. We studied the correlation between population-corrected combined wastewater viral concentrations to weekly positivity rates of each virus among in-patients who tested positive and were admitted to Stollery Children’s Hospital in Edmonton.

Figure SP020-1: Offsetting Wastewater Measurements forward with pediatric hospitalization data by 11 days.
RESULTS: Overall, 279 wastewater (WW) samples were tested. 55 samples (19.7%) and 118 samples (42.2%) were positive for influenza A and RSV, respectively, with influenza A concentration ranging from 8.1 to 1.09*10^3 copies/100 mL WW, and RSV concentrations ranging from 12.4 to 1.32*10^3 copies/100 mL WW. The correlation between WW and weekly positive rate of influenza A among inpatients (r=0.36) was higher than that of RSV (r=0.11). No influenza B was detected in WW and inpatients.

CONCLUSIONS: Influenza A and RSV can be monitored in wastewater with correlation between WW and influenza A higher than RSV in terms of pediatric inpatients. Inpatients with RSV are predominantly neonates and diaper users, which might explain the lower correlation. Results from wastewater can be available within 24 hours of sample collection, allowing real time information to inform public health response and clinical resource allocation.

SP022
Hospitalizations for acute respiratory diseases among children before and during the COVID-19 pandemic
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OBJECTIVES: Hospitalizations for acute respiratory diseases (ARD) among children are a significant healthcare burden most pronounced during the winter in Canada. This seasonal pattern of ARD was interrupted by SARS-CoV-2 and non-pharmaceutical interventions (NPI) in March 2020. Vaccine availability and increased population immunity allowed for relaxation of NPIs followed by a surge in ARD in autumn, 2022. We aim to describe the pattern of ARD among children and measure the impact of SARS-CoV-2 and NPIs on the weekly incidence of ARD at a provincial level.

METHODS: We developed a provincial surveillance system to monitor the weekly incidence of hospital discharges for ARD among children 0-17 years old. All hospital discharges for asthma, bronchiolitis, croup, and pneumonia were identified in the hospital Discharge Abstract Database from January 2012 to September 2022. Current data are added monthly. Incidence rates were calculated using population denominators, and ratios compared incidence rates between time periods. Disease severity was measured using admission to the pediatric intensive care unit (PICU) as a percentage of hospitalization.

RESULTS: Provincially, there were 53,258 hospital discharges of which 6,372 (11.96%) included a PICU stay for ARD. A biennial pattern emerged; while weekly incidence of ARD increased each winter, peak incidence was highest in January 2013, 2015, 2017, and 2020, ranging from 9.55 to 13.75 per 100,000 children per week (Figure SP022-1). Similar biennial patterns emerged for bronchiolitis and pneumonia, while unique annual patterns emerged for asthma and croup. The weekly incidence of ARD decreased by 7.13-fold between January 2020 and 2021 (10.92 to 1.53 per 100,000 children) and increased by 2.44-fold between September 2021 and 2022 (3.47 to 8.45 per 100,000 children).

CONCLUSIONS: SARS-CoV-2 and NPIs had significant impacts on seasonal patterns of ARD. Ongoing surveillance will capture the current surge of ARD among children to inform timely decision making in public health and health care.

SP023
WITHDRAWN

SP024
Clinic barriers and facilitators to the implementation of a decolonization strategy for Staphylococcus aureus in hip and knee arthroplasty: A qualitative study
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OBJECTIVES: The aim of this study was to qualitatively assess the barriers and facilitators of implementing an evidence-based decolonization strategy prior to hip and knee arthroplasty in Alberta, Canada.

METHODS: Leveraging ongoing quality improvement (QI) activity to reduce SSIs amongst hip and knee replacement patients in Alberta, Canada, qualitative methods were deployed. Semi-structured interviews (n=2) were conducted with surgeons and focus groups (n=9) were conducted with nurses and administrative staff to understand barriers and facilitators to the implementation of a provincial decolonization strategy. Interview questions were developed in conjunction with the Theoretical Domains Framework (TDF) and the research team. An inductive analysis derived from a Grounded Theory (GT) approach was conducted with the assistance of NVivo software.

RESULTS: Knowledge and understanding of the decolonization strategy were central to implementation. When present, they acted as facilitators, but when absent or inconsistent, they were significant barriers to implementation. Specifically, clinics needed more knowledge of, and direction on how to, deliver the decolonization strategy to patients: under homecare; who had second surgeries; who required surgery during COVID-19 outbreaks.

CONCLUSIONS: This study investigates the barriers and facilitators for a decolonization strategy prior to hip and knee arthroplasty in Alberta. We found that knowledge and understanding was a core category within our data. A successful decolonization strategy may benefit from adopting further planning and development for specific patients and respiratory outbreaks such as COVID-19. Further aspects that may act as facilitators include a champion within clinics, regular reporting, and audit and feedback strategies. Findings from our study can provide information on the barriers and facilitators of a decolonization strategy and can be used in making the decolonization strategy successful in Alberta.

SP025
Automating surveillance of Staphylococcus aureus bacteremia in two urban hospitals
Minh T Nguyen1,2, Shay-Anne Daniels3, Azra Sharma2, Sultan Alawfi2, Sulaiman Tabesh2, Jany Chan2, Elizabeth Martin6, Christopher F Lowe2, Victor Leung2
OBJECTIVES: To outline the implementation and automation of a surveillance system for the detection of hospital-acquired *S. aureus* bacteremia (HA-SAB) in two urban hospitals.

METHODS: We developed an algorithm for extracting cases that met the temporal case definition of hospital-onset *S. aureus* bacteremia. All cases which met the definition were followed by more in-depth clinical review by an ICP (infection control practitioner) and/or IPAC physician to ascertain type (hospital-acquired versus community-acquired) and source of infection.

RESULTS: Between the fiscal years 2015/2016 to 2021/2022, the rate of hospital-acquired *S. aureus* bacteremia per fiscal year was 12.06-27.26 per 10,000 patient admissions and 1.34-2.8 per 10,000 patient-days. Our automated process effectively screened 2,367 total cases of *S. aureus* bacteremia between fiscal years 2019/2020 and 2021/2022 and determined that 119 cases (5%) fit the temporal definition of hospital-onset *S. aureus* bacteremia. In the study period, the most common sources of HA-SAB were central lines (26.3%) and peripheral IVs (22.1%).

CONCLUSIONS: An automated process to screen cases of *S. aureus* bacteremia for surveillance filtered out 95% of cases. This can improve workflow of infection prevention and control programs to enable a sustainable *S. aureus* bacteremia surveillance program as a quality metric for institutions.

SP026

**Investigating the transmission of *Clostridioides difficile* from asymptomatic patients**

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OBJECTIVES: *Clostridioides difficile* (*C. difficile*) infection (CDI) is a common healthcare-associated disease. Testing for *C. difficile* and isolation is only recommended for those with symptomatic diarrhea. It has been proposed that identifying asymptomatic *C. difficile* carriers may reduce transmission. The goal of this study was to determine whether asymptomatic patients harbouring *C. difficile* contribute significantly to in-hospital transmission of CDI.

METHODS: Routinely collected rectal swabs for methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *Enterococcus* (admission and point prevalence tests) were additionally tested for *C. difficile* through molecular testing (laboratory-developed loop-mediated isothermal amplification, and majority of positives confirmed by PCR). Positive samples were incubated in an anaerobic chamber for 24 hours before successfully cultured samples were sequenced using NextSeq technology.

RESULTS: A total of 79/1469 (5.4%) patients tested positive in both LAMP and PCR, while another 88 (6%) were LAMP positive but PCR was not performed. Fifty of the 1469 patients tested were diagnosed with symptomatic CDI. Culture was positive in 78 of 154 swabs (51%). Of these 78, 47 (60%) successfully had their genome sequenced. Only one of these 47 sequenced samples was associated with a symptomatic CDI case. A single nucleotide polymorphism phylogenetic tree showed high genetic diversity, with sequences being grouped primarily by multilocus sequence type. Within these subgroupings of the tree, we analyzed patient metadata for patient stays within the same hospital ward within six weeks of each other and swabs that were taken at least 72 hours post-admission. This strategy revealed eight clusters suggestive of patient-to-patient transmission events. Not all clusters within the tree are explained by in-hospital spatial and temporal overlap, suggesting potential community transmission or transmission in another congregate setting.

CONCLUSIONS: While *C. difficile* colonization in admitted patients is much more prevalent than patient-to-patient in-hospital transmission, our study suggests that transmission among asymptomatic individuals occurs more frequently than thought.

SP027

**Comparison between electronic surveillance and infection control professionals reporting of healthcare-associated *Clostridioides difficile* infections**

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OBJECTIVES: *Clostridioides difficile* (*C. difficile*) infection (CDI) is a common healthcare-associated disease. Testing for *C. difficile* and isolation is only recommended for those with symptomatic diarrhea. It has been proposed...
Abstracts

SP028

Harmonization of quality indicators used in university-affiliated clinical microbiology laboratories

Jennifer Tat, Adriana Airo, Mohammed A Sarhan, Ghulam Dhabaan, Ellen Avery, Shawn T Clark, James Burns, Sandra Isabel, Ruchika Gupta, Manal Tadros, Gregory J German, Robert Kozak, Antoine Corbeil, Susan M Poutanen

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OBJECTIVES: There is a lack of consensus and standardization of microbiology quality indicators (QIs) used amongst clinical microbiology laboratories. Harmonization (i.e. obtaining consensus on how to select, monitor and benchmark a QI) will allow for integration, pooling of data and may identify practices that can result in improved patient safety, care, and increased quality of lab services. The aims of this project are A) To identify the QIs currently used in clinical microbiology laboratories and B) Review reference material and perform a scoping review of literature to identify any recommendations for harmonization.

METHODS: A survey was developed based on the Patterns of Practice survey (2012) issued by the Institute for Quality Management in Healthcare (IQMH) and distributed to clinical microbiology laboratories associated with the university microbiology training program. The reference material reviewed was a selection of standard documents that are used routinely in microbiology labs. The scoping review of literature was performed using the key terms: “Quality Indicators” and “Clinical Labs” with selected synonyms using the Medline database. In total, 1264 articles were screened, and nine articles were selected for full review.

RESULTS: The survey revealed that only one QI (blood culture contamination rate) was monitored at all participating sites. The review of reference material and scoping review of literature revealed few QIs were recommended in published works or by organizations. Blood culture contamination rate and blood culture volume...
were the only QIs that were recommended by multiple sources.

CONCLUSIONS: We conclude that there is heterogeneity among QIs that are currently monitored in participating clinical microbiology laboratories. Moreover, there are few recommendations for harmonization in published work or by organizations. This data will help inform the development of consensus practice recommendations for harmonization of QIs used in clinical microbiology laboratories.

SP029
Time to break the dogma?
Ruchika Bagga, Tony Mazzulli
Department of Laboratory Medicine and Pathobiology, Toronto, ON, Canada

OBJECTIVES: To evaluate current blood culture practices including length of incubation time and the clinical utility of aerobic and anaerobic blood cultures in adults.

METHODS: All blood culture samples received in Microbiology Department at Mount Sinai Hospital, Toronto between April 2020 - May 2021 were included. A total of ~152,000 blood cultures were analysed. Chart review was conducted for blood cultures that became positive > 96 hrs after incubation. An analysis of the % positivity of anaerobic vs aerobic cultures and assessment of the spectrum of pathogens isolated from these cultures was performed.

RESULTS: A total of 15,289 (9.7%) blood cultures were positive. ~ 0.156% (24/ 15289) organisms that were isolated after 96 hrs of incubation were clinically relevant. Repeat Staphylococcus aureus isolates in patients already on therapy and Candida species accounted for 17/24 isolates which grew after 96 hrs. Incubation of blood cultures > 4 days increased isolation of contaminants, increased unnecessary antibiotic usage, and led to additional lab burden in terms of manpower and reagent cost and additional calls to notify wards/clinicians/etc. of the results.

Of all blood cultures, 50.5% were aerobic cultures and 49.5% were anaerobic. Net positivity for aerobic cultures was 9.7% vs 8.4% for anaerobic cultures. Anaerobic cultures grew an additional 134 unique isolates. Average time to positivity (TTP) for aerobic cultures was ~ 14.5 hrs vs ~ 16.3 hrs for anaerobic cultures. Contaminants grew more frequently in aerobic cultures. In addition to obligate anaerobes, some Enterobacter (n=8) and E. coli (n=29) grew only in anaerobic media. TTP was reduced for some microorganisms in anaerobic cultures.

