ORAL PRESENTATIONS

Thursday, April 7
16:15–17:45 PDT SESSION A

A01

Impact of the SARS-CoV-2 pandemic on overall and diagnosis-specific antibiotic prescription rates in long-term-care facilities in British Columbia, Canada

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OBJECTIVES: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic had a major impact on all facets of health care. We aimed to describe oral antibiotic prescribing for various diagnoses in long-term-care facilities (LTCFs) in British Columbia, Canada, during the SARS-CoV-2 pandemic and resulting control measures, using a novel approach of linked administrative data.

METHOD: Antibiotic prescription data and physician billing data for patients aged 65 years and older residing in LTCFs in British Columbia from January 1, 2017, until December 31, 2020, were anonymously linked. Antibiotic prescriptions were matched to the most relevant diagnosis on the basis of a three-tiered hierarchy. Diagnoses of interest were respiratory tract infections (RTIs), urinary tract infections (UTIs), and skin and soft tissue infections (SSTIs). Weekly prescription rates, stratified by diagnosis, age group, sex, and antibiotic class, were calculated. Interrupted time series (ITS) analyses using seasonal autoregressive integrated moving average models were conducted to quantify the change in prescription rates in LTCFs since March 2020.

RESULTS: In total, 1,060,135 LTCF residents from 306 facilities were included. Overall, 168,538 antibiotic courses were prescribed during the 4 study years. The overall antibiotic prescription rates during the pandemic year were comparable to historical values, with an average 1.13 increase in weekly prescription rates (95% CI –1.30 to 3.56). Also, ITS analyses showed no significant effect of the pandemic on prescriptions for RTI or SSTI. However, an increase of 0.68 in weekly prescription rates was seen for UTI (95% CI 0.15 to 1.22) (see Figure A01-1).

CONCLUSION: In contrast to the community, in which antibiotic prescriptions decreased after the start of the pandemic

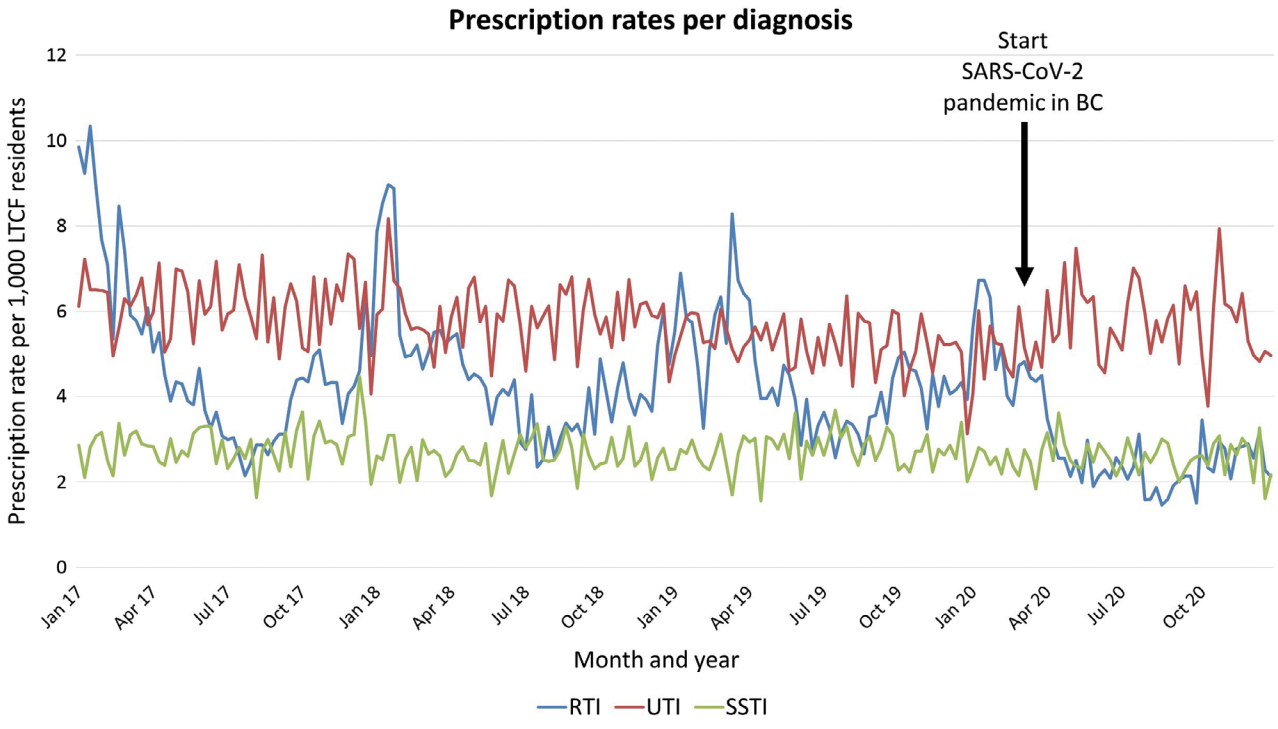

Figure A01-1: Prescription rates per diagnosis

in British Columbia, overall antibiotic prescription rates in LTCFs were not affected. However, an increase was seen in prescriptions for UTIs, despite the ongoing efforts to reduce prescribing for UTI in LTCFs. This will be further evaluated.

A02

Increased transmission efficiency of SARS-CoV-2 Delta and Omicron lineages are independent of viral load

Kyla Tozer[1,2], Calvin P Sjaarda[3], Emily Moslinger[2,4], Katya Douchant[2,5], Jummy Oladipo[1,2], April Saleem[2,4], Henry Wong[3], Danielle Brabrant-Kirwan[6], Prameet M. Sheth[1,2,3,4,5]

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OBJECTIVES: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has been punctuated by the emergence of distinct viral lineages designated as variants of concern (VOCs), notably the B.1.1.7 (Alpha), B.1.617.2 (Delta), and most recently B.1.1.529 (Omicron) variants. The emergence of each variant results in a dramatic increase in cases and hospitalizations. The rate of transmission of each variant appears to be different; here, we evaluate whether viral shedding of SARS-CoV-2 RNA is linked to the transmission efficiency of each of these VOCs.

METHOD: Nasopharyngeal swabs were tested using laboratory-developed dual-target (E-gene, 5' untranslated region) and a commercial VOC polymerase chain reaction (ORF1ab, N-gene, and S-gene) specific for SARS-CoV-2. Whole-genome sequencing on all isolates was performed using the Illumina COVIDSeq assay. Data were analyzed using PRISM 9.0 (GraphPad, San Diego, California) and Microsoft Excel (Microsoft Corp., Redmond, Washington).

RESULTS: A total of 3,418 individuals with SARS-CoV-2 were included, including Alpha (n = 1,048), Delta (n = 2,222), and Omicron (n = 148) VOCs. Using cycle thresholds (CTs) as a biomarker for viral load, we investigated the effects of viral lineage and biological sex on viral load. Viral lineages breakdown shows no significant difference between Alpha and Delta (20.21 versus 20.05, p = 0.0768). However, Omicron shows a higher CT than Delta (22.32 versus 20.05, p = 0.016). Further stratification of biological sex showed no significance between CT and sex across all lineages.

CONCLUSION: We show that individuals infected with Omicron had lower viral loads than other VOC lineages. There was no evidence to suggest biological sex affects viral load across all lineages. Despite the small number of individuals with Omicron in our study, we provide an early indication that increased viral loads, often seen as a viral strategy for increasing transmissibility, is not likely responsible for the increased transmission efficiency of the Omicron VOC.

A03

Prevalence of gastroenteritis viruses in wastewater in community and site-specific long-term-care facilities during the COVID-19 pandemic

Sudha Bhavanam[1], Bonita E. Lee[1], Xiaoli Lilly Pang[1,2]

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OBJECTIVES: The diversity of pathogenic viruses in wastewater (WW) reflects the status of infection in community and institutional settings. The main objective of this study was to evaluate the presence and temporal trend of gastroenteritis viruses (GEVs) in WW collected from WW treatment plants (WWTPs) across Alberta and from long-term-care facilities (LTCFs) during coronavirus disease 2019 (COVID-19) pandemic era.

METHOD: Post-grit raw influent WW samples (500 ml of 24-hour composite sample) were collected from 12 different WWTPs across 10 Alberta cities between May 2020 and July 2021. WW samples were collected from site-specific manholes from 10 LTCFs in Edmonton between January 2021 and August 2021. Viral RNA was extracted from ultrafiltration concentrates from 100 ml of WW using the MagMAX™-96 kits (ThermoFisher Scientific, Waltham, Massachusetts), and the nucleic acids were eluted in 100 µL of elution buffer. Detection and quantification of NoV genogroup I and II, AdV, RV, AstV, and SaV was performed by quantitative revers transcription polymerase chain reaction, as previously published.

RESULTS: Of the 2,458 samples tested from 12 WWTPs across Alberta, 953 (39%) tested positive for NoV GI, 1368 (56%) for NoV GII, 1,270 (52%) for AdV, 961 (39%) for RV, 251 (10%) for AstV, and 605 (25%) for SaV. In contrast, of 520 samples tested from LTCFs, 5 (0.9%) tested positive for NoV GI, 27 (5%) for NoV GII, 4 (0.8%) for AdV, 4 (0.8%) for RV, and 1 (0.2%) for AstV, but tests for SaV were negative during the study periods.

CONCLUSION: WW-based epidemiological surveillance (WBS) provided us an opportunity to study and compare the presence of GEVs in WW in different settings during the COVID-19 pandemic. The data in detail implies that WBS for GEV is a useful tool to monitor surging of pathogenic viruses in WW, providing early warning for potential imminent outbreaks in institutions and communities.

A04

Comparison of electronic medical record and paper-based health records on time to administration of first dose of IV antibiotics

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OBJECTIVES: Sepsis and septic shock are associated with significant morbidity and mortality,[1-3] with one study demonstrating a mortality rate of 46%.[4] The study by Kumar et al. observed a 7.6% increase in mortality with every hour delay in antimicrobial therapy in the first 6 hours of hypotension.[5] We aimed to study the time to actual antibiotic administration in the inpatient setting from physician order, comparing paper-based and computerized physician order entry systems in two hospitals.