CONCLUSIONS: Recent advances in blood culture media and technology necessitate re-evaluation of existing blood culture practices including length of incubation time which currently remains at 5 days for most blood cultures. Anaerobic cultures appear to add value in terms of additional isolates and should be continued in adults.

SP030
Turn-around time of positive blood culture in community hospitals in central zone Halifax: A quality assurance project
Yahya Shabi, Ross Davidson, David Haldane, Ian Davis, Joline Head, Paul Bonnar, Glenn Patriquin
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OBJECTIVES: Blood cultures are essential in diagnosing bloodstream infections and integral for patient management. Smaller facilities often lack the capability to perform blood cultures. Blood cultures are often sent to central laboratories. Bottles requiring transport may face delays in reporting given the time encountered in transportation. Delays could impact appropriate antimicrobial management, compromising the quality of care. Focusing on common bacterial organisms, Staphylococcus aureus, S. lugdenesis, Enterobacteriales, and afermenters (Pseudomonas, Acinetobacter, Burkholderia), we examined the effect of transport time between blood collection and arrival in the central laboratory on time to reporting results.

METHODS: Dates and times of sample collection, arrival at the laboratory, gram stain and final reports from both the community and central laboratory were examined. Retrospective data was collected from the LIS for 19 months. Time from collection to results was recorded and stratified by organism and location of blood collection. We also simulated potential delays of 0, 3, 12, and 24 hours at room temperature using self-inoculated bottles before placement on an instrument.
RESULTS:

<table>
<thead>
<tr>
<th>Organism</th>
<th>Transport time</th>
<th>Time to gram stain</th>
<th>Time of incubation</th>
<th>Turnaround time</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Central</td>
<td>Community</td>
<td>Central</td>
<td>Community</td>
</tr>
<tr>
<td>Staphylococi</td>
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<td>3:45</td>
<td>20:21</td>
<td>19:54</td>
</tr>
<tr>
<td>Enterobacteriales</td>
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<td>3:33</td>
<td>15:26</td>
<td>16:07</td>
</tr>
<tr>
<td>Afermenters</td>
<td>2:04</td>
<td>3:22</td>
<td>24:07</td>
<td>24:37</td>
</tr>
</tbody>
</table>

CONCLUSIONS: Despite prolonged transport to the central laboratory, the time required for preliminary and final reports between sites is insignificant. Our study supports the centralization of blood cultures.

SP031
Time-to-positivity of blood cultures collected from hospitalized children
Eugene YH Yeung¹,², Nadia P Sant¹,², Nicole MA Le Saux¹,³
¹University of Ottawa, Ottawa, ON, Canada; ²Eastern Ontario Regional Laboratory Association (EORLA), Ottawa, ON, Canada; ³Children’s Hospital of Eastern Ontario (CHEO), Ottawa, ON, Canada

OBJECTIVES: The current American Academy of Pediatrics guidance recommends reassessment of antimicrobial therapy at 48 hours when antimicrobials have been given for suspected sepsis with no source in infants and children. Using contemporary automated systems, the time to positivity (TTP) for blood cultures may be less than 48 hours. This study was conducted to investigate the TTP for pediatric blood cultures in order to provide evidence for earlier discontinuation of antibiotics.

METHODS: An audit was conducted on all first positive blood cultures from patients at CHEO from November 1, 2019, to October 31, 2020. Repeated positive blood cultures within 120 hours were not included unless a different microorganism was identified. TTP was defined as the time from the start of incubation to a positive signal from the automated incubators.

RESULTS: A total of 376 positive blood cultures were identified from 248 patients (mean age 6.27 years) during the study period. Overall, 268 unique episodes of positive blood cultures had a mean TTP of 28.81 hours [95%CI 25.89-31.73]. A weak, but statistically significant, positive correlation was observed between age and TTP (R=0.2077, p<0.05). The mean TTP in each age group was as follows: birth-27 days old (n=59), 24.75 hours; 1 months-2 years old (n=39), 27.45 hours; 3-11 years old (n=81), 31.56 hours*; 12-21 years old (n=61), 35.44 hours* (*p<0.05 vs. birth-27 days old). About 61.19%, 76.49% and 83.58% of blood cultures became positive within 24, 36, and 48 hours, respectively. Subgroup analysis of probable pathogens showed TTP of 20.80 hours [95%CI 16.56-25.04], compared to 33.07 hours of the probable non-pathogens [95%CI 29.33-36.81, p<0.05].

CONCLUSIONS: TTP for all microorganisms was shorter in the younger pediatric age groups. Empiric antimicrobials for infants should be reassessed at 24-36 hours as pathogens are likely to be detected prior to 48 hours.

SP032
Checkerboard assay: Synergistic anti-biofilm properties of Cannabinoids and commonly used antibiotics against pre-formed Biofilms of clinical multidrug-resistant strains of bacteria
Marissa T Yoneda, Aman Galymov, Keilin Gorman, Naowarat Cheeptham, Joanna Urban
Thompson Rivers University, Kamloops, BC, Canada

OBJECTIVES: A checkerboard assay was used to determine the synergistic effects between a cannabis extract (CBD) and a clinically relevant antibiotic (Ciprofloxacin) against pre-formed biofilms of multidrug-resistant strains of MRSA.

METHODS: MRSA biofilms were cultivated in the Innovotech MBEC Assay® Biofilm 96-well plates. A checkerboard challenge plate containing a mixture of cannabidiol (CBD) and Ciprofloxacin was prepared. Two-fold dilutions of the antimicrobials were set up to make a gradient of 77 unique combinations that were tested for a synergistic effect. Pre-formed biofilms were exposed to the antimicrobials for 16 hours. Metabolic activity of the biofilms post-exposure was assessed with 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) agent in addition to MIC values. For the quantification of the interactions between
cannabinoids and antibiotics, a fractional inhibitory concentration (FIC) index was calculated for each unique drug combination.

**RESULTS:** Control wells containing cannabidiol alone were more effective at eradicating pre-formed biofilms, as indicated by a lower MIC value compared to biofilm eradication properties of Ciprofloxacin. Out of the 77 unique drug combinations, 57 displayed clearing of the wells compared to the control mirror plate and were included as candidates for the observed synergy in the FIC index calculations. The MTT assay showed a decreased cell viability of the biofilms recovered from the 57 wells after exposure to the antimicrobials. Additional standardized trials for the quantification of the FIC index are under investigation.

**CONCLUSIONS:** Cannabis extracts have been gaining attention as novel antimicrobial agents that can serve as an effective alternative against gram-positive multidrug-resistant strains of bacteria in clinical settings. The checkerboard assay employed in this study would allow for the investigation of synergistic anti-biofilm properties of cannabis extracts and antibiotics. The findings will contribute to the ongoing research on alternative treatment options for multidrug-resistant bacterial infections in diagnostic and clinical microbiology.

**SP033**

**Evaluating the accuracy of the MBT Lipid Xtract Kit for assessing colistin resistance in comparison to broth microdilution**

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**OBJECTIVES:** Colistin destabilizes lipopolysaccharide-rich outer membranes of Gram-negative organisms. MBT Lipid Xtract Kit on MALDI Biotyper Sirius system can extend proteomic analysis to identify specific cell wall modifications related with colistin resistance, whether based on chromosomal or plasmid-coded modifications. Our study investigated whether MBT performed similarly to broth microdilution (BMD; ComASP Colistin, Liofilchem) in detecting colistin resistance across various Gram-negative bacteria.

**METHODS:** Gram-negative organisms (colistin non-resistant with MIC≤2, resistant with MIC≥4) by BMD were compared to MBT. Organisms intrinsically resistant to colistin were excluded. Each isolate was tested twice on MBT as per manufacturer’s recommendation. Testing was repeated for discordant results on the MBT. Categorical agreement between MBT and BMD MIC interpretation was analyzed, including a separate analysis for non- E. coli isolates which required manual analysis of the MALDI-TOF spectra.

**RESULTS:** Out of 36 Gram-negative isolates, 16 were phenotypically colistin-resistant per BMD. Colistin-intermediate isolates included ESBL (4/20), AmpC (4/20) and carbapenemase-producing organisms (8/20). 16 (44.4%) isolates were E. coli, 12 (33.3%) were K. pneumoniae and 8 were other Gram-negative organisms (C. freundii, P. aeruginosa, E. cloacae, A. baumannii, K. aerogenes).

There was an 80.6% concordance (29/36 isolates) between MBT and BMD. Amidst discordant isolates, 6/7 were with K. pneumoniae (1/6 falsely non-resistant, 4/6 discrepant I/R on initial run, 1/6 falsely resistant) and one with K. aerogenes. On repeat runs with discordant samples, 4/7 confirmed resistance and 1/7 confirmed non-resistance in keeping with BMD. 100% agreement was noted with E. coli; for non-E. coli isolates, C. freundii, E. cloacae and P. aeruginosa also had 100% agreement.

**CONCLUSIONS:** MBT Lipid Xtract Kit demonstrated 80.6% agreement with BMD with no identified discrepancies specifically for E. coli isolates. 85.7% of non-E. coli discrepancies were noted with K. pneumoniae. Further research is required for the assessment of colistin resistance in non-E. coli isolates.

**SP034**

**Hybrid whole-genome assembly allows for improved plasmid reconstruction and cluster identification of carbapenemase-producing organisms**

Darcy Sutherland1,2,3, Robert Azana1, Chris Kwan1, Benjamin Hon1, Aishwarya Sridhar1,2, Shannon Russell1, James Zlosnik1, Dan Fornika1, John Tyson1, Linda Hoang1,3

1BCCDC Public Health Lab, Vancouver, BC, Canada; 2BC Cancer’s Genome Sciences Centre, Vancouver, BC, Canada; 3University of British Columbia, Vancouver, BC, Canada

**OBJECTIVES:** The increasing incidence of antimicrobial resistance (AMR) in bacteria, or “superbugs”, represents a significant threat to public health. The spread of AMR genes occurs primarily through the dissemination of mobile genetic elements, such as plasmids. We investigated the utility of performing hybrid-assembly using both
long- and short-read whole-genome-sequencing for the surveillance and reporting of carbapenemase-producing organisms (CPO).

METHODS: Two different gDNA extraction methods were used and compared. Total genomic content was extracted from clinical CPO+ Gram-negative isolates using either the NucliSens easyMAG automated bead-based extraction method or Promega’s ‘salt-out’ gDNA extraction kit. Short and long reads were generated using Illumina MiSeq and Oxford Nanopore MinION instruments, respectively. Whole-genome assemblies taking short-reads, or hybrid assembly taking short and long reads were performed using Unicycler. Quast and Bandage/Flye bioinformatic tools were used to assess assembly quality, with Prokka and MOBsuite used for characterization of the reconstructed genomes and plasmids.

RESULTS: A hybrid assembly approach allows for improved bacterial core genome and plasmid reconstruction. Hybrid assemblies allowed the CPO+ clinical isolate genomes to be reconstructed into fewer pieces (5-10 vs 100-200 contigs), with greater depth and coverage when compared with the short-read-only approach. These improvements were the most notable when querying plasmid-derived sequences.

CONCLUSIONS: Performing hybrid assembly using both short and long reads allow for improved plasmid reconstruction and downstream AMR characterization. Hospital and community outbreaks of AMR pathogens, including CPO, are often implicated by plasmid-mediated transmission, indicating a requirement for improved interrogation of these mobile genetic regions. Improved reconstruction of these mobile elements will ultimately yield a more robust epidemiological surveillance and molecular characterization of these organisms.

**SP036**  
**Development of an assay on BD Max open system for detection of *Bordetella* species in clinical specimens**

Hanh Tran1,2, Shannon Schofield1, Ana Cabrera1,2,3

1Department of Pathology and Laboratory Medicine, London Health Sciences Centre, London, ON, Canada; 2Department of Pathology and Laboratory Medicine, Schulich School of Medicine and Dentistry, Western University, London, ON, Canada; 3Department of Microbiology and Immunology, Schulich School of Medicine and Dentistry, Western University, London, ON, Canada

OBJECTIVES: Pertussis or whooping cough is a contagious respiratory disease caused by *Bordetella* species, primarily, *B. pertussis* and *B. parapertussis*. Although pertussis is vaccine preventable, there are about 20-40 million pertussis cases and 400,000 deaths from the disease each year, worldwide. Canada has 1000-3000 cases each year. To efficiently detect pertussis infection, we developed and validated a fully automated multiplex assay to identify Bordetella spp., by detection of IS481 and IS1001, on the BD Max open system. IS481 is present in *B. pertussis*, *B. holmesii* and some *B. bronchiseptica*, while IS1001 exists in *B. parapertussis* and *B. bronchiseptica*. This assay also replaced our in-house polymerase chain reaction (PCR) assay, which detected IS481 only.