METHOD: Retrospective chart review was conducted in the two facilities from September 4 to October 18, 2018. Admitted patients receiving their first dose of intravenous (IV) antibiotics in medical and surgical wards were included, whereas those receiving the first dose in the intensive care unit and emergency room were excluded. Patients receiving oral and pre- or post-operative antibiotics were also excluded.

RESULTS: The population consisted of 107 patients from the first institute, which uses a paper-based system, and 159 patients at the second institute, which uses an electronic medical record (EMR) system. The most common indication at hospital 1 was bloodstream infections (n = 27; 25.2%); at hospital 2, it was sinorespiratory infections (n = 29; 37.2%). Average time to antibiotic administration was longer at the second hospital which uses an EMR system (M = 344.6 min, SD = 391.86, versus M = 209 min, SD = 134.7; $t < 0.01$). Of the 40 longer durations, 39 were within the EMR-based institute, the longest being 23 hours, 32 minutes. The greatest delay at both sites was consistently the delivery time from inpatient pharmacy to the ward.

CONCLUSION: This study shows that an EMR system was slower in timing to administration of first dose of IV antibiotics. Unfortunately, the specific reasons for such delays were out of the scope of our project but are a starting point for future studies and quality improvement endeavours.

A05

Introducing the escalation antibiogram: A simple tool to inform changes in empiric antimicrobials in the non-responding patient

Daniel Teitelbaum[1], Marion Elligsen[2], Kevin Katz[3,4,5], Philip W Lam[1,6], Jennifer Lo[2], Derek R MacFadden[7], Christie Vermeiren[4,5], Nick Daneman[1,6,8]

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OBJECTIVES: Hospital antibiograms guide initial empiric antibiotic treatment selections but do not directly inform escalation of treatment among non-responding patients. Our objective is to introduce the concept of an escalation antibiogram that can use hospital antibiogram data to inform antibiotic susceptibility in patients with resistance to initial empiric therapy for appropriate escalation.

METHOD: Using gram-negative bacteremia (GNB) as an exemplar condition, we sought to introduce the concept of an escalation antibiogram. Among GNBs between 2017 and 2020 from six hospitals in the Greater Toronto Area, we generated escalation antibiograms for 12 commonly used agents. Among organisms resistant to an antibiotic, we calculated the likelihood of susceptibility to each of the other 11 agents. In subgroup analyses, we examined escalation antibiograms across study years, individual hospitals, community versus hospital onset, and pathogen type.

RESULTS: Among 6,577 GNB isolates, the likelihood of coverage was as follows: ampicillin, 31.8%; cefazolin, 62.7%; ceftriaxone, 67.1%; piperacillin–tazobactam, 72.5%; ceftazidime, 74.1%; trimethoprim–sulfamethoxazole, 74.4%; ciprofloxacin, 77.1%; tobramycin, 88.3%; gentamicin, 88.8%; ertapenem,

91.0%; amikacin, 97.5%; and meropenem, 98.2%. The escalation antibiograms revealed marked shifts in likelihood of coverage by the remaining 11 agents. For example, among ceftriaxone-resistant isolates, piperacillin–tazobactam susceptibility (21.2%) was significantly lower than trimethoprim–sulfamethoxazole (54.2%; $p < 0.0001$), ciprofloxacin (63.0%; $p < 0.0001$), ertapenem (73.4%; $p < 0.0001$), tobramycin (80.1%; $p < 0.0001$), gentamicin (82.8%; $p < 0.0001$), meropenem (94.3%; $p < 0.0001$), and amikacin (97.1%; $p < 0.0001$). Trimethoprim–sulfamethoxazole was the second-ranked agent in the meropenem escalation antibiogram (49.6%) and the first-ranked agent in the amikacin escalation antibiogram (86.0%). Escalation antibiograms were consistent across 4 study years and six hospitals.

CONCLUSION: Escalation antibiograms can be generated to inform empiric treatment changes in non-responding patients. These tools can yield important insights, such as avoiding the common maneuver of escalating from ceftriaxone to piperacillin–tazobactam in suspected GNB.

ORAL PRESENTATIONS

Thursday, April 7
16:15–17:45 PDT SESSION B

B01
Evolving acquisition of carbapenemase-producing Enterobacterales in Canadian acute-care facilities, 2017–2020

Robyn Mitchell[1], Laura F Mataseje[2], Ghada N Al-Rawahi[3], Ian RC Davis[4], Chelsey Ellis[5], Joanne Embree[6], Susy S Hota[7], Pamela Kibsey[8], Jerome A Leis[9], Allison J McGeer[10], Jessica Minion[11], Michael Mulvey[2], Sonja Musto[12], Ewa Rajda[13], Stephanie W Smith[14], Jocelyn A Srigley[3], Kathryn N Suh[15], Nisha Thampi[16], Jennifer Tomlinson[12], Titus Wong[17], Kevin Katz[18], on behalf of the Canadian Nosocomial Infection Surveillance Program[1]

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OBJECTIVES: We describe trends in carbapenemase-producing Enterobacterales (CPE) rates and sources of acquisition reported by the Canadian Nosocomial Infection Surveillance Program (CNISP) sentinel hospital network.

METHOD: CNISP conducts surveillance for CPE among inpatients of all ages. 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: In 2020, 72 CNISP hospitals in 10 provinces participated in CPE surveillance. CPE colonization rates steadily increased from 0.12 per 1,000 admissions in 2017 to 0.21 per 1,000 admissions in 2019 ($p < 0.001$). A plateau in CPE colonization rates was observed in 2020 (0.20 per 1,000 admissions). CPE infection rates remained low and stable from 0.02 per 1,000 admissions in 2017 to 0.04 per 1,000 admissions in 2020 ($p = 0.7$).

The proportion of patients who acquired CPE in health care outside of Canada was steadily decreasing even before the pandemic (45% in 2017 to 17% in 2020; $p < 0.001$). CPE acquisition in Canadian facilities has been on the rise (52% in 2017 to 75% in 2020; $p < 0.001$), and this increase is primarily driven by hospitals in Ontario and Quebec. Limited data show that the majority of patients (80%; 100/124) from 2018 to 2020 acquired CPE from another patient while in a Canadian health care facility. Trends in the proportion of CPE have shown New Delhi metallo-β-lactamase and OXA-48 acquired in Canadian facilities have increased from 2017 to 2020 (25% to 69%, $p < 0.001$, and 35% to 55%, $p = 0.2$, respectively). The majority of KPC (67%) were acquired in Canadian facilities, and this trend did not change over time.

CONCLUSION: CPE rates remain low in Canada; however, national surveillance data suggest that nosocomial transmission of CPE in Canadian health care facilities is increasing. The impact of screening practices on these trends requires further investigation.

B02

Duration of antibiotic prescription for community infections in British Columbia, Canada: Room for improvement

Abdullah A Mamun[1], Max Xie[1], Anastasiia Lisovskaia[2], Hannah Lishman[1,3], Nick Smith[1], Lynsey Hamilton[1], Sade Stenlund[1,3], Fawziah Marra[4], David M Patrick[1,3]

[1]British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada; [2]Simon Fraser University, Vancouver, British Columbia, Canada; [3]School of Population and Public Health, University of British Columbia, Vancouver, British Columbia, Canada; [4]Faculty of Pharmaceutical Sciences, University of British Columbia, Vancouver, British Columbia, Canada

OBJECTIVES: Community antibiotic stewardship has focused on eliminating unnecessary prescriptions, but studies now also support shorter duration of therapy (DOT) for many indications. This population-based study explored the DOT for common infections and compared them with Canadian guidelines.

METHOD: Prescription and physician billing data generated during the last pre-pandemic year (2019) were anonymously linked to determine prescriptions associated with specific diagnoses. We calculated the distribution and median (first quartile [Q1], third quartile [Q3]) DOT per prescription from PharmaNet by overall prescriptions, prescribing profession, indication, and drug. Physician prescriptions (~85% of total) were anonymously linked to billing data to describe DOT distribution by indication (community-acquired pneumonia [CAP], cystitis, acute bronchitis, pyelonephritis, cellulitis). DOTs for notable diagnoses were compared with recent Canadian guidelines.

RESULTS: During 2019, median DOT (Q1, Q3) for all prescriptions was 7 (7, 10) days and was similar across all health care professions except naturopathic doctors (14 d). The median DOT was 7 days across all diagnoses, but the DOT distribution skewed further right for cellulitis, pyelonephritis, and acute bronchitis. Median (Q1, Q3) DOT for CAP and cystitis was 7 (5–7) days; for pyelonephritis and acute bronchitis, it

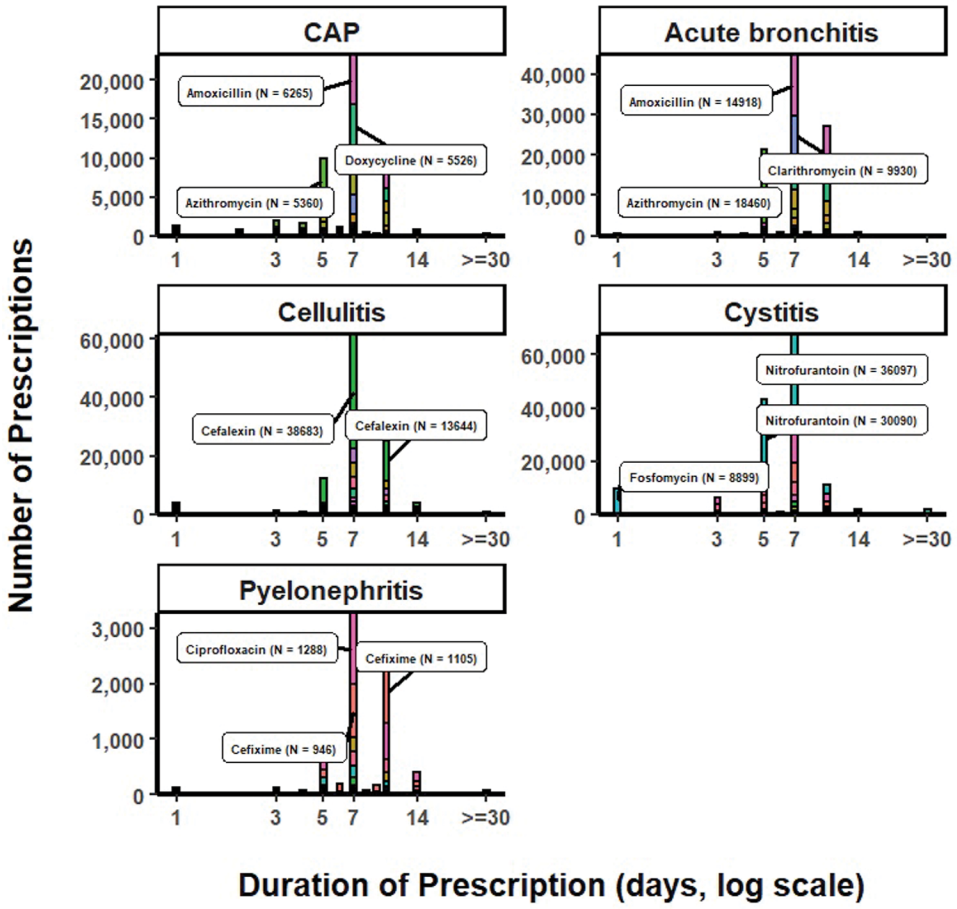

Figure B02-1: Duration of antibiotic prescription for community infection
CAP = Community-acquired pneumonia