METHODS: Patient specimens positive for IS481, from in-house PCR assays, were collected. *B. pertussis* and *B. parapertussis* DNA controls were independently spiked into negative nasopharyngeal swabs in transport media to generate contrived specimens. Nucleic acid extraction and PCR were performed using the BD Max ExK TNA-2 kit (Becton, Dickinson, Maryland, USA) and a premade PCR master mix. The master mix consisted of Luna Universal Probe One-Step RT-qPCR Reaction Mix (NEB, Massachusetts, USA) with primers and probes for IS481, IS1001 and the internal control RNase P. Agreement, analytical sensitivity and specificity, and precision were calculated.

RESULTS: The observed accuracy was 98.43% (confidence interval-CI: 95.48-99.67%) for IS481 and 97.41% (CI: 95.43-99.67%) for IS1001. The analytical specificity was 97.83% with no cross-reactivity detected among tested viruses and bacteria, except *Streptococcus pneumoniae*. Limit of detection was 20 genomic copies/mL specimen for IS481 and 0.2 pg/mL specimen for IS1001. The coefficients of variation (CV) were calculated as 3.25% and 3.09% for IS481 and IS1001, respectively, from triplicates over four days.

CONCLUSIONS: The assay described here performed well, expediting testing and reporting of pertussis cases. Automation on the BD Max system facilitated the workflow and decreased hands-on time.

**SP037**  
**Human enhancing technology in the microbiology laboratory: Analytical performance and validation of MetaSystems for detection of respiratory mycobacterial infections and implementation considerations**

Claudine Desruisseaux1,2, Conor J Broderick2, Kim Sy1, Gaurav Barot1, Duang-Jai Garcia1, Kerstin Locher1,2, Charlene Porter1, Méllisa Caza3, Valéry Lavergne1,2, Marthe K Charles1,2

OBJECTIVES: Pertussis or whooping cough is a contagious respiratory disease caused by *Bordetella* species, primarily, *B. pertussis* and *B. parapertussis*. Although pertussis is vaccine preventable, there are about 20-40 million pertussis cases and 400,000 deaths from the disease each year, worldwide. Canada has 1000-3000 cases each year. To efficiently detect pertussis infection, we developed and validated a fully automated multiplex assay to identify Bordetella spp., by detection of IS481 and IS1001, on the BD Max open system. IS481 is present in *B. pertussis*, *B. holmesii* and some *B. bronchiseptica*, while IS1001 exists in *B. parapertussis* and *B. bronchiseptica*. This assay also replaced our in-house polymerase chain reaction (PCR) assay, which detected IS481 only.

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CONCLUSIONS: The assay described here performed well, expediting testing and reporting of pertussis cases. Automation on the BD Max system facilitated the workflow and decreased hands-on time.
OBJECTIVES: The primary objective of this study is to establish the analytical performance and to validate the Metafer software from Metasystem (Altlussheim, Germany) on respiratory samples submitted for mycobacteriology screening. The secondary objective was to measure the impact of the level of expertise of the reviewer required to operate the instrument. Lastly, this study sought to establish a framework & considerations checklist for implementation.

METHODS: Microscopy slides of respiratory samples: Sputum & tracheal aspirate (n = 104), bronchoalveolar lavage & bronchial wash BAL/BW (n = 145) & pleural fluid (n = 37) were archived between August 31st, 2021, & May 25th, 2022. The slides were chosen to represent an array of grading (1+, 2+, 3+, 4+, and negative). A total of 320 slides were scanned using the MetaSystem platform & Neon Metafer AFB Module (version 4.3.130). The images were reviewed by 3 different levels of expert reviewers. The probability threshold (PT) on the instrument was set at 96% & tiles with inferior PT were rejected.

RESULTS: A total of 286 slides were fit for interpretation by Neon Metafer AFB Module for a total failure rate of the instrument of 10.6%. The limit of detection of digital microscopy was similar to manual microscopy for both TB & MAC. The overall agreement between digital microscopy & manual microscopy was 94.4% after discrepant analysis. The positive percentage agreement and negative percentage agreement between digital microscopy and culture was 89.3% (95 CI 80.1-95.3%) and 91.9% (95 CI 87.4-95.2%). The 2 most experienced reviewers had an interrater agreement of 0.838.

CONCLUSIONS: Metasystem Mycobacteria Scanner provides automation of reading and classification of AFB smear. In the context of an incidence-low, resource rich setting, this instrument has an acceptable performance for testing of respiratory samples at a PT of 96% combined with an expert reviewer. Further testing will be required to establish the clinical performance of this instrument within a prospective study.

SP038
Performance of an in-house PCR assay for the detection of Mycobacterium tuberculosis complex and Mycobacterium avium complex in various specimen types

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1 Department of Pathology and Molecular Medicine, McMaster University, Hamilton, ON, Canada; 2 Public Health Ontario, Toronto, ON, Canada; 3 Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada

OBJECTIVES: Infections caused by Mycobacterium tuberculosis complex (MTBC) and Mycobacterium avium complex (MAC) have high morbidity and mortality. Traditional diagnostic methods such as Acid Fast Bacilli (AFB)-smear or culture have imperfect sensitivity and do not permit timely species identification. Nucleic acid amplification tests are fast and accurate, but most studies have focused on commercial tests, which can be prohibitively expensive. We completed a retrospective review of records to assess the accuracy of our in-house multiplex MTBC/MAC polymerase chain reaction (PCR) assay.

METHODS: All clinical specimens tested by real-time MTBC/MAC PCR and mycobacterial culture from June 2016 to August 2021 were included. Sensitivity/specificity of PCR was calculated using culture as the reference.

RESULTS: 7160 specimens were included, with an overall MTBC PCR positivity rate of 26.6% compared with 23.0% for culture. Most specimens were respiratory (83.6%), followed by tissues (8.3%), body fluids (5.2%), and CSF (1.9%). MTBC PCR had an overall sensitivity of 96.1% (95% CI: 95.1-97.0%) and overall specificity of 94.1% (95% CI: 93.4-94.7%). Stratifying by specimen type, respiratory specimens had similarly high accuracy as the overall data, and most extrapulmonary specimens had good accuracy. Sensitivities were lower for non-lung, non-lymph-node tissue (85.7%, 95% CI: 80.0-90.3%) and CSF (42.1%, 95% CI: 20.3-66.5%). Stratifying by AFB-smear positivity for all specimen types, sensitivity of PCR for smear-positive specimens was significantly higher (98.4%, 95% CI: 97.6-99.0%) than for smear-negative specimens (57.1%, 95% CI: 46.3-67.5%). MAC PCR had lower overall sensitivity (66.6%; 95% CI: 64.9-68.4%) but similar overall specificity (95.3%; 95% CI: 94.6-95.9%) compared to the MTBC target.
CONCLUSIONS: Our in-house multiplex PCR for MTBC demonstrated excellent diagnostic accuracy when compared with culture for AFB smear-positive specimens. PCR is relatively insensitive for AFB smear-negative specimens and cannot be used to rule out MTBC infection. MAC PCR had lower sensitivity but good specificity.

SP039
Development and validation of RT-qPCR panel for the detection and quantification of polioviruses in wastewater
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OBJECTIVES: Occasional wild-type polio infections and recent clusters of acute flaccid paralysis from oral vaccine-derived poliovirus type 2 (VDPV2) in some countries and, the case in New York highlighted the ongoing risk of Polio. Our study aims to develop and validate a RT-qPCR panel that employs RT-qPCR assays using different primers and probes but have identical thermal-cycle conditions that can be run together to simultaneously detect poliovirus targets including vaccine (Sabin 1, 2, and 3) and wild-type (WPV 1, 2 and 3) in wastewater samples.

METHODS: Positive controls including inactivated poliovirus vaccine (IPV) of Sabin-1,2,3 and engineered DNA fragments (eDNAf) of 3 Sabin and 3 WPV, were used to develop the RT-qPCR panel: 1) optimize primers, probes, and use identical thermal-cycle conditions for each PCR reaction, 2) determine the limit of detection (LOD) of each target using serial dilutions and probit analysis, 3) evaluate the recovery rate of spiked IPV (Sabin 1) from wastewater.

RESULTS: The RT-qPCR panel detected Sabin 1 in IPV, and eDNAf of Sabin 1, 2 and 3, WPV1 and WPV3. However, WPV2 was not detected. No cross reaction was observed indicating that each RT-qPCR assay was specific, and the panel could differentiate various VDPV and WPV strains. The LOD of IPV Sabin 1 was at 1.60 x10-6 d-antigen units/PCR reaction and all the other polio targets at 1 copy/PCR reaction. The recovery for IPV Sabin 1 ranged from 48-100% with significantly higher recovery rate at lower concentrations of spiked IPV from wastewater (95% CI, p < 0.05).

SP040
Verification and clinical evaluation of the cobas CMV assay: Commutability with the CAP/CTM CMV assay
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OBJECTIVES: Despite the World Health Organization’s development of a cytomegalovirus international reference standard, inter-assay and inter-institution variability of CMV quantification persists. We sought to explore this issue of commutability between two commercial assays for CMV quantification: the cobas CMV and the cobas AmpliPrep/cobas TaqMan (CAP/CTM) CMV.

METHODS: A commercial linearity panel and 205 archived clinical samples were used for verification studies to assess cobas CMV performance in terms of linearity, precision, accuracy, correlation of agreement, and systemic bias relative to CAP/CTM CMV. Accuracy, correlation of agreement, and systemic bias were further evaluated with a 16-week clinical evaluation using 809 prospective patient samples.

RESULTS: The cobas CMV was linear and met precision claims across the reportable range of the assay. Between the two assays, paired archived and prospective samples qualitatively concurred 82.9% and 77.8% of the time, respectively. 9.8% (n = 20) of archived samples and 11.7% (n = 95) of prospective samples were undetected or unquantifiable on CAP/CTM CMV but were quantified on cobas CMV. In terms of agreement and bias between the assays, archived and prospective samples had linear correlations of agreement according to equations y = 0.97x + 0.35, R² = 0.95 and y = 1.04x - 0.13, R² = 0.93, and systemic shifts of -0.25 log10 IU/mL (95% CI -0.66–0.14 log10 IU/mL) and -0.0075 log10 IU/mL (95% CI -0.42–0.41 log10 IU/mL), respectively.
CONCLUSIONS: The cobas CMV met the requirements of a Health Canada-approved quantitative assay. With a lower limit of quantification, cobas CMV demonstrated a greater ability to quantify viral loads than CAP/CTM CMV. In terms of commutability, the cobas CMV assay reported viral loads that were higher than CAP/CTM CMV, but this systemic shift was not statistically significant and was further minimized when using prospective samples.

SP041
Improved Test Sensitivity of Direct Gram stain and Calcofluor in the Diagnosis of Blastomycosis after Repeated Microscopic Examination

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OBJECTIVES: Blastomyces spp. is a dimorphic fungi that is endemic around the Great Lakes, Mississippi and Ohio rivers. Early diagnosis of blastomycosis is fundamental in starting empiric therapy. Fungal culture is the gold standard and the most sensitive and specific diagnostic method, but it requires days to weeks to get a definitive diagnosis. Direct examination of clinical specimens using Gram stain or Calcofluor White stain are simple and rapid techniques to provide presumptive diagnosis. However, the yield of direct specimen examination is reported to be low (36-46%). The objective of this study was to document the sensitivity of direct examination compared to culture.

METHODS: A retrospective study was conducted on all confirmed cases with positive Blastomyces cultures at a tertiary-care centre in the Toronto region between 2010 and 2021 inclusive. The laboratory information system record was reviewed to document the yield of Gram stain and Calcofluor White stain. The specimen type, region, and year of each case was documented.

RESULTS: 82 fungal cultures were positive for Blastomyces spp. from 33 cases (7 females and 26 males) distributed mainly in the Greater Toronto Area (55%). Increased numbers were identified in recent years. Positive specimens included BAL (70%), sputum (10%), and other (20%). The sensitivity of Gram stain and Calcofluor White stain direct examination was 30% and 61% respectively. Repeated examination of direct Gram and Calcofluor white smears, after culture results were available or after re-review by a senior technologist, increased the yield to 52% and 70%, respectively.