was 7 (7–10) days. Each diagnosis-specific DOT distribution was also informed by which antibiotic was used (see Figure B02-1). For cystitis, fosfomycin was prescribed for 1 day, but ciprofloxacin, cefixime, and nitrofurantoin were more frequently prescribed for ≥7 days than for shorter durations. When compared with recent Canadian and US guidelines, there is room to reduce duration of prescription for most of the drug–indication combinations studied (Figure B02-1).

CONCLUSION: In British Columbia, there are opportunities to improve prescription practices by not only reducing unnecessary antibiotic prescriptions but by also shortening the duration of indicated antibiotic therapy while maintaining clinical effectiveness. Continuing education targeting professions and optimal DOT for indication–drug combinations should be accelerated.

B03

Coping with the grey area of antibiotic prescribing: A theory-informed qualitative study exploring family physician perspectives on antibiotic prescribing

Michelle (Shelly) Simeoni[1], Marianne Saragosa[2], Celia Laur[3], Laura Desveaux[4], Kevin L Schwartz[1,5], Noah Ivers[5,6]

[1]Public Health Ontario, Toronto, Ontario, Canada; [2]Mount Sinai, Toronto, Ontario, Canada; [3]Women's College Hospital Institute for Health System Solutions and Virtual Care, Toronto, Ontario, Canada; [4]Trillium Health Partners, Toronto, Ontario, Canada; [5]Dalla Lana School of Public Health, Toronto, Ontario, Canada; [6]Women's College Hospital Institute for Health System Solutions and Virtual Care, Toronto, Ontario, Canada

OBJECTIVES: Unnecessary antibiotic use is associated with adverse side effects and rising rates of resistance at the individual and population levels. This study used a theory-informed approach to identify potentially modifiable determinants of antibiotic prescribing for patients presenting to primary care with symptoms of upper respiratory tract infection.

METHOD: Qualitative interviews were conducted with primary care physicians in Ontario, Canada, who were identified as medium- or high-volume antibiotic prescribers (high volume defined as top 20th percentile, medium volume defined as 40th–60th percentile). The interview guide and analysis were informed by the Theoretical Domains Framework. Each interview was coded by two research team members. Sampling and analysis continued until thematic saturation was achieved.

RESULTS: Physicians felt that many decisions about prescribing for symptoms of upper respiratory tract infection were straightforward (ie, black and white). However, the intention to avoid prescribing in cases in which an antibiotic was not clinically indicated did not always align with provider action or patient expectation. Clinical decisions were influenced by elements that were both internal (knowledge, skills, social or professional role, and belief about capabilities) and external (resources, social influence, belief about consequences, reinforcement, emotions, and behavioural regulation) to the physician. The nature of the physician–patient relationship seemed to moderate the role of these factors in the decision-making process in cases in which there was diagnostic uncertainty.

CONCLUSION: Antibiotic prescribing in primary care is a complex decision-making process in which context may outweigh biology during encounters of clinical uncertainty. Differential skill in handling uncertainty and applying guidelines in practice seems to contribute to observed variation in prescribing patterns, rather than differences in foundational knowledge of best practices. Thus, interventions to reduce inappropriate antibiotic prescribing should provide communication strategies for managing uncertainty and address the application of guidelines to situations with uncertain diagnoses.

B04

The Alberta Telestewardship Network: Building a platform to enable capacity building in antimicrobial stewardship—results of an initial pilot study

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OBJECTIVES: Resources to improve antimicrobial stewardship (AS) are limited, but a telestewardship platform can enable capacity building and scaling. The Alberta Telestewardship Network (ATN) was designed to focus on outreach across Alberta and facilitate AS activities where they are underdeveloped or not as readily available or accessible.

METHOD: Outreach occurred virtually between pharmacists and physicians in urban, rural, and long-term-care settings in Alberta. With the Alberta Health Services (AHS) Virtual Health team, we integrated secure, enterprise Zoom software (Zoom Video Communications, San Jose, California) on both desktop and mobile devices into clinical workflows. We purchased 10 iPads (Apple Inc., Cupertino, California) and 5 Tryten stands for mobile sessions. The Telehealth Usability Questionnaire was adapted to capture the health provider's experience, including usefulness, ease of use and learnability, interface quality, reliability and satisfaction, and future use. We sought to determine the impact and accessibility of telestewardship, describe characteristics of patient and clinician participants, and evaluate participant satisfaction.

RESULTS: A total of 33 pilot consultations (adult and pediatric) were completed from July 6, 2020, to December 15, 2021. The majority of respondents agreed that virtual care via iPads or desktop computer and Zoom was an acceptable means to provide health care ($n = 22$; 85%), they would use virtual care via Zoom again ($n = 22$; 85%), and that they were able to express themselves effectively to other health care professionals ($n = 23$; 88%). Respondents agreed that the system was simple to use ($n = 23$; 96%) and that they could quickly become productive using the system ($n = 23$; 88%). Overall, 24 (92%) respondents were satisfied with the virtual care platform.

CONCLUSION: We aim to implement and evaluate a telehealth inpatient consultation and collaborative care service between AS providers and regional centers in Alberta. AHS has since prioritized similar workflows, including access to specialists in acute care, as part of their Virtual Health Strategy. Evaluation results will be shared with provincial stakeholders for further development of strategic planning for the ATN.

B05

Rising prevalence of extended spectrum beta-lactamase–producing *Escherichia coli* infections in Toronto

Parva Thakker[1], Shaista Anwer[1], Yerin Lee[1,2], Justin Callahan[1,2], Susan M Poutanen[1,2]

[1]Mount Sinai Hospital, Toronto, Ontario, Canada; [2]University of Toronto, Toronto, Ontario, Canada

OBJECTIVES: Extended spectrum beta-lactamase (ESBL) are enzymes capable of hydrolyzing most non-carbapenem β-lactams and are encoded on mobile genetic elements with other resistance determinants, leaving limited treatment options. We previously identified a rise in the prevalence of ESBL-producing *Escherichia coli* bloodstream infections in Toronto between 2006 and 2016 linked to the introduction of ST131 *E. coli*. This study determined whether this rise has continued over the past 5 years.

METHOD: This study included 6,354 *E. coli* isolates from blood between 2006 and 2020 from a large tertiary-care microbiology laboratory in Toronto. *E.coli* isolates were phenotypically screened for ESBL production following a validated modified Clinical and Laboratory Standards Institute double-disk test method. Proportions of *E. coli* that were phenotypic ESBL producers were graphed. Linear trendlines and χ^2 tests for trend were calculated using Excel (Microsoft Corp., Redmond, Washington) and GraphPad Instat (GraphPad, San Diego, California), respectively.

RESULTS: The proportions of ESBL-producing *E.coli* bloodstream infections have continued to increase over the past 5 years, with a dramatic rise from 6.4% (19/296) in 2006 to 26.5% (57/272) in 2020 ($p < 0.0001$, χ^2 test for trend; Figure B05-1).

CONCLUSION: Our data indicate an ongoing, concerning rise in prevalence of ESBL-producing *E. coli* bloodstream infections in Toronto. Correlation with changes in prevalence of ST131 *E. coli* is ongoing, along with determination of community acquisition, to better understand the underlying contributors to this dramatic change.

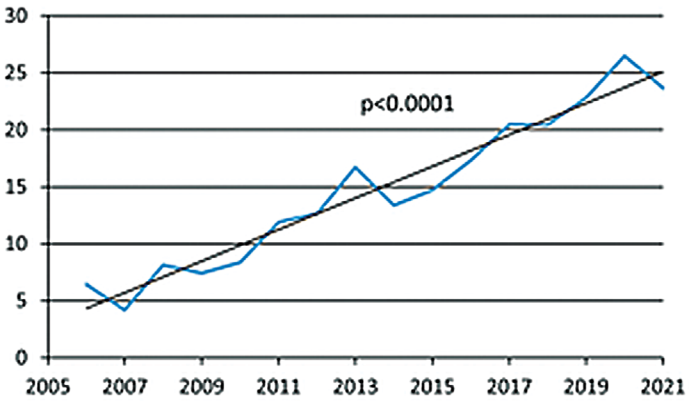

Figure B05-1: Proportion of extended spectrum beta-lactamase–producing *Escherichia coli* bloodstream infections from 2006 to 2021

ORAL PRESENTATIONS

Friday, April 8
10:15–11:30 PDT SESSION C

C01
External quality assessment for community-based testing using the Xpert® Xpress SARS-CoV-2 and Xpert Xpress SARS-CoV-2/Flu/RSV in northern, remote, and isolated communities in Canada

Margot Plews[1], Dana Cabiles[1], Micah Venus[1], Linda Ares[1], Tomasz Bielawny[1], Max Abou[1], Leanne Pukalo[1], Emma R Lee[1], Adrienne FA Meyers[1,2], Paul Sandstrom[1,2]

[1]National STBBI Laboratory Division for Underserved Population Health, JC Wilt Infectious Diseases Research Centre, National Microbiology Branch, Public Health Agency of Canada, Winnipeg, Manitoba, Canada; [2]Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, Manitoba, Canada

OBJECTIVES: In response to the coronavirus virus disease 2019 (COVID-19) pandemic, northern, remote, and isolated communities across Canada received GeneXpert® (Cepheid, Sunnyvale, California) instruments to perform community-based testing (CBT) for detection of severe acute onset respiratory syndrome coronavirus 2 (SARS-CoV-2). CBT is essential for equitable access to health care, linkage to treatment, and limiting the spread of SARS-CoV-2 in these communities. To support and maintain the success of CBT for SARS-CoV-2, an external quality assessment (EQA) program for the Xpert® Xpress SARS-CoV-2 and Xpert® Xpress SARS-CoV-2/Flu/RSV assay was implemented in July 2020.