CONCLUSIONS: The sensitivity of direct examination with Calcofluor White stain and Gram stain is increased with repeated examination with sensitivities as high as 70% and 52%, respectively. Laboratories should recognize the importance of thorough direct examination and staff training in this regard given the value added to the early diagnosis of blastomycosis.

SP042
Methodological and reporting quality of non-inferiority randomised controlled trials comparing antiretroviral therapies: A systematic review

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1Division of Medical Microbiology, Department of Pathology and Molecular Medicine, McMaster University, Hamilton, ON, Canada; 2Department of Health Research Methodology, Evidence, and Impact, Faculty of Health Sciences, McMaster University, Hamilton, ON, Canada; 3Division of Infectious Diseases, Department of Medicine, McMaster University, Hamilton, ON, Canada; 4Transplant Infectious Diseases and Ajmera Transplant Centre, University Health Network, University of Toronto, Toronto, ON, Canada; 5Division of Medical Microbiology, Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada; 6Division of Internal Medicine, King Faisal University, Hofuf, Saudi Arabia; 7Division of Infectious Diseases, Department of Medicine, McMaster University, Toronto, ON, Canada; 8Shared Hospital Laboratories, Toronto, ON, Canada; 9Division of Infectious Diseases, Georgetown Public Hospital Corporation, Georgetown, Guyana; 10Michael G. DeGroote School of Medicine, McMaster University, Hamilton, ON, Canada; 11Division of Infectious Diseases, Department of Medicine, Queen’s University, Kingston, ON, Canada

OBJECTIVES: Non-inferiority randomized controlled trials (NI-RCTs) should be reported following the CONSORT reporting standards, particularly because these trials are used to inform the standard of care. No empirical data exist illustrating whether antiretroviral NI-RCTs are adequately CONSORT compliant. Our primary objective was to assess whether CONSORT reporting requirements are met in NI-RCTs comparing ≥2 antiretroviral regimens.
used to treat or prevent HIV infection. We also assessed reporting quality by publication year and funding source.

METHODS: We systematically searched Medline, Embase, and Cochrane Central from inception to 14 November 2022. We included NI-RCTs comparing two or more antiretroviral regimens used for HIV treatment, pre-exposure, or post-exposure HIV prophylaxis. We performed blinded, duplicate assessments of articles and extracted relevant CONSORT reporting items. We assessed risk of bias using the Cochrane RoB 2.0 tool. Descriptive statistics were used for results synthesis; statistical tests were two-sided. (PROSPERO CRD42022328586)

RESULTS: 160 articles reporting 171 trials were included; 101 of 160 articles (63.1%) did not justify the non-inferiority margin used, and 28 (17.5%) did not provide sufficient information for sample size calculation. Eighty-nine of 160 articles (55.6%) reported both intention-to-treat (ITT) and per-protocol (PP) analyses, while 118 (73.8%) described missing data handling. Ten of 171 (5.9%) trials reported potentially misleading results. Trials funded by pharmaceutical industry were more likely to be double blinded (28.1% vs. 10.3%, p=0.029), and to describe missing data handling (52.9% vs. 43.6%, p=0.021). The proportion of trials reporting both ITT and PP analyses increased over time, while the proportion of trials reporting missing data handling decreased. Overall risk of bias was low in 96 studies (60%), moderate in 47 (29.3%), and high in 17 (10.6%).

CONCLUSIONS: Antiretroviral NI-RCTs should improve non-inferiority margin justification, reporting of ITT and PP analyses, and missing data handling to increase CONSORT adherence.

SP043
Pre-analytical optimization of Dermacentor tick species processing for molecular identification

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

OBJECTIVES: In our province, routine tick identification is performed by microscopy, and Dermacentor andersoni account for over 90% of Dermacentor ticks identified. In contrast, a recent tick identification survey based on ITS-2 targeted sequencing suggested D. variabilis may predominate. Given the potential advantage of molecular testing, this study investigated pre-analytical optimization of tick processing for downstream polymerase chain reaction (PCR) and whole genome sequencing (WGS) testing for Dermacentor species identification.

METHODS: A subset of D. andersoni ticks submitted for surveillance testing underwent DNA extraction utilizing the Qiagen Blood and Tissue kit. Pre-analytical variables investigated included tick body content (one or three legs, half body, whole body), gut content (with, without) and tissue preparation (cutting, grinding). Additional variables of micropestle components and Proteinase K digestion time were explored. Data were generated in duplicate for different scenarios across a range of tick weights. DNA concentration was assessed by Qubit and Nanodrop. PCR amplicons of extracted DNA were generated using previously described ITS-2 primers and assessed by automated electrophoresis (TapeStation).

RESULTS: Thirty-six ticks were tested in the study, with weights ranging from 2 to 11 mg. DNA extraction of half a tick body with gut or greater yielded DNA levels (2.7 ± 1.6 μg) appropriate for downstream molecular applications. Grind- ing tissue yielded higher DNA concentrations than cutting. Overnight and 10-minute Proteinase K digestion yielded similar DNA concentrations. On average, a 17 ng/μL DNA concentration difference was identified in weight and sex-matched ticks across all weights. TapeStation revealed a thick ITS-2 band of ~450 bp from extracted D. andersoni DNA.

CONCLUSIONS: Grinding half a tick body with gut using matching micropestle components and 10-minute Proteinase K digestion for DNA extraction appeared appropriate for downstream molecular testing, and optimized processing time and cost. Further work will incorporate these optimized steps for molecular characterization and expand the approach to additional tick species.

SP044
The period prevalence of a beta-lactam allergy label in patients prescribed carbapenems: A retrospective cohort study

Shealynn Carpenter, Jackson J Stewart, Cecilia Lau, Karen Fong, Dima Kabbani, Stephanie W Smith, Karen Doucette, Justin Z Chen

University of Alberta, Edmonton, AB, Canada

OBJECTIVES: The rate of reported beta-lactam allergies is significantly higher than that of true hypersensitivity
reactions. Inappropriate allergy labels are associated with adverse patient outcomes. Our primary objective was to evaluate the period prevalence of beta-lactam allergy labels in patients prescribed carbapenems at a major tertiary care centre. Secondary objectives included identifying the frequency of carbapenems prescribed explicitly because of an allergy label, stratifying allergy risk to determine opportunities for delabeling, and quantifying the potential days of carbapenem use that could be saved through allergy reconciliation.

METHODS: A retrospective chart review was performed on inpatients who were prescribed a carbapenem and prospectively audited by the antimicrobial stewardship program from July 2020 to July 2022. Subgroup analysis was completed regarding allergy reconciliation based on validated and previously published beta-lactam allergy delabeling algorithms.

RESULTS: Of 1815 carbapenem prescriptions audited, 360 were associated with a beta-lactam allergy label. Duplicate patients were removed resulting in a beta-lactam allergy period prevalence of 276/1399 (20%). Of all the carbapenem prescriptions in those with listed beta-lactam allergies, 139/360 (39%) were directly related to the allergy label, representing 745 potential days of carbapenem use that could have been avoided through allergy reconciliation.

Amongst the total number of unique (non-cross-reactive) beta-lactam allergies, 273/312 (88%) were candidates for allergy delabeling through: immediate allergy removal 67/312 (21%), oral challenge 24/312 (8%), or skin test 18/312 (6%). Additionally, 96/312 (31%) were candidates for either an oral challenge or skin test but required additional allergy details to clarify. Finally, 68/312 (22%) of allergies could not be risk stratified due to insufficiently documented allergy history.

CONCLUSIONS: Beta-lactam allergies among patients prescribed carbapenems is overrepresented and is the primary reason for prescribing a carbapenem in over one third of cases. Allergy reconciliation represents an important intervention that could lead to a reduction in unnecessary carbapenem prescribing at our centre.

SP045
Adherence to recommendations from antimicrobial stewardship audit and feedback rounds in academic intensive care units

Kari A Griffore1, Keerthika Selvakumar2, Michael Wan3, Linda R Taggart4, Elizabeth Leung5,6

1Leslie Dan Faculty of Pharmacy, University of Toronto, Toronto, ON, Canada; 2University of Toronto, Toronto, ON, Canada; 3St. Joseph’s Health Centre/ Unity Health Toronto, Toronto, ON, Canada; 4Li Ka Shing Knowledge Institute, Interprofessional Practice Based Research, Toronto, ON, Canada

OBJECTIVES: Antimicrobial stewardship programs (ASPs) can improve patient outcomes and decrease emergence of antimicrobial resistance. ASP guidelines recommend prospective audit and feedback (PAF) as it has been shown to reduce inappropriate antimicrobial use. Factors associated with variable PAF acceptance rates are not well studied. Identifying predictors of successful recommendations may help optimize PAF processes.

METHODS: The setting was a large, academic teaching hospital in Toronto, Canada. Data were recorded from verbal recommendations made during selected ASP rounds conducted in 3 ICUs between April 2013 and September 2022. ASP recommendations were categorized using standardized definitions. The primary outcome was acceptance of ASP recommendations.

RESULTS: Overall, 85.7% of ASP recommendations were accepted. Interventions aimed at promoting appropriate antimicrobial coverage were less likely to be accepted in comparison to all other recommendations combined (OR 0.47, 95% CI 0.27-0.82). Recommendations within the “promote appropriate coverage” category were further classified to demonstrate that recommendations to expand antimicrobial coverage were more likely to be accepted than recommendations to narrow coverage (OR 2.37, 95% CI 1.08 - 5.19). There were no statistically significant differences in acceptance rates between ICUs or intervention categories.

CONCLUSIONS: Most of the recommendations made during ASP rounds were accepted by the ICU teams. Recommendations that suggested expanding antimicrobial coverage were more likely to be accepted than those that suggested de-escalation. This finding is consistent with studies that looked at predictors of ASP intervention success in similar institutions. These results highlight important considerations for optimizing PAF process measures within institutional ASPs.

SP046
Changes in physician outpatient antibiotic prescribing from 2019 to 2021 during the COVID-19 pandemic

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OBJECTIVES: Antimicrobial stewardship programs (ASPs) can improve patient outcomes and decrease emergence of antimicrobial resistance. ASP guidelines recommend prospective audit and feedback (PAF) as it has been shown to reduce inappropriate antimicrobial use. Factors associated with variable PAF acceptance rates are not well studied. Identifying predictors of successful recommendations may help optimize PAF processes.

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Objectives: Our objective was to evaluate inter-physician variability and predictors of changes in antibiotic prescribing before (2019) and during (2020/2021) the COVID-19 pandemic.

Methods: We conducted a retrospective cohort analysis of physicians in Ontario, Canada prescribing oral antibiotics in the outpatient setting between 1 January 2019 and 31 December 2021 using the IQVIA Xponent dataset. The primary outcome was the change in the number of antibiotic prescriptions between the pre-pandemic and pandemic periods. Secondary outcomes were changes in the selection of broad-spectrum agents and long-duration (>7 days) antibiotic use. We used multivariable linear regression models to evaluate predictors of change.

Results: There were 17,288 physicians included in the study with substantial inter-physician variability in changes in antibiotic prescribing (median decrease of 43.5 antibiotics per physician, IQR 5.0 to 136.5). In the multivariable model, male physician gender (adjusted beta [β] -14.3, 95% confidence interval [CI] -19.6 to -8.9, p<.001), later career stage (β -45.3, 95% CI -52.9 to -37.8, p<.001), family medicine specialty (β -46.0, 95% CI -62.5 to -29.4, p<.001 compared to emergency medicine), urban location (β -33.3, 95% CI -43.9 to -22.7, p<.001), patient age <18 years (β -117.6, 95% CI -135.5 to -99.6, p<.001), male patient sex (β -52.4, 95% CI -71.1 to -33.7, p<.001), low patient comorbidity (β -42.5, 95% CI -50.3 to -34.8, p<.001), and high prescribing to new patients (β -216.5, 95% CI -223.5 to -209.5, p<.001) were associated with a decrease in antibiotic initiation. Family medicine specialty and high prescribing to new patients were associated with a decrease in selection of broad-spectrum agents and prolonged antibiotic use.

Conclusions: Antibiotic prescribing changed throughout the COVID-19 pandemic with overall decreases in antibiotic initiation, use of broad-spectrum agents, and prolonged antibiotic courses with inter-physician variability. These findings present opportunities for community antibiotic stewardship interventions.