METHOD: A proficiency panel, consisting of four blinded non-infectious specimens to be handled and tested in the same manner as patient specimens, is shipped every 3 months. Results are submitted to a website for confidential group analysis. Feedback is provided in the form of individual performance reports for each community and, if necessary, corrective and preventive actions to maintain the highest quality testing.

RESULTS: Since inception in July 2020 to December 2021, there have been eight EQA sessions. The pilot session consisted of 40 GeneXpert users. The program has grown to include 188 GeneXperts from communities and laboratories in seven provinces and three territories. In the eight sessions, 2,957 samples have been tested correctly and 7 samples were reported to have a discordant result. The average rate of community proficiency across the eight sessions is 89%, with 8% no submission, 2% unable to report and 1% corrective action.

CONCLUSION: This EQA program shows that quality-testing standards for CBT are being maintained for SARS-CoV-2 diagnosis in Canada. The success of CBT requires ongoing EQA to ensure confidence in equipment, kit performance, ability of test operator, and reliability of test results. We will continue to administer the EQA program quarterly in 2022 to ensure sustainability and help build capacity for CBT across Canada.

C02
Genetic preparedness: A strategy to identify and assess the impact of target site mutations in commercial SARS-CoV-2 diagnostic tests

Carolyn Smith[1], Gregory R McCracken[2], Kalen Spinney[3], Daniel Gaston[2], Janice Pettipas[4], Glenn Patriquin[2,3], Ross J Davidson[2,3], Jason J LeBlanc[2,3]

[1]Acadia University, Wolfville, Nova Scotia, Canada; [2]Department of Pathology and Laboratory Medicine, Nova Scotia Health, Halifax, Nova Scotia, Canada; [3]Dalhousie University, Halifax, Nova Scotia, Canada; [4]Nova Scotia Provincial Public Health Laboratory Network, Halifax, Nova Scotia, Canada

OBJECTIVES: Throughout the coronavirus disease 2019 (COVID-19) pandemic, polymerase chain reaction (PCR) has been an essential tool for the detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) detection. Over time, SARS-CoV-2 genomic mutations arose, resulting in diversity between and within circulating lineages. Mutations causing PCR target mismatches could affect assay performance; therefore, monitoring for mutations and assessing their impact is crucial for accurate PCR results. However, the exact location of commercial PCR targets is proprietary. This study developed a strategy to estimate the genetic location of commercial PCRs and assess mutation impact.

METHOD: The Xpert® Xpress (Cepheid, Sunnyvale, California) SARS-CoV-2 target sites were estimated using various conventional reverse transcriptase polymerase chain reactions performed with primer pairs targeting overlapping segments of the E or N genes (ie, amplicon tiling), followed by refinements with different combinations of overlapping forward and reverse primers (ie, primer tiling) spanning the regions delineated with amplicon tiling. Each amplicon was purified by gel extraction, diluted, and subjected to Xpert testing. Next, synthetic DNAs were used to assess the impact of every single point mutation possible in the N2 target. Each DNA was concatenated to a wild-type E gene sequence (ie, calibrator),

allowing comparisons of cycle threshold value differences between this gene and wild-type or mutated N2 sequences. Results were classified as no impact, reduced sensitivity, or detection failure.

RESULTS: Amplicon and primer tiling experiments deduced that the Xpert E and N gene targets were between genomic positions 26269 and 26381 and 29164 and 29230, respectively. Of 201 possible mutants evaluated in the N2 target region, 22 resulted in target detection failure, and 59 showed reduced sensitivity.

CONCLUSION: Amplicon and primer tiling effectively deduced PCR target sites, defining the genomic region to monitor for mutations through sequence-based surveillance. Coupled with the proposed method for mutation impact assessment, these strategies ensure ongoing quality assurance for SARS-CoV-2 PCR testing using Xpert and could be adapted to any molecular test.

C03

Environmental sampling for SARS-CoV-2 virus in a tertiary hospital

Alex Oxley[1], Alon Vaisman[1], Samira Mubareka[2], Allison J McGeer[3], Kavitha Ramaraj[1], Carly Rebelo[1], Krista Marquis[1], Kimberly Gibbens[1], Tiffany Liang[1], Susy S Hota[1]

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OBJECTIVES: Understanding the mechanism of nosocomial transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has become a key focus for health facilities. The objective of this study was to explore the potential role of environmental reservoirs and surface contamination during coronavirus disease 2019 (COVID-19) outbreaks and in high viral-volume areas at an acute-care setting.

METHOD: Surface testing for SARS-CoV-2 viral RNA was conducted in three inpatient internal medicine units that recently (0–2 d) experienced outbreaks of COVID-19 or housed patients with COVID-19 in May and June 2020. Surface types were categorized as high-touch surfaces; elevated surfaces; or heating, ventilation, and air-conditioning (HVAC) components. Samples were tested using polymerase chain reaction assays. Culture for viability was performed if cycle thresholds for a sample were sufficiently low (<30 units).

RESULTS: SARS-CoV-2 viral RNA was detected (21/121; 2%) or indeterminate (5/121; 4%) in samples collected from surfaces of all three pre-determined categories, including 1/30 (3%) of high-touch surfaces, 6/39 (15%) of HVAC surfaces, and 6/39 (30%) of elevated surfaces. No SARS-CoV-2 RNA was detected in the samples collected in the air supply ductwork. None of the positive samples met the assigned criteria to proceed with culturing.

CONCLUSION: Although cycle thresholds were not suggestive of the presence of viable virus, the recovery of SARS-CoV-2 RNA on various surfaces was indicative of the potential for diffuse environmental contamination. The detection of low quantities of SARS-CoV-2 RNA on a few elevated surfaces more than 2 metres from the patient's head of bed implies the possibility of dispersion of viral RNA fragments more than 2 meters via smaller respiratory particles and aerosols from infected individuals. The low inoculum of virus from the positive samples is consistent with the existing literature and suggestive of a low risk of transmission via fomites and the lower likelihood of transmission from distantly dispersed viral particles.

C04

Comparison of auto sampling and passive sampling methods for SARS-CoV-2 detection in wastewater

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OBJECTIVES: Wastewater-based surveillance is emerging as an important tool for coronavirus disease 2019 (COVID-19) pandemic trending. Current methods of wastewater collection, such as grab and auto-composite sampling, have drawbacks that impede effective surveillance, especially from small catchments with limited accessibility. Passive samplers are promising candidates for monitoring wastewater for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). We compared SARS-CoV-2 detection in wastewater using traditional auto-sampling and passive sampling.

METHOD: The torpedo passive sampler containing both cotton swabs and electronegative filter membranes was used. Between April and June 2021, 15 passive samplers were placed at a local hospital wastewater outflow alongside an auto sampler. Quantitative reverse transcription polymerase chain reaction was used to detect the N1 and N2 genes of SARS-CoV-2 after sample processing and RNA extraction.

RESULTS: Among the 15 collected passive samples and grab or composite samples, SARS-CoV-2 was detected in 12 (80%) passive samples and 10 (67%) grab or composite samples. There was no significant difference in the cycle threshold (Ct) value for SARS-CoV-2 N1 and N2 genes between grab/composite (Ct = 26.6–30.1 for N1 and 26.7–32.2 for N2) and passive samples, as well as membrane (Ct = 29.5–36.2 for N1 and 30–35.9 for N2) and cotton swab (Ct = 29.1–35.3 for N1 and 30.4–36.4 for N2). There were discrepant results on 2 days with negative grab or composite samples and positive passive samples, which might be related to the longer duration of passive sampling in the study.

CONCLUSION: Compared with traditional grab or composite sampling methods, the passive sampler is more cost-effective and less labour intensive and has a shorter sample processing time. Requiring fewer resources makes passive sampling a good choice for long-term monitoring efforts and monitoring in resource-poor countries. Overall, our results demonstrate that passive sampling has valuable potential for monitoring COVID-19 prevalence in small catchment areas and could be used as an alternative sampling method for detection of SARS-CoV-2 in wastewater.

ORAL PRESENTATIONS

Friday, April 8
10:15–11:30 PDT SESSION D

D01
Seroprevalence, morbidity, and health care utilization costs of varicella-zoster virus infection in adults with HIV, 2000–2020

Jason Zou[1], Hartmut Krentz[2], Brenda Beckthold[2], Quang Vu[2], M John Gill[1,2]

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OBJECTIVES: Varicella-zoster virus (VZV) infection disproportionately affects people with HIV (PWH) who are at high risk for herpes zoster and its complications. However, VZV seroprevalence and its association with zoster-related clinical outcomes remain understudied in PWH in the modern era of antiretroviral therapy (ART). We assessed VZV seroprevalence, rates of VZV-related illness, and the associated health care costs in a large cohort of PWH over 20 years.

METHOD: We performed retrospective chart review of patients seen from 2000 to 2020 at a large regional HIV clinic. Serological, clinical, immunization, and costing data were extracted from in-house databases. VZV-related inpatient admissions, emergency department (ED) visits, and urgent care (UC) visits in our region were identified using relevant ICDN codes and validated when possible by two-physician chart review. Associated health care utilization costs were adjusted for inflation.

RESULTS: A total of 3,006 PWH were identified. VZV serology was available for 2,628, of whom 2,503 (95.2%) were seropositive. Only 39% of 102 seronegative patients and 1% of 2,503 seropositive patients were subsequently immunized for varicella (provided free) or shingles (insurance covered), respectively. A total of 38 hospitalizations and 138 ED or UC visits among mostly seropositive PWH (91.3%) were identified during 29,768 years of patient follow-up. Nearly a quarter of hospitalizations were due to laboratory-confirmed VZV meningitis or encephalitis. Notably, most patients (82%) with VZV-related illness were aged <50 years. After inflation adjustment, the average admission cost was $33,001 and the total cost of VZV-related illness was $1,257,691 during the study period.

CONCLUSION: VZV still causes significant morbidity and costs for PWH despite use of ART and availability of chickenpox and shingles vaccines. Herpes zoster occurs at significantly younger ages among PWH than among the general population. Increased use of the shingles vaccine through dedicated program funding may reduce VZV illness and hospitalization costs among PWH.

D02
Evaluating the optimal time for blood culture incubation: Is it time to change?

Ruchika Gupta[1], Tony Mazzulli[1]

[1]University of Toronto, Toronto, Ontario, Canada

OBJECTIVES: To assess the optimal incubation time for blood cultures based on time-to-positivity (TTP) data using the new continuous blood culture system (bioMérieux Virtuo; bioMérieux, Marcy-l'Étoile, France) and to compare the TTP across different subsets of patients, including post-transplant, immunocompromised, medical, and surgical patients.

METHOD: TTP data were retrieved from the Lab Information System. Cultures with TTP >96 hours were followed by accessing patient medical records for clinical data, reason for admission, and mortality data. An isolate was considered significant if it influenced clinical decision making (eg, antibiotic initiation or change or assessment by an infectious

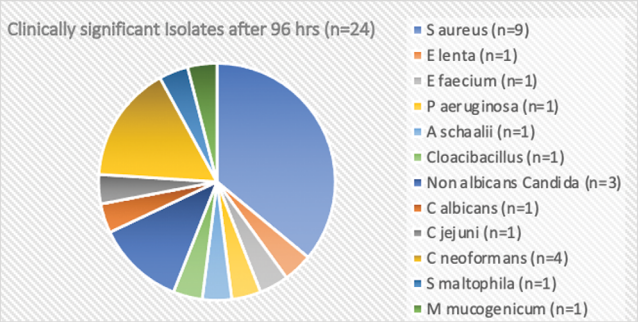

Figure D02-1: Clinically significant isolates

diseases physician). Data were segregated by transplant, medical, and surgical patients.

RESULTS: More than 100,000 blood culture samples were reviewed, with 15,296 positive cultures. Of these, 98.13% cultures were positive within the first 72 hours, and 99.37% were identified by the end of 96 hours of incubation; 91.3% (253/277) of isolates that grew after 72 hours were contaminants. Of microorganisms recovered after 96 hours, 0.156% (24/15,296) were clinically relevant. Sixteen of 24 (66.66%) clinically significant isolates—including *Staphylococcus aureus* (8 /9), *Cryptococcus neoformans* (4/4), gram-negative bacilli, and *Eggerthella lenta*—were repeat isolates in patients on treatment, and 17/24 (70.8%) were isolated in immunocompromised patients, of whom 14/17 were post-transplant patients (Figure D02-1).

CONCLUSION: Our study revealed that consideration can be given to reducing blood culture incubation times to 96 hours, although more studies and larger data sets are needed. With <0.5% clinically relevant new isolates identified after 72 hours, antibiotics can be deescalated or discontinued at 3 days with reasonable surety. Reducing incubation time would reduce laboratory costs by decreasing processing of contaminants, instrument usage, and manpower hours. More caution with immunocompromised patients is needed, especially with transplant patients. New, more efficient, continuous monitoring blood culture systems demand review of existing incubation policies to determine optimal duration.

D03

Survival of blood-borne and neonatal meningitic *Escherichia coli after* wastewater treatment: The prospect of septicaemia and meningitis becoming water borne

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OBJECTIVES: Wastewater reuse represents an emerging strategy to address growing water sustainability issues. Of concern, pathogenic strains of *Escherichia coli*, such as the uropathogenic *E. coli*, appear to differentially survive wastewater treatment, representing a potential risk associated with wastewater reuse. Whether this observation extends to other extraintestinal pathogenic *E. coli* (ExPEC) pathotypes is unclear; thus, we sought to assess the septicaemic and meningitic potential of *E. coli* strains surviving wastewater treatment.

METHOD: *E. coli* isolates were collected from wastewater samples received from treatment plants across Alberta and screened for ExPEC genetic markers using polymerase chain reaction. Presumptive wastewater ExPEC were genome sequenced and analyzed against a genomic library of clinical blood-borne *E. coli* (BBEC) and neonatal meningitic *E. coli* (NMEC) strains. Multi-locus sequence typing (MLST), pairwise genomic alignments, and virulence gene and antibiotic resistance gene screening were performed to assess the degree of genomic similarity between wastewater and clinical isolates.

RESULTS: Six hundred thirty-seven isolates were collected from chlorinated sewage and finished effluents, of which 86 represented presumptive ExPEC. MLST clustered the isolates into several pandemic, ExPEC-associated lineages, including ST131 and ST95. Pairwise alignments revealed that wastewater isolates shared between 96.04% and 99.74% whole-genome similarity with a BBEC or NMEC strain and differed from their clinical counterpart by as few as two single nucleotide polymorphisms in an approximately 417 kbp core genome backbone. Wastewater and clinical isolates also shared an extremely similar complement of antibiotic resistance genes and virulence genes.

CONCLUSION: Several *E. coli* isolates recovered from treated wastewater were virtually identical to a clinical BBEC or NMEC strain across the whole, core, and accessory genome. Collectively, this suggests that *E. coli* isolates surviving

wastewater treatment, and present in treated wastewater matrices, may possess the capacity to cause extraintestinal diseases such as septicaemia and meningitis. Our work calls for further research into the public health risks associated with wastewater reuse.

D04

Improving antimicrobial stewardship in the treatment of *Streptococcus pneumoniae* respiratory infections

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OBJECTIVES: In the clinical laboratory, *Streptococcus pneumoniae* is frequently tested against oxacillin to predict susceptibility to penicillin. In isolates with an oxacillin zone <20 mm, penicillin is tested and, if resistant, many clinicians assume that amoxicillin will also be resistant. As such, oxacillin non-susceptible, penicillin-resistant isolates may be managed with second-line agents such as macrolides or fluoroquinolones. These broader-spectrum agents potentially expose patients to more side effects and increase the risk of development of antimicrobial resistance. Oral amoxicillin could potentially be a narrower-spectrum option; however, susceptibilities are frequently not provided.

METHOD: Susceptibility testing was performed on 64 oxacillin non-susceptible *S. pneumoniae* isolated from respiratory specimens by our clinical laboratory since 2010. Amoxicillin and penicillin diffusion gradient testing and susceptibility were interpreted using published clinical standards from the Clinical Laboratory Standards Institute (CLSI).

RESULTS: Of the 64 oxacillin non-susceptible isolates, 49% ($n = 31$) were penicillin resistant using oral penicillin minimum inhibitory concentration (MIC) breakpoints. Testing against amoxicillin demonstrated that 97% ($n = 62$) were sensitive using the CLSI amoxicillin non-meningitis MIC breakpoints.

CONCLUSION: This study demonstrates that oral amoxicillin is often susceptible against oxacillin non-susceptible *S. pneumoniae* and that reporting only a penicillin result could potentially lead clinicians to prescribe broader-spectrum agents when amoxicillin, a narrower therapeutic choice, might be a more favorable option. Clinical laboratories should consider testing both penicillin and amoxicillin against oxacillin non-susceptible *S. pneumoniae* in settings in which an oral agent would be appropriate.

E-CASE REPORTS

CR01

Citrobacter freundii and non-tuberculous mycobacteria cervical lymphadenitis in an adult

Devika Singh[1], Shirley Sit[2], Narendra Singh[2,3]

[1]Michael G DeGroote School of Medicine, McMaster University, Hamilton, Ontario, Canada; [2]Humber River Hospital, Toronto, Ontario, Canada; [3]McMaster University, Hamilton, Ontario, Canada

OBJECTIVES: Currently, no cases of cervical lymphadenitis caused by *Citrobacter freundii* have been reported in the literature. In addition, *Mycobacterium avium* complex lymphadenitis, also referred to as *non-tuberculous Mycobacterium* (NTM), which includes *Mycobacterium paragordonae*, is rare and is typically found among children. Very few reported cases of NTM are reported among immunocompetent adults. Adult cervical lymphadenitis caused by *Mycobacterium* is typically a result of infection by *Mycobacterium tuberculosis*. Surgical excision is recommended and appears to be the definitive treatment. The objective of this case report is to describe a rare case of infectious cervical lymphadenitis that was positive for both *C. freundii* and NTM on core biopsy.

CASE SUMMARY: A 21-year-old woman presented to the emergency department with lymphadenitis that was subsequently positive for *C. freundii*, *M. avium*, and *M. paragordonae* on needle biopsy. Multiple ultrasounds were taken that showed a 3 cm hypoechoic lymph node in the right neck. The patient was placed on trials of five antibiotics throughout the course of this disease. Chest X-ray was normal. A computed tomography scan showed sub-mandibular swelling in addition to the enlarged lymph node. The patient was followed up for 3 months with regular clinical examinations and ultrasounds and is currently asymptomatic with no visible cervical swelling. The excisional biopsy was cancelled as a result.

DISCUSSION: When evaluating a patient with an atypical lymphadenitis with a suspected infectious cause, *C. freundii* should be considered in the etiology. In addition, NTM lymphadenitis can also occur in young, immunocompetent adults, and conservative management should be considered as one of the treatment options, despite most cases being treated surgically. This approach can be beneficial if the

patient is asymptomatic. This case report can be used to inform future cases of NTM and *C. freundii* lymphadenitis in immunocompetent adult patients.

CR02
Recurrent breast abscesses with mixed anaerobes: Zuska's disease

Amro Qaddoura, Stan Houston, Stephanie W Smith

University of Alberta, Edmonton, Alberta, Canada

OBJECTIVES: To describe an uncommon condition and highlight the importance of maintaining a broad differential diagnosis (DDx) and considering non-infectious causes of disease.