Objectives: There are limited data on pharmacokinetics (PK) of cefazolin in hemodialysis (HD) patients and no information on protein binding (PB), i.e., the pharmacologically active free fraction. Without evidence-based guidelines, cefazolin dosing is often a one-size-fits-all approach without considering the diverse HD population. The objective was to characterize the concentrations and PB of cefazolin in infected patients undergoing chronic intermittent high-flux HD.

Methods: A clinical PK study was conducted in 20 patients receiving cefazolin (2 g post-HD 3x/week) in an outpatient HD setting. A post-dose peak and two pre-HD troughs were collected from each patient. Total cefazolin serum concentrations were measured in all samples using UHPLC-MS/MS. Free concentrations were determined in the ultrafiltrate of 20 samples, i.e., one peak and trough from 10 patients. Cefazolin concentrations and PB were described, and factors associated with particularly low (<10 mg/L), or high (>100 mg/L) pre-HD troughs were investigated.

Results: Total peaks and pre-HD troughs were 237.0±47.7 mg/L and 70.1±37.7 mg/L, respectively. Pre-HD troughs were extremely variable (3.7–149.4 mg/L) with values <10 mg/L in two patients (10%) and >100 mg/L in five patients (25%). Most of the variability was explained by the wide range of cefazolin half-lives off dialysis, presumably due to residual renal function (R²=0.71, P<0.0001). Cefazolin half-lives <14 hours and >40 hours were predictive of low and high pre-HD troughs, respectively. Cefazolin PB was concentration-dependent and significantly lower in peaks compared to pre-HD troughs (59.5% versus 81.8%, P<0.0001). PB in pre-HD troughs had a positive correlation with serum albumin (R²=0.29, P=0.04) and was more consistent with values in other populations.

Conclusions: The current study shows limitations in using standard cefazolin dosing for all HD patients. The
data will be used to investigate other dosing strategies that could improve therapy in this under-studied, high-risk population.

**SP048**

**Verification of antimicrobial susceptibility testing methods for new agents against challenging multi-drug resistant Gram-negative organisms**

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¹University of Toronto, Toronto, ON, Canada; ²University Health Network/Mount Sinai Hospital, Department of Microbiology, Toronto, ON, Canada; ³Department of Laboratory Medicine and Pathobiology & Medicine, University of Toronto, Toronto, ON, Canada

**OBJECTIVES:** The rise of antimicrobial-resistant bacteria is a rapidly growing threat, particularly among multi-drug resistant Gram-negative (MDR GN) organisms. Timely completion of antimicrobial susceptibility testing (AST) is therefore critical, and laboratories often rely on commercial automated AST methods, rather than the more time-consuming gold-standard, frozen broth microdilution (BMD). Newer drugs are often not included in these automated ASTs, forcing laboratories to turn to alternate AST methods that may not have been well-verified. Previously we verified different methods to test newer agents (ceftriaxone, cefiderocol, ceftolozane/tazobactam, ceftazidime/avibactam, meropenem/vaborbactam, imipenem/relebactam, tigecycline, and plazomicin). The purpose of this study was to compare different methods against one another.

**METHODS:** A custom frozen BMD Sensititre panel (ThermoFisher Scientific) served as gold-standard. Verification data for a custom lyophilized BMD Sensititre panel (ThermoFisher Scientific), Etest gradient strips (bioMerieux), MIC Test Strips (Liofilchem), and Kirby-Bauer disks were compared. A total of 90 Enterobacterales, 46 Pseudomonas aeruginosa, 39 Acinetobacter spp., and 15 non-lactose fermenters, were used for each verification. Very major errors (VME), major errors (ME), minor errors (MinE), and categorical/essential agreements (CA/EA) were calculated, and acceptability was determined using both Cumitech31A and EUCAST thresholds and 95% confidence intervals. A heat maps of acceptability was created to facilitate between method comparisons.

**RESULTS:** For non-lactose fermenters, all methods are acceptable for newer antimicrobial agents. For Enterobacterales, all methods are acceptable for newer agents, except tigecycline. For *P. aeruginosa* and *Acinetobacter* spp., only the lyophilized BMD Sensititre is acceptable for all newer agents (Figure SP048-1).

**CONCLUSIONS:** Testing new antimicrobial agents that are included in automated susceptibility testing platforms poses challenges to laboratories. Not all alternate methods have acceptable performance compared to gold standard BMD testing. Laboratories should take this into consideration when choosing their testing methodologies and should complete verification of the accuracy of their chosen testing method.

**CASE REPORTS SYMPOSIUM**

**Thursday, March 30**

**17:15 – 18:15**

**CR001**

**Severe leptospirosis following a rat bite in an urban setting: A case report**

Maxime Arbour¹, Marc Brosseau², Xavier Marchand-Sénécal³

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**DISCUSSION:** Rat bite fever and leptospirosis can both present as life-threatening infections after a rat bite. These diagnoses are challenging since their causative bacteria cannot be isolated from conventional blood culture. Universal 16S PCR with sequencing on blood specimen can be helpful in these situations. Severe leptospirosis can present with fever and jaundice, disproportionate renal failure, pulmonary hemorrhage or severe thrombocytopenia. Given the vasculitic nature of the disease, steroids are sometimes
administered based on little evidence. This patient improved after administration of this treatment.

**OBJECTIVES:** Establish the differential diagnosis of sepsis following a rat bite. Recognize the presentation of severe leptospirosis.

**CASE SUMMARY:** A 76-year-old man presented to the emergency department following a rat bite on two fingers. He was discharged after basic wound care. Eighteen days later, he came back with a 3-day history of fever, headache, and abdominal pain. He had no respiratory symptoms, arthralgias or urinary complaints.

The patient was hypotensive and tachycardic, without hypoxemia. Mental status was normal. The abdomen was soft with mild diffuse tenderness. Skin was unremarkable. There was no jaundice and the conjunctivae were normal. There was mild erythema around the bite wound, without purulent discharge.

The patient was admitted to the intensive care unit and received empiric treatment with piperacillin-tazobactam. Despite the resolution of hypotension after aggressive fluid resuscitation, the acute kidney injury he had on arrival deteriorated from a creatinine of 162 to 518 μmol/L. He also had severe thrombocytopenia (nadir 17 × 10^9/L). Liver enzymes remained normal. Rat bite fever and leptospirosis were both suspected from the exposure and the presentation. The patient received intravenous steroids and immunoglobulins. He got better with normalization.

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<tr>
<th>Enterobacterales</th>
<th>Sensititre</th>
<th>Etest</th>
<th>MIC Strip</th>
<th>KB Disk</th>
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<tr>
<td>Pseudomonas aeruginosa</td>
<td>Sensititre</td>
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<tr>
<td>Acinetobacter spp.</td>
<td>Sensititre</td>
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<tr>
<td>Non-Lactose Fermenters</td>
<td>Sensititre</td>
<td>Etest</td>
<td>MIC Strip</td>
<td>KB Disk</td>
</tr>
</tbody>
</table>

**Figure SP048-1:** Results of the custom lyophilized BMD sensititre panel, Etest gradient strip, Liofilchem gradient strip, and Kirby-Bauer disk diffusion test, compared to the custom frozen BMD sensititre panel. Green = optimal, yellow = acceptable, red = not recommended, gray = not tested.
of creatinine and platelet count. Treatment was completed with amoxicillin. Leptospirosis was confirmed with 16S rRNA broad-range PCR and sequencing performed on the negative blood culture specimen.

**CR002**

**A confounding headache**

Curtis Quan¹, Ling Yuan Kong²

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**DISCUSSION:** Rodents are known reservoirs of LCMV. Humans commonly acquire LCMV via direct contact with contaminated feces or inhalation of aerosolized viral particles. Clinical presentation of LCMV meningitis involves an influenza-like illness followed by headache and meningismus. CSF analysis demonstrates a lymphocytic pleocytosis with elevated protein levels, usually more pronounced than more common viral causes of meningitis such as enterovirus. There is no directed antiviral treatment for LCMV; management is supportive. This case illustrates the importance of obtaining complete exposure history and recognizing when CSF parameters are out of keeping with other causes of meningitis. LCMV testing should be obtained in patients presenting with aseptic meningitis and exposure to rodents.

**CASE SUMMARY:** A 53-year-old woman presented with a 1-day history of right ear pain with purulent discharge. She was treated with amoxicillin/clavulanate for otitis media, but over the next ten days developed headaches, vomiting, lethargy, and inability to tolerate oral intake. The patient is originally from Iran and works in a food-packaging factory. Upon return to the hospital, the patient had a fever of 39.5 °C with mild neck stiffness. Bloodwork including white blood cell count (WBC), electrolytes and C-reactive protein were within normal limits. Blood cultures were negative. CT and MRI scans of the head were normal. Cerebrospinal fluid (CSF) analysis showed elevated WBC of 851x10⁶/L (98% lymphocytes), elevated total protein of 1.47 g/L and a normal CSF/serum glucose ratio. CSF Gram stain, acid-fast smear and bacterial, fungal and mycobacterial cultures were negative. Upon further history, the patient reported seeing mice at her workplace. Due to this exposure, lymphocytic choriomeningitis virus (LCMV) serology was requested and returned positive for IgM. Repeat serologies 5 weeks later demonstrated seroconversion with positive LCMV IgM and IgG confirming the diagnosis of LCMV meningitis.

**CR003**

**A case report of Medicopsis romeroi cutaneous nodules in a liver transplant patient**

JeongMin Kim, Allison Mah

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**DISCUSSION:** Medicopsis romeroi, previously known as Pyrenochaeta romeroi, is a dematiaceous fungus that is widely distributed in the environment. The phaeohyphomycoses can cause numerous clinical entities, including localized cutaneous nodules. These are usually secondary to trauma, but the time of symptom onset may be years after the exposure, especially in the context of new immunosuppression. There are at least 12 cases of Medicopsis romeroi infection in solid organ transplant patients in literature, though none have been reported in North America. Treatment can include voriconazole or itraconazole. If resectable, local excision has highest rates of cure, and was a successful option for our patient while also avoiding hepatotoxic medications.

**OBJECTIVE:** To describe the clinical presentation, diagnosis, and management of cutaneous phaeohyphomycosis in an immunocompromised person who immigrated more than 30 years ago from an endemic country.

**CASE SUMMARY:** We present the case of a 69-year-old man with a recent liver transplant, on mycophenolate, tacrolimus, and prednisone. Two months after transplantation, he developed painful erythematous swelling to his right second metacarpophalangeal joint (MCP). He had immigrated from Vietnam in the 1980s. There was no history of trauma to the finger, and no systemic signs or symptoms. He presented to the hospital where he received an incision and drainage and started on empiric cefazolin. His lab-work was normal, including eosinophils of zero. His finger improved minimally. Two weeks later, his cultures returned positive for Medicopsis romeroi. A CT scan showed minimal capsular thickening at the MCP with no features suggestive of osteomyelitis or soft tissue collections. He was seen by the plastics surgery team and received complete incisional biopsy of the lesion, which on pathology showed multiple coalescing nodules of granulomatous inflammation with fungal organisms suggestive of yeast forms and pseudohyphae. He was asymptomatic without relapse six months later.
**CR004**

**A case of cutaneous diphtheria by Corynebacterium ulcerans, its identification and public health implications**

Charlotte A Fuller, Sharon Grad, Cheryl Main

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**DISCUSSION:** Toxin detection testing is routinely performed for C. diphtheriae isolates but it is less clear when to perform for other toxin producing Corynebacteria, especially when found in mixed cultures. *C. ulcerans* was initially misidentified as *C. pseudotuberculosis* by the VITEK MS PRIME, which raises concerns for the reliability of this method for identification for possible toxin producing Corynebacteria. As per Ontario’s Public Health Standards, *C. ulcerans* contacts should be treated similarly to *C. diphtheriae*, with contact tracing, surveillance, and chemoprophylaxis for close contacts regardless of vaccination status.

**OBJECTIVES:** Corynebacterium diphtheriae is a toxin producing bacteria and the causative agent of diphtheria. This case highlights toxin production by other Corynebacterium species. We will review their ability to cause clinical disease and the role for prophylaxis as per current public health recommendations. We will also review current identification and toxin detection methods and discuss their possible limitations.

**CASE SUMMARY:** We report a case of toxin producing *C. ulcerans* in a 23-year-old male presenting with a skin and soft tissue infection. The organism was initially identified as *C. pseudotuberculosis* by our VITEK MS PRIME (bioMérieux Canada) in a mixed flora culture. The organism was sent for toxin detection testing as a deviation from internal standard operating procedures for mixed cultures for teaching purposes. The organism was identified by 16S Sequencing as *C. ulcerans* and found to be positive for toxin production by modified Elek test and PCR for diptheria toxin gene by the National Microbiology Laboratory. Following identification of toxin production, Public Health Ontario was involved for contact tracing. Prophylaxis was administered to the patient’s contacts as per currently provincial guidelines.

**DISCUSSION:** Vancomycin dependent *Enterococcus* (VDE) are not routinely reported in microbiology samples. The unique feature of these isolates is that not only are they resistant to vancomycin, they need vancomycin for their growth. In patients with VDE, vancomycin cannot be used as therapy. On retrospective analysis of one-year data we had at least three such isolates, all among oncology / transplant population from screening swabs. Is it time to incorporate VDE screening in wound swabs from such patients?

**OBJECTIVE:** To highlight the need for screening for vancomycin dependence in Enterococci among immunocompromised/ transplant patients.

**CASE SUMMARY:** 59-year-old male status post orthoptic liver transplant X 2 admitted with pancytopenia and disseminated varicella zoster infection. Patient had liver transplant for alcoholic end stage liver disease in October 2021, but the post-transplant course was complicated by acute cellular rejection and biliary stricturing. He received solumedrol and multiple courses of antibiotics [AV1]. He subsequently had a second liver transplant in March 2022 with post-transplant course complicated by aspergillosis for which he received voriconazole for 3 months, CMV viremia on valganciclovir and had recent admissions for *C. difficile* colitis as well. Currently he was on valganciclovir for CMV viremia, amoxicillin/ clavulanic acid for perianal abscess, vancomycin po BID (prophylaxis while on amox/clav) and on atovaquone prophylaxis.

His surveillance screening swabs grew *Enterococcus faecium* which did not grow on blood agar (BAP) but grew well on VRE agar. This led to the suspicion of vancomycin dependence in this isolate. The isolate was then streaked on a BAP with a standard vancomycin disc and grew well around the disc which confirmed the diagnosis of vancomycin dependent *Enterococcus* (VDE).
CASE REPORT POSTER PRESENTATIONS

CRP001
The sinister spread of Streptococcus: A complicated case of Streptococcus pneumoniae bacteremia with pyogenic ventriculitis, osteomyelitis, and lumbar abscess in a patient with polysubstance use disorder

Samantha Peterson, Omar Akhter, Shanaz Azad, George Gueorguiev
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DISCUSSION: While Streptococcus pneumoniae is commonly associated with the eponymous respiratory infection, its ability to escape phagocytosis and invasive nature can lead to severe infections of other organ systems. Ventriculitis is a rare central nervous system infection often caused by Streptococcus pneumoniae and is frequently linked to spinal cord infections. This patient’s polysubstance use by way of insufflation and intravenous injection may have predisposed him to his diffuse spread of Pneumococcal infection, both by introducing bacteria that typically colonize the nasopharynx as well as by weakening his overall immunity. He may have also had infection with a particularly virulent strain. Prompt recognition of severe complications associated with Pneumococcal disease can minimize adverse effects, and may be prevented by vaccination.

CASE SUMMARY: A 63-year-old male with a history of hypertension and polysubstance use disorder presented with altered mental status. He was initially febrile and labs demonstrated leukocytosis. Chest X-ray showed infiltrates consistent with pneumonia, and blood cultures were positive for Streptococcus pneumoniae. Urine antigen was also positive for Streptococcus pneumoniae. He was intubated and started on ceftriaxone. After several days he showed minimal clinical improvement, and due to persistent fevers and altered status, an MRI was performed and revealed pyogenic ventriculitis. Antibiotics were changed to linezolid and cefepime, and his mental status slightly improved. Given generalized weakness throughout all four limbs, an MRI of the entire spine was performed, which showed multilevel spinal discitis/osteomyelitis throughout the cervical, thoracic, and lumbar spine as well as a lumbar epidural abscess. He underwent L2-L5 laminectomy with drainage of lumbar abscess. High-dose ceftriaxone was restarted, which he continued for 6 weeks after he was discharged in stable condition.

CRP002
Barking up the wrong tree: An unusual case of Capnocytophaga ochracea complicated skin and soft tissue infection in an immunocompetent individual

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DISCUSSION: Infections with Capnocytophaga species, gram-negative facultative anaerobes found in oral flora of humans and animals, are relatively uncommon and are generally seen in patients who are immunocompromised, most often manifesting as sepsis. While Capnocytophaga canimorsus is typically associated with animal oral flora, particularly dog bites, Capnocytophaga ochracea is more commonly associated with human oral flora, and may rarely lead to infections such as periodontitis, septic arthritis, or septic shock. Given that the patient’s cultures grew Capnocytophaga ochracea, this indicates that the patient’s inoculation source was likely from a toothpick used by a human despite her recollection of the puppy chewing the toothpick. Regardless of the source, skin and soft tissue infections associated with any involvement of oral flora should be covered appropriately with amoxicillin-clavulanate, clindamycin, or imipenem to prevent more severe forms of Capnocytophaga illness.

CASE SUMMARY: A 66-year-old female with a history of hypertension presented with right lower extremity pain for approximately ten days, at which time she had stepped on a toothpick she believes was chewed on by her puppy. She removed the toothpick but experienced progressively worsening swelling and pain associated with purulent and malodorous drainage. Upon presentation, her labs demonstrated leukocytosis of 15.9 x 10^3/ul as well as an elevated sedimentation rate to 130 mm/h. An X-ray showed diffuse soft tissue swelling of the right foot, and an MRI showed no evidence of osteomyelitis. She was started on daptomycin with piperacillin-tazobactam and underwent an incision and drainage of the area. Intraoperative cultures revealed Capnocytophaga ochracea, Staphylococcus epidermidis, and Streptococcus species. She was discharged in stable condition with a 3-week course ertapenem.
CRP003
Traceback investigation of a suspect case of transfusion-transmitted malaria

Bryan Tordon1, Steven J Drews23, Francine Flahr4, Kathleen Bennett5, Teresa Gaziano6, Danielle Anderson7, Susan Nahiriak1378, Hanan Gerges3, Gregory J Tyrrell3A9, Momar Ndao1011, Mark Bigham23, Matthew Seftel24

1Canadian Blood Services, Toronto, ON, Canada; 2Canadian Blood Services, Edmonton, AB, Canada; 3University of Alberta, Edmonton, AB, Canada; 4University of Alberta, Edmonton, AB, Canada; 5Canadian Blood Services, Regina, SK, Canada; 6Canadian Blood Services, Ottawa, ON, Canada; 7Canadian Blood Services, Brampton, ON, Canada; 8Alberta Precision Laboratories (APL), Edmonton, AB, Canada; 9Alberta Health Services, Edmonton, AB, Canada; 10APL Public Health, Edmonton, AB, Canada; 11National Reference Centre for Parasitology, Montréal, QC, Canada; 12Department of Medicine, Division of Infectious Diseases, McGill University, Montréal, QC, Canada; 13Department of Medicine, Division of Infectious Diseases, McGill University, Montréal, QC, Canada; 14Canadian Blood Services, Vancouver, BC, Canada; 15Department of Medicine, University of British Columbia, Vancouver, BC, Canada.

DISCUSSION: This is the first probable case of transfusion-transmitted malaria (TTM) in Canada in over 25 years. Although TTM risk is low (<1 in 20 million cellular donations), blood operators continue to pursue malaria-risk mitigation efforts in blood donors.

CASE SUMMARY: A 4-month-old infant hospitalized since birth received multiple blood transfusions. In March 2022, P. falciparum was incidentally identified in a peripheral blood film. As an initial investigation did not implicate the mother as the source of infection, we initiated a traceback investigation for potential blood donor source. The patient had received 13 red blood cell (RBC) units, 3 apheresis platelet (PLT) units and 16 pooled PLT units. With 77 donors initially implicated, initial focus was on donors of cellular (RBC and PLT) components. Thirteen donors were contacted and assessed using a categorization approach (Table).

Table CRP003-1: Blood donor categorization.

<table>
<thead>
<tr>
<th>Time/behaviour-based categories</th>
<th>Action-oriented-based categories</th>
</tr>
</thead>
<tbody>
<tr>
<td>Low</td>
<td>No history of birth, travel, or residence in malaria-endemic region</td>
</tr>
<tr>
<td>Intermediate</td>
<td>Short term travel (&lt;1 month) and/or residence (&lt;6 months) in malaria-endemic region</td>
</tr>
<tr>
<td>High</td>
<td>History of birth, travel (&gt;1 month), and/or residence (&gt;6 months) in malaria-endemic region</td>
</tr>
<tr>
<td></td>
<td>Donor malaria testing not indicated</td>
</tr>
<tr>
<td></td>
<td>Donor malaria testing may be indicated if other sources ruled out</td>
</tr>
<tr>
<td></td>
<td>Donor malaria testing indicated</td>
</tr>
</tbody>
</table>

Using this assessment tool, three RBC donors were deemed high potential: donor 1, born in an endemic region (West Africa); donor 2, born in an endemic region and having travelled to Mexico; and donor 3, with extended travel to endemic regions in South America and Asia. These donors consented to P. falciparum serology (immunofluorescence assay [IFA]) and nucleic acid testing (NAT). Donor 1 was P. falciparum NAT-positive (Ct > 32, estimated 0.0004% parasitemia), and P. falciparum IFA-positive. Donors 2 and 3 were NAT and IFA-negative. Lookback investigation of all prior transfused fresh products from donor 1 identified no malaria-positive blood recipients.

CRP004
Withdrawn

CRP005
A real pain in the neck - rat bite fever complicated by spinal epidural abscess

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1Division of Medical Microbiology, Department of Pathology and Molecular Medicine, McMaster University, Hamilton, ON, Canada; 2Division of Infectious Diseases, McMaster University, Hamilton, ON, Canada; 3Division of General Internal Medicine, Department of Medicine, McMaster University, Hamilton, ON, Canada

DISCUSSION: Rat bite fever caused by S. moniliformis classically presents with fevers, polyarthralgia, and non-specific flu-like symptoms, and it can mimic common rheumatological disorders such as rheumatoid arthritis. A subset of patients may present with serious complications such as spinal epidural abscess. This case highlights the importance of maintaining a broad differential when approaching spinal infections as well as the value of a thorough exposure history in such cases. Clinicians should carefully assess patients with S. moniliformis infection for metastatic complications including spinal infections.

OBJECTIVES:

1. Review the presentation of rat bite fever and its clinical mimics.
2. Highlight Streptobacillus moniliformis as a potential cause of spinal infections.

CASE SUMMARY: A 56-year-old woman presented to hospital with a three-day history of severe neck pain that was preceded by one week of fevers, headaches, and
polyarthritis. On exam, she had cervical spine tenderness and arthritis of some interphalangeal joints of her fingers. She had no nuchal rigidity or focal neurological deficits. Workup showed leukocytes of 12.6 [4.0-11.0x10^9/L], platelets of 64 [150-400x10^9/L] with splenomegaly, C-reactive protein of 277 (≤8 mg/L), and rheumatoid factor of 22 (≤14IU/mL). Nasopharyngeal swab was positive for SARS-CoV-2. Her presentation was attributed to acute viral infection with possible rheumatoid arthritis, and antibiotics were not initiated. Progressive upper limb paresthesia and hyperreflexia prompted a cervical spine MRI that showed an early abscess in the anterior spinal epidural space from C4 to C6 with mild to moderate spinal canal stenosis. She was started empirically on piperacillin-tazobactam and then underwent posterior C3-C7 decompression, instrumentation, and fusion. Post-operatively, blood cultures collected at the time of admission grew Streptococcus moniliformis. Antibiotics were switched to intravenous penicillin G for six weeks with subsequent clinical and radiographic improvement. Further history revealed that she kept pet rats at home that she would often feed by hand.

**CRP006**

**Vertebral osteomyelitis with coccidioidomycosis: A case report and review of the literature**

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**DISCUSSION:** We have discussed in this paper the limited evidence in this topic for antifungal selection and duration of therapy within the IDSA 2016 guidelines. We have also provided some teaching points from this textbook case and a review of the literature for treatment.