CASE SUMMARY: A female patient in her 30s was referred for evaluation of recurrent right breast abscesses over 2 years. She had multiple aspirations and antibiotic courses (including clindamycin and amoxicillin–clavulanate). All cultures grew mixed anaerobes (gram-positive and gram-negative), including *Prevotella bivia* and *Actinotignum schaalii*.

When evaluated in the infectious diseases clinic, she did not have active infection. However, she had a left-sided breast abscess 2 weeks prior (contralateral from her prior infections), which also grew mixed anaerobes and resolved with aspiration and a 7-day course of clindamycin. Her only identified risk factor was a piercing placed 20 years prior and not used for 10 years. She had no children and did not breastfeed. She reported good hygiene practices and denied contaminating the area in any way. As a result of the recurrence of abscesses, she had bilateral lumpectomy (right sided, then left sided) with biopsies that were consistent with Zuska's disease (ZD) with squamous metaplasia of lactiferous ducts (SMOLD).

DISCUSSION: ZD is due to SMOLD and presents as recurrent central or peri-areolar non-puerperal abscesses associated with lactiferous fistulas. It typically affects young to middle-aged women who are not breastfeeding. It rarely affects men. Risk factors include cigarette smoking, diabetes mellitus, and nipple piercing. Treatment involves abscess drainage and antibiotics and, if recurrent, complete excision of the affected duct may be required. It was important to be open-minded in this case because, given the unusual combination of anatomy and microbiology, self-induced contamination was initially considered in the DDx. However, maintaining this as a diagnosis of exclusion facilitated a histopathologic diagnosis and ultimately allowed the patient to have definitive treatment with resection of the draining sinuses and duct excision.

CR03
Mycobacterium mucogenicum bloodstream infection due to central venous catheter infection

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OBJECTIVES: To outline the challenges associated with treatment of *Mycobacterium mucogenicum* bloodstream infection in a patient with short gut syndrome (SGS).

CASE SUMMARY: A male patient in his 40s had chills and night sweats for 2 weeks after a camping trip. He had a central venous catheter (CVC) for nutrition as a result of SGS from

Table CR03-1: Blood culture site, type, and time to positivity for *Mycobacterium mucogenicum*

Timing	Type/Location	Days Positive
Day -6	BCx / unknown	6 days
Day 0 (admission)	mBCx / central line	2 days
Day 0	mBCx / Peripheral (2)	3 and 5 days
Day 0	BCx / central line	2 days:10 hours
Day 0	BCx / Peripheral (2)	No growth
Day +2	BCx & mBCx, periph	No growth
Day +3	Central line tip culture	MSSA*, Yeast*, Coryneforms**

BCx – blood culture; mBCx: mycobacterial blood culture; MSSA – methicillin-susceptible *Staphylococcus aureus*. Positive refers to *Mycobacterium mucogenicum* unless otherwise specified.
* $>10^{15}$ colony forming units; ** $<10^{15}$ colony forming units.

Mycobacterium mucogenicum/phocaicum group

Description	Value
Microbiology Comment [Note:]	* (MIC (mg/L))
	Results obtained using microbroth dilution.
Amikacin	Susceptible
Cefoxitin	Susceptible
Ciprofloxacin	Susceptible
	For non-tuberculosis Mycobacterium species (NTM), Ciprofloxacin is the class representative for fluoroquinolones.
Clarithromycin	Susceptible
Doxycycline	Susceptible
Imipenem	Susceptible
Linezolid	Susceptible
Meropenem	Susceptible
Moxifloxacin	Susceptible
Tigecycline	0.12 (MIC (mg/L))
Trimethoprim+Sulfamethoxazole	Susceptible

MIC – minimal inhibitory concentration.

Figure CR03-1: Susceptibility profile for the *Mycobacterium mucogenicum isolate*

multiple operations for inflammatory bowel disease. He had blood cultures collected in the emergency department, was assessed to not require admission, and discharged home. He was advised to return 6 days later because blood cultures grew *M. mucogenicum*. Repeat blood cultures are shown in Figure CR03-1. Amikacin, cefoxitin, and ciprofloxacin were initiated empirically; these had to be given parenterally because of SGS. Blood cultures on day 2 of admission did not demonstrate growth, and the CVC was removed on day 3. As shown in the figure**,** the CVC tip grew several organisms that were not targeted therapeutically given the patient's clinical stability and lack of growth on other cultures. A new CVC was placed on day 11. He was discharged with a planned treatment duration of 4 weeks. In follow-up toward the end of therapy, he had a recurrence of symptoms similar to his initial presentation. Several investigations were ordered, including blood cultures. He subsequently developed full-body erythematous macules, and blood cultures were negative. His antimicrobials were stopped with resolution of symptoms and clinical stability on follow-up.

DISCUSSION: *M. mucogenicum* is a rapid-growing nontuberculous mycobacterium. Bloodstream infections are associated with indwelling CVCs. Typical treatment includes three antimicrobials, with definitive therapy guided by drug susceptibility results. This case had several challenges: an inability to use oral antimicrobials, growth of different organisms on catheter tip culture, and recurrence of similar index symptoms toward the end of therapy that were ultimately due to antimicrobial adverse effect as opposed to recurrent infection.

CR04

Pediatric case of extensively drug-resistant *Salmonella* Typhi infection in a patient returning from Pakistan

Amro Qaddoura, Joan L Robinson

University of Alberta, Edmonton, Alberta, Canada

OBJECTIVES: To describe a pediatric case of extensively drug-resistant *Salmonella enterica* serovar Typhi (XDR-Typhi) and its implications for empiric antimicrobial therapy.

CASE SUMMARY: An 8-year-old girl had two febrile illnesses while in Pakistan and was treated with unknown oral antibiotics. Her fever recurred 10 days later when back in Canada. She had abdominal pain and emesis but no diarrhea. She was seen in an emergency department (ED) and discharged with no specific therapy but was called back when blood culture (BCx) grew gram-negative bacilli. Meropenem was started empirically with clinical improvement within 24 hours. When the BCx was speciated as *Salmonella* (ultimately Typhi) on the second day of admission, she was transitioned to ceftriaxone. The following day, drug susceptibility testing (DST) demonstrated resistance to ampicillin, ceftriaxone (due to an extended-spectrum beta-lactamase), ciprofloxacin, and trimethoprim–sulfamethoxazole and susceptibility to azithromycin, ertapenem, and meropenem. Despite 24 hours of ceftriaxone, she was clinically well and afebrile. Repeat BCx were negative. Therefore, we advised discharge with a 7-day course of azithromycin.

DISCUSSION: A large outbreak of XDR-Typhi was identified in Pakistan in 2016. The US Centers for Disease Control and Prevention has since identified XDR-Typhi in US residents without international travel and a separate strain of ceftriaxone-resistant Typhi from Iraq. It is difficult to know whether the risk is now sufficiently high that all patients with suspected typhoid with travel to Pakistan or Iraq should be treated for XDR-Typhi pending DST. If one chooses to do so, the options are a carbapenem or azithromycin because almost all XDR-Typhi remain susceptible to both. Ceftriaxone remains the optimal empiric choice for patients with travel to all other countries. However, this may change at any time as the plasmid-mediated transmission of XDR-Typhi resistance is especially concerning.

CR05

Detection of anti–SARS-CoV-2 IgG antibodies in the breast milk of a COVID-19 patient post-bamlanivimab infusion: A case report

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[1]University of British Columbia, Vancouver, British Columbia, Canada; [2]Surrey Memorial Hospital Clinical Research Unit, Surrey, British Columbia, Canada; [3]Fraser Health, Surrey, British Columbia, Canada; [4]CIHR Canadian HIV Trials Network, Vancouver, British Columbia, Canada; [5]Centre for Health Evaluation & Outcomes Sciences, Vancouver, British Columbia, Canada; [6]British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada

OBJECTIVES: The coronavirus disease 2019 (COVID-19) pandemic presents challenges for newborn care, with no vaccines currently approved for infants. Monoclonal antibodies (mAb) targeting severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike protein, such as bamlanivimab, may mitigate detrimental impacts of COVID-19; however, little is known about transfer of maternal antibodies through breastmilk. We evaluated whether administration of bamlanivimab early

postpartum leads to antibody transfer into breastmilk and whether they persist over time.

CASE SUMMARY: A 36-year-old woman, early postpartum and unvaccinated for SARS-CoV-2, presented with moderate cough, shortness of breath, mild loss of appetite, severe loss of taste and smell, and fatigue since May 3, 2021. She tested polymerase chain reaction–positive for SARS-CoV-2 on May 5, 2021, when her infant was 1 week old. Bamlanivimab was administered intravenously on May 7, 2021. Daily breastmilk samples were collected immediately pre-mAb infusion (baseline) and for the first 14 days, then weekly until 102 days post-infusion. Mother and infant sera were also collected at 102 days post-infusion. Anti-SARS-CoV-2 spike, nucleocapsid, and receptor binding domain (RBD) immunoglobulin G (IgG) in breastmilk and sera were quantified using a multiplex immunoassay. Anti-spike and anti-RBD IgG first peaked within 3 days post-infusion and rapidly declined, showing evidence of mAb transfer into breastmilk. Anti-nucleocapsid IgG increased slowly and peaked at 29 days post-infusion, coinciding with a second peak in anti-spike and anti-RBD IgG, suggesting a natural immune response. At 102 days post-infusion, all three antibodies remained present in breastmilk, and the infant was also found seropositive for all SARS-CoV-2 targets; however, the infant was never symptomatic or tested for SARS-CoV-2 infection; thus, infant infection status is unknown.

DISCUSSION: We demonstrate strong evidence of mAb transfer into breastmilk. It is unclear whether antibodies detected in infant serum were acquired through breastfeeding or development of a natural immune response secondary to horizontal transmission of SARS-CoV-2. Our case raises the importance of including pregnant and lactating women in clinical and vaccine research to inform potential therapeutic benefits for both women and their infants.

CR06

Successful treatment of suspected early form of chronic Chagas cardiomyopathy

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OBJECTIVES: Chagas disease, caused by the protozoan *Trypanosoma cruzi*, is the most common parasitic etiology of non-ischemic cardiomyopathy in the Americas, resulting in heart failure, arrhythmias, and death. The American Heart Association suggests possibly treating early chronic Chagas cardiomyopathy. We describe a patient with probable Chagas disease and early cardiomyopathy who demonstrated significant sustained improvement in cardiac function as a result of timely benznidazole therapy.