**CASE SUMMARY:** The dimorphic fungi Coccidioides spp. cause a systemic fungal infection, coccidioidomycosis, also known as Valley fever by inhaling arthroconidia which is the infectious form of this fungus. One-half to two-thirds of all infections caused by Coccidioides spp. are either asymptomatic or mild, requiring no seeking for medical evaluation. About 1%-0.5% of all infections in the general population cause extra-pulmonary dissemination. We report a case of a previously healthy 32-year-old male who had acquired Valley fever just after a hiking trip during his residence in an endemic region of Coccidioides spp. Despite receiving fluconazole for a total of 4 months for his primary infection, he then presented with a compression fracture of C5 and prevertebral abscess secondary to disseminated coccidioidomycosis. His management was optimized by surgical intervention plus Amphotericin B, then step down to Itraconazole twice daily.

**CRP007**

**Persistent SARS-CoV-2 infection in an immunocompromised patient**

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**DISCUSSION:** Resolution of COVID-19 infection is based on time post onset of illness and clinical. Cases are considered active for 10 days post onset of illness, or 20 days in severe illness or immunocompromise. A “test of cure” based resolution is not advisable, as resolved cases may continue to test positive for weeks to months post initial infection. Cycle Threshold (Ct) values of the PCR reaction has been used to differentiate between an acute infection versus a post-acute positive, with Ct < 30 indicative of active infection. In this case, we review an immunocompromised patient with what appeared to be persistent SARS-CoV-2 infection requiring multiple hospitalizations over a two-month period. This case highlights a need for additional research to understand patterns of SARS-CoV-2 shedding in immunocompromised hosts, and how to manage protracted infections from both a clinical management and infection control perspective.

**CASE SUMMARY:** A 69-year-old male with a history of acute myeloid lymphoma status post allogeneic stem cell transplant, and on prednisone for delayed graft versus host disease, presented to a community COVID care centre with new onset respiratory illness. COVID-19 infection was confirmed via PCR, and the patient was prescribed nirmatrelvir/ritonavir. Chest radiography at the time showed no pulmonary involvement. Twenty-eight days post onset of infection, the patient was admitted to hospital with progressive dyspnea and radiographic airspace disease, COVID-19 positive on PCR with cycle threshold (Ct) values in the mid 20s. Patient was started on prednisone 60 mg daily for organizing pneumonia and discharged on a six-week tapering dose. On day 55 post onset of infection, he again presented to hospital requiring ICU admission for hypoxemic respiratory failure, again testing positive for COVID-19 with Ct values in the low 20s. Whole-genome sequencing of specimens taken at initial infection, day 28, and day 57 were all confirmed as Omicron BA.2.9.
**CRP008**

A rare mimic of a common foe: A case of *Aerococcus urinae* infective endocarditis, complicated by renal abscess and multiple strokes

Alison Sumner, Matthew Clifford-Rashotte

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**DISCUSSION:** *Aerococcus urinae* is a gram-positive coccus appearing in tetrads/clusters on gram stain (similar to staphylococci) and displays alpha hemolysis on blood agar (similar to viridans group streptococci). Further, it is catalase negative; this unique combination of characteristics can make initial lab identification challenging. Primarily identified in the urinary tract, *Aerococcus urinae* is a rare cause of bacteremia, with ~20% of cases complicated by infective endocarditis. Most cases of endocarditis occur in male patients with underlying urinary pathology, likely due to ascending infection. Interestingly, our patient had no change in his urinary symptoms (intermittent urgency, and mild straining) for months prior to hospitalization. *Aerococcus urinae* is generally susceptible to penicillins, ceftriaxone, and vancomycin, and case series have described combination therapy with beta-lactam and aminoglycoside antibiotics (based on *in vitro* synergy), with a duration of 4-6 weeks for endocarditis. Definitive management of obstructive urinary pathology likely reduces the risk of invasive infection with *Aerococcus urinae*.

**CASE SUMMARY:** We discuss a rare case of gram-positive bacteremia and infective endocarditis due to *Aerococcus urinae*, including pitfalls in initial lab identification, risk factors, and treatment strategies. A 57-year-old man presented to hospital with fevers, transient vision loss, and flank pain. Past medical history included lichen sclerosis of the urethra. On assessment he was febrile, with an apical murmur, and a normal neurologic examination. CT abdomen revealed a right renal abscess, and echocardiogram revealed a 2 cm mitral valve vegetation. MRI brain showed multiple cerebral infarcts. Blood cultures were initially reported as gram-positive cocci in clusters, and he was treated with vancomycin for suspected staphylococcal bacteremia. Subsequent testing identified the organism in blood culture to be *Aerococcus urinae*, and antibiotics were changed to ceftriaxone. He underwent mitral valve replacement and completed a 6-week course of antibiotics. Urology was consulted for definitive management of his urethral lichen sclerosis.

**CRP009**

Disseminated *Metamycoptasma hominis* infection in a renal transplant recipient

Matthew Spear, Mark Robbins

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**DISCUSSION:** *M. hominis* is a rare cause of bacteremia but is capable of causing disseminated disease in immunocompromised patients. *M. hominis* isolates are predictably susceptible to tetracyclines and levofloxacin but are intrinsically resistant to macrolides. Laboratory detection is challenging as standard techniques have suboptimal sensitivity, although 16S and prolonged incubation of cultures may help identify the organism in challenging cases such as this. This case highlights a complex presentation and associated challenges in identification of *M. hominis* infection in an immunocompromised host.

**CASE SUMMARY:** *Metamycoptasma hominis* is a commensal organism of the genital tract but has been implicated in systemic disease particularly in immunocompromised hosts and can be challenging to identify with standard laboratory techniques. This report describes a case of *M. hominis* bacteremia, epidural abscess and native joint septic arthritis with diagnosis requiring molecular techniques and prolonged incubation of microbiologic samples. A 58 year old immunocompromised male presented to hospital with subacute low back pain, lower extremity weakness and acute history of right knee pain, swelling and erythema. His past medical history included remote renal transplantation in 2016 secondary to Fabry disease, mechanical aortic valve and pacemaker. Right knee synovial fluid analysis revealed white blood cell count of 77440 x10^3/L with 97% neutrophils, negative bacterial culture and indeterminate 16S testing. He underwent MRI which demonstrated L4/L5 discitis, osteomyelitis with vertebral bone biopsy culture yielding no growth. Follow-up of the indeterminate 16S RNA result from synovial fluid revealed that *Metamycoptasma spp.* was identified with 80% certainty. Subsequently, 16S RNA testing of lumbar spine samples were positive for *M. hominis*. Blood cultures drawn at this time reported growth of *M. hominis* after 21 days incubation. He was treated with 18 weeks of doxycycline with clinical, biochemical, and radiographic resolution.

**CRP010**

A case of human Eastern Equine Encephalitis Virus (EEEV) infection acquired in Canada

Swati Chavda1, Anna Cvetkovic1, Alireza Eshaghi2, Jonathan B Gubbay2, Kai Makowski1, Moiz Mikail1, Samir Patel2, John
**Abstracts**

**DISCUSSION:** EEEV encephalitis is an arthropod-borne arboviral disease. EEEV-positive mosquito pools (vector) were reported in the Parry Sound, Windsor-Essex, and Simcoe-Muskoka regions in 2021 and Eastern Ontario in 2013. EEEV in horses has been reported in rural areas in southern Ontario, Quebec, and Nova Scotia. A single case of human EEEV was previously reported in Ontario in 2016. This is the first known fatal case of EEEV infection in Ontario. Due to the scarcity of cases in Canada, epidemiology of EEEV is not well defined. Human EEEV infection should be considered for patients with exposure to mosquitoes in Southern and Eastern Ontario and Southern Quebec.

**CASE SUMMARY:** Discuss a case of human EEEV infection and review its epidemiology in Canada. A 68-year-old man presented to the emergency department in August 2022 with a fever and headache. His level of consciousness rapidly deteriorated secondary to seizures requiring intubation. He was empirically treated for bacterial and viral meningitis. His cerebrospinal fluid (CSF) analysis demonstrated a leukocytosis (115.3x10^6 L – 50% monocytic) and elevated protein (1.69 g/L). Two weeks prior to his presentation, he visited a cabin in Mont-Tremblant and had exposure to mosquitoes. Serology was positive for EEEV, and PCR of CSF (but not serum) was positive. Serology was negative for West Nile, Western Equine encephalitis, and St. Louis encephalitis. MRI showed an abnormal T2 signal in the bilateral basal ganglia and thalamus, with cytotoxic edema and intraventricular purulent material in the left occipital horn. He had further neurologic decompensation within a week of his admission, with a repeat CT showing diffuse cerebral edema and anoxic brain injury with herniation. After discussion with family, palliation was pursued, and he died shortly thereafter. An autopsy confirmed viral meningoencephalomyelitis with PCR and whole genome sequencing from brain tissue confirming Eastern equine encephalitis virus RNA.

**CRP011**

*Pluralibacter gergoviae in a postoperative brain abscess*

Sonya J Ramondino, Omar Mourad

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**DISCUSSION:** *Pluralibacter gergoviae* is a rare human pathogen which is most commonly nosocomial in origin with the potential to cause opportunistic infection. It has also been isolated from cosmetics requiring recall of various products. Limited clinical data exists surrounding the management of human infection, including resistance profiles and antibiotic selection.

**OBJECTIVES:** *Pluralibacter gergoviae* is a facultatively anaerobic Gram-negative environmental bacterium and an uncommon cause of human disease. We intend to review existing cases in the literature as well as present our case of *Pluralibacter gergoviae* post-surgical resection of a brain mass.

**CASE SUMMARY:** A 59-year-old man initially presented to hospital with left-sided weakness and confusion. He was subsequently found to have a small infarction associated with subarachnoid hemorrhage, which was treated non-operatively. Later in the month he was re-admitted to hospital with persistent neurologic symptoms. Serial MRIs revealed an underlying mass which was eventually resected and confirmed to be a high-grade glioma. The patient underwent six weeks of temozolomide therapy with radiation, followed by 12 cycles of adjuvant temozolomide monotherapy. He was concurrently treated with a one-week course of cephalexin due to notable discharge from his wound. Upon completion of his radiation therapy, a repeat MRI was performed with concern for a post-operative abscess given evidence of persistent discharge and wound dehiscence. The MRI was suggestive of an abscess, and the patient underwent surgical exploration approximately three months after his original resection. Tissue and fluid cultures from the operating room grew *Pluralibacter gergoviae*. The patient was originally treated with meropenem and stepped down to ceftriaxone after susceptibilities were reported.

**CRP012**

*A national response to the 2022 monkeypox virus outbreak*

Kristina D Dimitrova, Anders Leung, Mable Hagan, Kaylie Doan, Geoff Soule, Yvone Deschambault, Shihua He, Jim Strong, David Safronetz

National Microbiology Laboratory, Winnipeg, MB, Canada

**DISCUSSION:** In early May 2022, a suspect case of mpox was detected in the United States with recent travel history to Quebec. On May 19, 2022, confirmation of the first mpox positive case in Canada was made by real-time PCR within 24 hrs of receiving the sample. All suspect samples underwent validated high consequence pathogen inactivation protocols prior to transferring to a containment level 2 laboratory for diagnostic detection of mpox virus. Viral
Abstracts

**CASE SUMMARY:** Mpox is a Orthopoxvirus from the same Poxviridae family as smallpox and is transmitted through close contact with an infected person or animal. Symptoms include a rash that goes through several stages, swollen lymph nodes and flu-like symptoms. Most cases are self-resolving and less than 6% of are fatal. Mpox infections primarily occur in central and west Africa and are occasionally exported to other regions around the World. On May 6, 2022, an outbreak of mpox was identified in United Kingdom, the first cluster of non-endemic cases since 2003. Mpox cases were quickly identified to over 70 countries. Of the 11 pre-remediation specimens collected by the PHU, 64% (7) detected presence of Legionella species by PCR. One specimen obtained from the ice machine used by the resident was positive on culture (L. anisa). Of the 52 subsequent pre-remediation specimens collected for qPCR, 7.7% (4) and 5.8% (3) detected 10 to 100 genomic equivalents (GE)/mL of L. pneumophila and non-pneumophila Legionella species, respectively. Post-remediation, two specimens from the ice machine and one specimen from the resident’s room sink detected ≥100 GE/mL of Legionella species. All cultures were negative. The ice machine was removed from service and the sink faucet was replaced. No further cases of legionellosis were identified during the subsequent 3-months of heightened surveillance.