CASE SUMMARY: A 75-year-old expatriate woman from El Salvador presented to our Canadian tertiary centre with dyspnea in the context of heart failure and atrial fibrillation and flutter. Her past medical history was notable for hypertension, diabetes, and chronic kidney disease. Tranesophageal echocardiogram revealed dilated cardiomyopathy with left ventricular ejection fraction (LVEF) 15%–20%. She underwent direct-current cardioversion to restore sinus rhythm with clinical improvement and was discharged. Work-up for non-ischemic cardiomyopathy was positive for *T. cruzi* IgG antibody serology by enzyme-linked immunosorbent assay IgG. She re-presented 3 weeks later with a similar presentation and LVEF 25%–30%, complicated by ventricular tachycardia requiring cardiac device implantation. After discussion between Infectious Diseases and Cardiology, her overall presentation was in keeping with early Chagas cardiomyopathy. Although a second *T. cruzi* confirmatory test was delayed as a result of the coronavirus disease 2019 pandemic, the constellation of clinical findings and initial positive serology strongly indicated this diagnosis. She completed 60 days of benznidazole with marked symptomatic improvement. Subsequent LVEF was 45%–50%, which was sustained on 12-month follow-up.

DISCUSSION: This case highlights the importance of multidisciplinary collaboration in the diagnosis of early Chagas cardiomyopathy and timely treatment with benznidazole, as there is no response in late disease due to myocardial cell death program. While the BENEFIT study did not demonstrate mortality reduction, we advocate that the significant reduction in cardiovascular-related hospitalizations should be considered for symptomatic patients. Our patient avoided cardiac transplantation through opportune timing of benznidazole, in comparison to cardiac medication and device therapy alone.

CR07

Ticked off: False-positive cerebrospinal fluid West Nile virus serology in a patient with Lyme neuroborreliosis

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OBJECTIVES: We present a case of bilateral facial nerve palsy secondary to Lyme disease with associated false-positive West Nile virus (WNV) serology. We discuss the infectious differential diagnosis and highlight options for confirmatory testing with suspected false-positive WNV results.

CASE SUMMARY: A 70-year-old man presented to hospital with bilateral cranial nerve (CN) VII palsy. MRI of the brain demonstrated abnormal enhancement of bilateral CNs III, V, and VII. Cerebrospinal fluid (CSF) analysis demonstrated lymphocytic pleocytosis (white blood cell [WBC] 291 × 10E6/L), with elevated protein of 1,618 mg/L. CSF bacterial and fungal cultures and polymerase chain reaction (PCR) for herpes viruses were negative. CSF WNV immunoglobulin (Ig) M antibody was positive. Serum WNV IgG and IgM, CSF WNV PCR, and plaque reduction neutralization testing (PRNT) were negative. Serum Lyme IgM enzyme immunoassay (EIA) and Western Blot were reactive, and IgG was non-reactive. The patient was treated with 2 g of intravenous ceftriaxone every 12 hours for 14 days for probable Lyme neuroborreliosis, with complete symptom resolution. On convalescent serology, Lyme IgM and IgG EIA and Western Blot were reactive. Convalescent serum WNV IgG and IgM remained non-reactive.

DISCUSSION: This case highlights the differential diagnosis of bilateral facial nerve palsy and the further diagnostic possibilities with suspected false positive flavivirus serology. Cranial neuropathies are uncommon with WNV infection: fewer than 1% of individuals with WNV infection will develop neuroinvasive disease; of those, only 20% will have cranial neuropathy. The main infectious etiologies causing bilateral facial nerve palsy are tuberculosis and Lyme disease. Although this patient's acute and convalescent serology confirmed Lyme neuroborreliosis, his CSF WNV IgM was positive. Given the clinical incompatibility and alternative diagnosis, this was considered a false-positive result. In cases of diagnostic uncertainty for WNV encephalitis, concomitant serum serology (acute and convalescent), CSF PCR, and PRNT can provide diagnostic clarification. To our knowledge, this is the first reported case of false-positive WNV serology due to Lyme disease.

CR08

Gordonia sputi–associated bloodstream infection in a renal transplant patient with a chronic indwelling central venous catheter: A case report and literature review

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OBJECTIVES: *Gordonia* species are ubiquitous gram-positive bacilli under the Actinomycetales order. We describe a case of *Gordonia sputi* bacteremia in a renal transplant patient with an indwelling intravenous catheter. Current strategies and challenges for initial identification and workup of aerobic actinomycetes, including *Gordonia* species, are discussed.

CASE SUMMARY: A 62-year-old renal transplant patient on tacrolimus and mycophenolate was admitted to hospital with a 2-month history of dry cough and fevers after weekly electrolyte infusions via Groshong line. Blood cultures on three occasions over a 2-week period grew gram-positive bacillus, each in one (aerobic) of two bottles. matrix assisted laser desorption ionization time of flight VITEK MS V3 (bioMérieux, Marcy-l'Étoile, France) was unable to identify the organism, whereas the API Coryne system (bioMérieux) gave an identification of *Rhodococcus* species. Empiric vancomycin was started. Transthoracic and transesophageal echocardiograms were negative for endocarditis, but chest computed tomography (CT) showed multifocal lung opacities. The Groshong line was removed, and the line tip grew the same organism. Blood cultures on antibiotic day 5 (1 day after line removal) were negative. Isolate was sent to reference lab for 16S-rRNA sequencing and subsequently identified as *Gordonia sputi;* oral ciprofloxacin was added. After 6 weeks of dual antibiotic therapy, repeat chest CT showed marked improvement of pulmonary opacities, and treatment was stopped. The patient remains symptom free 3 months after completion of therapy.

DISCUSSION: This case illustrates the challenges surrounding the workup for *Gordonia* species, including misidentification by API Coryne and lack of identification by VITEK MS. 16S-rRNA sequencing may be the preferred identification method in this scenario, as shown by previous literature on peritoneal dialysis–related peritonitis due to *Gordonia*. A formal literature review on *Gordonia* will be performed, because developing a strategy for earlier identification of Actinomycetes, including *Gordonia*, is necessary to facilitate directive antimicrobial therapy.

CR09

Disseminated tuberculous lymphadenopathy in an immunocompetent teenager: A rare presentation of *Mycobacterium tuberculosis*

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OBJECTIVES: *Mycobacterium tuberculosis* (TB) remains prevalent in persons who are Indigenous, born in TB-endemic countries, or have close contact with persons born in TB-endemic countries. The most common sites of non-respiratory TB disease in Canada are unilateral cervical lymph node, intra-abdominal, and bone and joint. We describe a case of an immunocompetent teenager with disseminated TB lymphadenopathy and highlight the importance of investigating both infectious and non-infectious causes with this presentation.

CASE SUMMARY: A 15-year-old girl was transferred from a remote First Nations community with complaints of abdominal pain and swelling above her clavicle. Review of systems was notable for 1 week of nausea, emesis, and fatigue with long-standing night sweats, decreased appetite, and poor weight gain. She had two previous exposures to family members with respiratory tuberculosis at ages 7 and 9 years. She completed directly observed INH preventive therapy after the second exposure. Computed tomography (CT) scans showed enlarged and necrotic lymph nodes in the mediastinum, perihilar regions, supraclavicular and infraclavicular regions, and mesentery, retroperitoneum, and iliac chains (Figure CR09-1). Excisional biopsy of a left cervical chain lymph node showed caseating granulomatous lymphadenitis and acid-fast bacilli on microscopy. Tissue culture grew pan-sensitive *M. tuberculosis*. She was prescribed first-line therapy and has shown good clinical response to date.

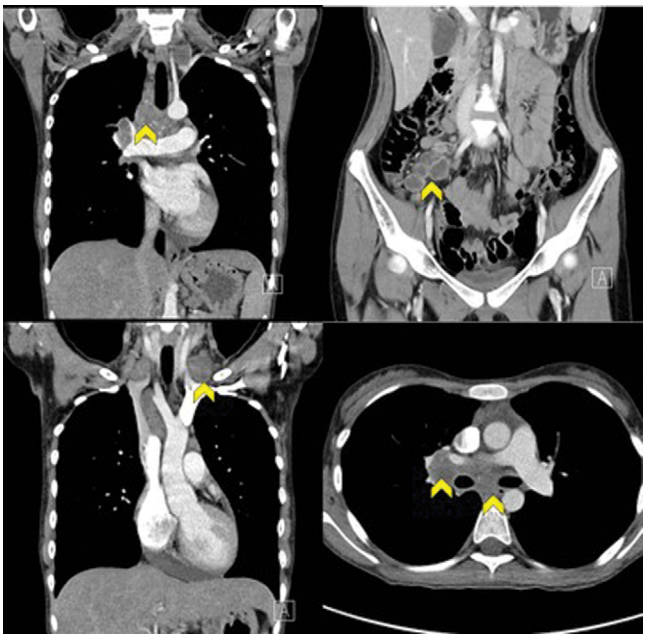

Figure CR09-1: Computed tomography scan with coronal and transverse views showing multiple enlarged and necrotic lymph nodes

DISCUSSION: Disseminated lymphadenopathy can be caused by lymphoproliferative disease, metastasis, and sarcoidosis in addition to generalized infections. Regional lymph nodes are the most common site of TB disease after the lungs. Disseminated mycobacterial lymphadenopathy is rare in immunocompetent patents and is more commonly described in patients with HIV. This case demonstrates that TB remains a diagnostic consideration in populations with epidemiologic risk and also highlights the classic radiographic and histologic findings of lymph node tuberculosis.

CR10

Clostridium septicum endocarditis associated with colonic malignancy: Case report and literature review

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OBJECTIVES: Anaerobic bacteria account for 2%–16% of infective endocarditis, of which a quarter is due to *Clostridium* spp We review the literature of metastatic *Clostridium septicum* infections and describe a case of *C. septicum* causing native valve endocarditis associated with colonic malignancy.