**RESULTS:** Our experience highlights the potential for nosocomial transmission of non-pneumophila Legionella species and the importance of timely investigation, remediation measures, and iterative review of ice machine maintenance.

**CRP013**

**Nosocomial case of Legionella bozemanii pneumonia in a long-term care setting**

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**OBJECTIVES:** To describe a case of Legionella pneumonia acquired in a long-term care facility (LTCF), and the associated investigation and remediation measures.

**METHODS:** A 68-year-old long-term care resident with chronic myelomonocytic leukemia was transferred to acute care with symptoms concerning for healthcare-associated pneumonia. Diagnostic bronchoscopy was performed for non-response to empiric piperacillin-tazobactam. Legionella polymerase chain reaction (PCR) returned positive, with culture confirming L. bozemanii. Given the resident’s prolonged stay, this was considered a nosocomial acquisition to the LTCF and was reported to the public health unit (PHU). After environmental testing by PCR identified possible contamination of the water system, remediation occurred using thermal disinfection to ≥70 °C and copper-silver ionization, in collaboration with a consultant and the PHU. To assess the effectiveness of remediation, pre-and post-remediation specimens from specified plumbing infrastructure and ice machines throughout the LTCF were collected for quantitative PCR (qPCR).

**CONCLUSIONS:** Our experience highlights the potential for nosocomial transmission of non-pneumophila Legionella species and the importance of timely investigation, remediation measures, and iterative review of ice machine maintenance.
maternal infertility). He was admitted to NICU at birth for prematurity. In the NICU, he had prolonged periods of bradycardia and was subsequently diagnosed with Long QT Syndrome (LQTS). Initial genetics and metabolic work up were unremarkable. Once stable, he was discharged home on propranolol with close cardiology followup. However, he was readmitted at two months of age to the pediatrics ICU with hypercapnic respiratory failure of unclear etiology requiring intubation. He developed worsening signs of heart block with ECG pattern suggestive of Brugada syndrome. Chest x-ray showed multinodular nodular opacities in both lungs. The baby progressed on standard ventilation and was actively being workup and prepared for ECMO (Extracorporeal membrane oxygenation). Given his worsening condition, he underwent diagnostic bronchoscopy and bronchoalveolar lavage, sputum cultures came back positive for Mycobacterium tuberculosis. Although neither of the parents had disease symptoms, both parents were screened for TB (negative induced sputum x3). There had been no overseas visitors or exposures to other people at risk for TB. As these tests were negative, it was suggested the mother have an endometrial biopsy and it showed necrotizing granulomatous inflammation. Endometrium and urine culture were positive for Mycobacterium tuberculosis. The diagnosis of congenital TB was confirmed, the baby was treated with anti-TB medications, which had better outcomes, including the complete resolution of LQTS.

**CRP015**

**Vesiculopustular rash in a 2-month-old infant... not only for adult!**

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**DISCUSSION:** Mpox may be underdiagnosed in pediatrics, as the rash can easily be confused with other childhood illnesses. Treatment may be considered for patients at high risk of severe disease including children. Tecovirimat as first-line therapy for Mpox infection in young children was shown here to be safe and effective, even when started late in the evolution.

**OBJECTIVES:** Recognize Mpox presentation in infants and safety of Tecovirimat

**CASE SUMMARY:** A 2-month-old infant consulted for a disseminated vesiculopustular rash. Parents noticed an initial cluster of 3 vesicles on the infant’s forehead a week before and one spike of temperature three days prior to the visit. On examination, a dozen umbilicated vesiculopustules were observed with minimal surrounding skin inflammation. They ranged from 2 to 5 mm in size and were scattered over the face, trunk and limbs including palms and soles. In addition, 3 crusted umbilicated lesions (2 cm x 2 cm) were found on the forehead. Differential diagnosis included varicella zoster virus, herpes simplex virus, syphilis and enteroviral infections. An extensive work-up was ordered as neonatal herpes infection could not be ruled out. Skin and CSF specimens were sent for bacterial and viral testing. Pending results, acyclovir was initiated. New lesions continued to be observed daily. Results came back negative on all specimens. Due to ongoing transmission of Mpox in the community, PCR for orthopoxvirus was sent to the reference laboratory and came back positive on the skin and negative in CSF. Because of the patient’s age and ongoing new lesions, Tecovirimat, was administered on day 10 of symptoms. After 24 hours, new lesions stopped appearing and crusting of active lesions was noted. Although parents denied symptoms initially, the mother remembered in retrospect having a mild rash that consisted of 10 pustules on her hands and arms two weeks prior to her child.

**CRP016**

**Septic transfusion reaction related to platelet contamination is rare but is still happening. Would you recognize it?**

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**DISCUSSION:** Hema-Quebec performs large volume delayed sampling (LVDS) approach for all platelets products. This approach consists of sampling 20 ml of room temperature platelets product 48 hours after collection. This method has been shown to be more sensitive than previous protocol and was introduced in 2016. Since its introduction, no proven case of septic transfusion reaction had been described in Quebec. In case of “suspicious” septic transfusion reaction, clinicians should perform culture of blood products as described in RMTC 2007. Coagulase negative staphylococcus (SCoN) are often considered “culture” contamination in this setting. However, it is the most frequent cause of platelets product contamination recognized before transfusion by the LVDS approach. This case highlights the possibility of SCoN product contamination probably
coming from donor skin and suggests that other cases might be misclassified as “culture” contamination instead. Even if LVDS is very sensitive, bacterial contamination may still be overlooked and cause septic transfusion reaction. Pathogen Reduction Technology will soon be deployed on a larger scale in Canada and should contribute to reduce this risk even more.

**OBJECTIVES:** Recognize septic transfusion reaction related to platelet contamination and its risk mitigation strategies

**CASE SUMMARY:** An adult patient with hematologic malignancy was hospitalized for neutropenic fever and treated with meropenem and vancomycin. He/She developed high fever (39 degree) and significant hypotension while receiving a platelet transfusion. Transfusion was stopped, platelets product was sent to the microbiology laboratory for culture and blood cultures were collected from the patient 2 hours and 12 hours after the septic transfusion reaction. Direct gram stain from the residual platelets product showed gram positive cocci in clusters. All blood cultures and platelets product cultures grew Staphylococcus epidermidis which were proven to be from the same pulsivar according to PFGE. Patient recovered over the next days.

**CRP017**

**Antibody detection using phage immunoprecipitation sequencing to directly link enterovirus D68 infection to a pediatric case of severe Guillain-Barré Syndrome**

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**DISCUSSION:** Where viral diagnostic yield by NAT is low, such as in cases of neurological complications following EV-D68 infection, a comprehensive method for antibody detection such as PhIP-Seq can directly and rapidly link a pathogen to clinical outcomes.

Enterovirus D68 (EV-D68) can cause neurologic complications following respiratory illness, particularly in children. However, cerebrospinal fluid (CSF) in these cases is often negative for EV-D68 by nucleic acid testing (NAT).

**OBJECTIVES:** In an effort to directly link EV-D68 to neurologic disease, we explored the use of phage immunoprecipitation sequencing (PhIP-Seq) to detect enterovirus group D (EV-D) specific antibodies in CSF.

**CASE SUMMARY:** A 6-year-old was diagnosed with severe Guillain-Barré Syndrome with widespread sensory and motor peripheral demyelinating neuropathy and secondary axonal loss following laboratory-confirmed infection with EV-D68. CSF from the case was PCR negative for enterovirus RNA. We used a phage display library called VirScan encoding for peptides of 206 human viral pathogens on the patient’s serum and CSF to detect EV-D antibodies. Anonymized sera from residual serology testing were used as uninfected/distantly infected controls to evaluate case serum/CSF seropositivity. Normalized hits for case samples were notably higher than those for control samples for the following EV-D epitopes, which include capsid protein VP4 (serum: 106.77; CSF: 89.99; controls: 0), non-structural proteins 3A (serum: 59.60; CSF: 76.31; controls: 0) and 3D (serum: 62.06; CSF: 77.47; controls: 0). Hierarchical clustering analysis revealed two main groups in the assay run, with both case samples (serum and CSF) clustering into a separate group from the control samples, further supporting the presence of antibody production in serum and CSF of the case. The ratio of averaged normalized EV-D enriched epitope hits between the serum and CSF samples of the case was 11:1, lower than typically observed, suggesting local central nervous system antibody production.

**CRP018**

**Bartonella Henselae infection with concurrent latent Syphilis in a patient with unexplained generalized Lymphadenopathy: A Case Report**

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**DISCUSSION:** Cat scratch disease (CSD) remains an uncommon clinical diagnosis. The causative organism, *Bartonella henselae*, is an intracellular gram-negative bacillus transmitted by cat fleas to cats, and to humans via contact with cat saliva. The clinical presentation is marked by lymphadenopathy. Immunocompromised individuals can present with invasive disease including various neuro-ophthalmic manifestations. It is therefore imperative to assess vision in confirmed cases of CSD. Given *Bartonella henselae* is fastidious and difficult to grow microbiologically. Therefore, we rely on indirect detection with antibody serology and direct confirmation through Warthin-Starry
staining of infected tissue. Treatment is a five day course of oral azithromycin. The patient received oral doxycycline and rifampin due to suspected neuroretinitis.

Complicating this patient’s diagnosis further was the fact that syphilis is also a known cause of various neuroophthalmal manifestations that overlap with CSD. This patient’s CSF was negative with both VDRL screening and FTA-ABS. The former is more sensitive and the latter highly specific for neurosyphilis. Overall, the pertinent negative findings supported a provisional diagnosis of ocular bartonellosis.

**CASE SUMMARY:** A 32-year-old, previously healthy female presented with a 5-week history of progressive bilateral cervical and groin lymphadenopathy, as well as constitutional symptoms including 35-lb weight loss and significant fatigue. Notable exposures included living with a roommate’s cat and typically unprotected vaginal intercourse. Two separate lymph node biopsies were non-revealing. Syphilis testing was positive and the patient underwent treatment for presumed early syphilis. Despite treatment, she developed ocular symptoms and peripheral neuropathy, with normal neuroimaging and bland CSF. She was nevertheless treated for presumed neurosyphilis. Weeks later, serologies returned positive for *Bartonella henselae* IgG with a titre of 1:128. This prompted a re-evaluation of her case given her initial presentation was not fully accounted for by syphilis. She was started on treatment for ocular bartonella with clinical and serological improvement.

**CRP019**

*Mycobacterium abscessus* scalp infection following a hair transplant in Central America

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**DISCUSSION:** With the increased popularity of medical tourism, infectious complications pose a challenge for our healthcare system. *M. abscessus* is a ubiquitous environmental pathogen which colonizes inadequately sterilized medical instruments leading to iatrogenic infections. We report a case of multi-drug resistant *M. abscessus* (subsp. *massiliense*) scalp infection. This organism is a non-tuberculous mycobacteria containing a non-functioning *erm* gene, with susceptibility to macrolides. There is a paucity of literature guiding management of *M. abscessus* cutaneous infections. Case reports and small case series suggests that dual-therapy antibiotics are more effective than monotherapy. Our patient experienced mild tinnitus after 1 month of dual therapy and debridement, but also showed clinical improvement. We continued Clarithromycin monotherapy for another 5 months with clinical success. This case contributes to the limited literature documenting success of treating multi-drug resistant *M. abscessus* surgical site infections.

**OBJECTIVES:**

- *Mycobacterium abscessus* is an uncommon cause of iatrogenic infections due to inadequate sterilization and instrument contamination
- *M. abscessus* (subspecies *massiliense*) is a non-tuberculous mycobacteria which contains a non-functioning *erm* gene conferring macrolide susceptibility.
- The treatment of *M. abscessus* cutaneous infections is based on the combination of surgical debridement and multiple antimicrobial agents.

**CASE SUMMARY:** A 53-year-old man presented with painful, red nodules on his anterior scalp 3 weeks following a hair transplant in Central America. He failed initial therapy with 6 days of Doxycycline and 1 day of Cephalexin. The scalp abscesses were aspirated and grew *Mycobacterium abscessus* (subsp. *massiliense*), susceptible to Amikacin, Clarithromycin, and Linezolid. He underwent surgical debridement and combination Clarithromycin and Amikacin for 1 month. Amikacin peak and trough concentrations were monitored in addition to weekly audiometry assessments to ensure safety. After 1 month he developed mild tinnitus, so Amikacin was discontinued. He completed another 5 months of Clarithromycin and experienced resolution of nodules and tinnitus at the end of therapy.