CASE SUMMARY: A 64-year-old man with underlying coronary artery disease underwent a planned hemicolectomy for local adenocarcinoma of the sigmoid colon. He was re-admitted post-operative day 1 for myocardial infarction and congestive heart failure exacerbation requiring supplemental oxygen. He had leukocytosis and maximal temperature of 38.1°C; however, other constitutional symptoms were confounded by the underlying malignancy and transfusion-requiring anemia. A trans-esophageal echocardiogram showed two vegetations on the mitral valve measuring 13 × 15 mm and 6 × 10 mm. Peri-operative blood cultures were negative; however, subsequent blood cultures on post-operative day 8 grew

C. septicum in three sets for 3 days before achieving sterility on intravenous penicillin and clindamycin. The *C. septicum* isolate was susceptible to penicillin and metronidazole, but it was resistant to clindamycin, thus prompting a subsequent change to intravenous metronidazole. He developed multiple acute cerebral infarcts suggestive of cardioembolic events. A cardiac surgery assessment recommended medical management only with 6 weeks of intravenous (IV) penicillin.

DISCUSSION: *C. septicum* is associated with colonic malignancy and can cause non-traumatic gas gangrene; however, it rarely causes metastatic infection, including endocarditis, septic arthritis, endophthalmitis, and intra-abdominal abscesses. Colonic malignancy is present in nearly all cases associated with major embolic phenomena. Despite treatment with IV penicillin alone or in combination with metronidazole, mortality rates remain high, with estimates at 20%–40%. Data are limited by small numbers, historical reporting, and outcomes confounded by underlying comorbidities, including malignancy. Given the heterogeneity of anaerobic bacteria in the *Clostridium* genus, risk factors differ depending on the species and include colonic malignancy, history of trauma, injection drug use, and post-abortion complications.

CR11

Disseminated visceral Kaposi sarcoma without cutaneous involvement presenting as gastrointestinal bleeding in a patient with HIV/AIDS

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OBJECTIVES: AIDS-related Kaposi sarcoma (KS) is the most common cancer seen in HIV-infected individuals. Affecting predominantly men, cutaneous manifestations are the most common initial presentation. We present a case of disseminated visceral KS without cutaneous involvement in an AIDS patient presenting with gastrointestinal (GI) bleeding.

CASE SUMMARY: A 30-year-old woman presented with a 3-month history of abdominal pain, nausea, vomiting, diarrhea, weight loss, and melena. She denied any fevers or night sweats. She was diagnosed with HIV 10 years prior but was lost to follow-up. Her hemoglobin was 69 g/L (previously normal), and her CD4 count was 75 and HIV viral load was 67,880 IU/mL. Chest CT revealed

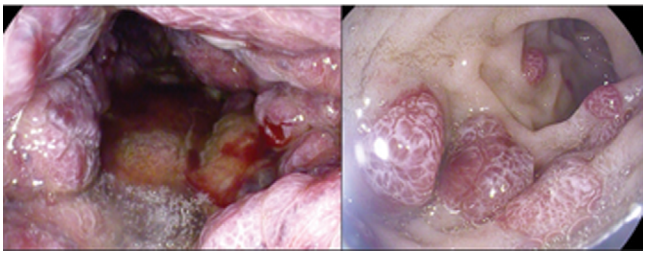

Figure CR11-1: Upper endoscopy showing erythematous vascular polypoid like lesions throughout the stomach (left) and duodenum (right)

bilateral interlobular septal thickening with randomly distributed pulmonary nodules. Abdominal CT revealed ascites, lymphadenopathy and small bowel intussusception. Bronchoscopy with endobronchial biopsy of the lymphadenopathy and nodules followed. Multiple microbiological samples were sent for culture and nucleic acid amplification, and all were negative. She was started on intravenous pantoprazole, and upper endoscopy revealed multiple polypoid vascular lesions in the gastric body and duodenum with biopsies taken. Excisional biopsy of her inguinal lymph node was performed.

All tissue specimens revealed highly vascular malignant spindle cell tumour staining CD31, ERG, and D2-40 positive, suggestive of KS. The patient had detectable HHV-8 DNA in serum. Physical exam did not reveal cutaneous involvement.

DISCUSSION: Disseminated visceral KS without cutaneous involvement is a rare presentation of AIDS-related KS seen in <1% of cases. Gastrointestinal KS is seen in approximately 40% of individuals with AIDS and is under-diagnosed because it is largely asymptomatic. When symptoms are present, they are non-specific and include abdominal pain, weight loss, vomiting, GI bleeding, intestinal obstruction, and diarrhea. The lymphadenopathy and bilateral pulmonary infiltrates in our patient posed a wide range of possibilities, which included common and opportunistic infections. This underscores the importance of obtaining tissue in the treatment of AIDS-related conditions and maintaining a comprehensive differential.

CR12

Infection with an unclassified member of Burkholderiaceae in a patient with CGD leading to HLH and death: A case report

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OBJECTIVES: Chronic granulomatous disease (CGD) is a primary immunodeficiency caused by mutations in one of the five subunits of nicotinamide adenine dinucleotide phosphate

(NADPH) oxidase wherein affected patients are susceptible to recurrent infections caused by specific bacteria and fungi. Members of the Burkholderiaceae family are known causes of potentially fatal infection in individuals with CGD. We describe a patient with CGD infected with an unclassified member of Burkholderiaceae that resulted in hemophagocytic lymphohistiocytosis (HLH) and death.

CASE SUMMARY: A 26-year-old man with CGD presented to an urgent care facility with fever, cough, and congestion of 1 week onset. Rapid coronavirus disease 2019 (COVID-19) testing was negative, and he was discharged home. The next day he went to an emergency room confused, febrile, tachycardic, jaundiced, and hypotensive. Liver function tests were elevated, and influenza and COVID-19 tests were negative. He required pressors, was started on broad-spectrum antibiotics, and was transferred to a tertiary care facility's intensive care unit. Blood culture subsequently identified a coagulase-negative *Staphylococcus.* Upon transfer, he had neutropenia, thrombocytopenia, transaminitis, and persistent hypotension. Twenty-four hours after transfer, he went into pulseless electrical activity with return of spontaneous circulation after multiple rounds of cardiopulmonary resuscitation in the setting of clinical HLH. High-dose steroids, meropenem, and levofloxacin treatment was attempted; however, the next day the patient declined further, requiring hemodialysis and additional pressors, until ultimately suffering disseminated intravascular coagulation and death. The patient was transferred to the National Institutes of Health for autopsy. Culture from both lung and liver specimens grew bacterial isolates that were identified as unclassified Burkholderiaceae; 16S rRNA gene sequencing revealed the isolates likely represent a novel organism.

DISCUSSION: This case presents an opportunity to discuss infections with members of Burkholderiaceae in patients with CGD and the associated risks of HLH. To our knowledge, this case also represents the first known instance of infection with this unclassified member of Burkholderiaceae.

CR13

Two times lucky: Fungal keratitis picked up on *Acanthamoeba* culture

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OBJECTIVES: Fungal keratitis (FK) is a severe sight-threatening condition associated with poor clinical outcomes. Diagnosis and treatment are often delayed by lack of clinical suspicion of a fungal infection, non-specific clinical presentation, and suboptimal sensitivity of microbiological methods. We describe two cases of FK diagnosed on the basis of growth of fungi on *Acanthamoeba* culture plates, despite negative or absent initial dedicated fungal work-up.

CASE SUMMARY: In case 1, corneal scrapings from a 58-year-old woman were sent to the regional hospital laboratory for Gram stain and bacterial culture, to the provincial reference laboratory for viral polymerase chain reactions (PCRs; herpes simplex virus, vesicular stomatitis virus, and adenovirus), and inoculated at bedside for fungal culture (on Sabouraud agar) and *Acanthamoeba* culture (on *Escherichia coli* seeded non-nutrient agar). Viral PCRs and bacterial and fungal cultures were negative. Fungal elements were detected along the inoculation line on the *Acanthamoeba* culture plate on day 5 post-inoculation. Direct internal transcribed spacer (ITS) sequencing of the sample collected for viral studies identified *Fusarium oxysporum*. Agar excised from the *Acanthamoeba* culture plate also grew *F. oxysporum* in culture. A repeat corneal scraping collected 2 months after the initial diagnosis remained culture positive for *F. oxysporum*. In case 2, contact lens and corneal scrapings from a 45-year-old man were sent to the provincial reference laboratory for viral PCRs and *Acanthamoeba* culture. Viral PCRs were negative. Fungal elements were seen on day 4 along the inoculation lines of the *Acanthamoeba* culture plates inoculated with the contact lens and corneal scrapings. Direct ITS sequencing was negative on the sample collected for viral studies, but agar excised from the *Acanthamoeba* culture plates grew *Purpureocillium lilacinum* in culture.

DISCUSSION: FK remains challenging to diagnose, and meticulous examination of all corneal scraping cultures is required for microbiological result interpretation. These cases highlight the ongoing need for improved diagnostics for FK due to challenges with specimen scarcity, need for invasive sampling, and variable organism burden.

CR14

Two unusual presentations of human protothecosis in Canada: A case series

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OBJECTIVES: *Prototheca* are achlorophyllous algae that have been implicated in rare opportunistic human infections, including cutaneous disease, olecranon bursitis, and disseminated disease. Diagnosis of protothecosis can be challenging in the lab given its rarity and its similarity to yeast in both its microscopic and culture appearance. In this case series, we describe two cases of human protothecosis in immunocompetent patients, one with an olecranon bursitis accompanied by a hardware infection, and one with persistent respiratory colonization over 7 years.

CASE SUMMARY: In case 1, a 59-year-old man, with a history of K-wire fixation of the right elbow, was seen in the emergency department with right elbow pain and swelling. Bursa aspiration revealed growth of yeast-like colonies. Gram stain of these colonies revealed round yeast-like structures that were identified presumptively as *Prototheca wickerhamii* on the basis of wet mount appearance. He underwent surgical debridement and K-wire removal 17 days later, with cultures growing *P. wickerhamii* and *Staphylococcus aureus*. He received 6 weeks of itraconazole and doxycycline without evidence of relapse. In case 2, a 65-year-old woman, with a history of bronchiectasis secondary to childhood tuberculosis, underwent a bronchoscopy for worsening respiratory symptoms. Cultures from bronchoscopy yielded growth of yeast-like colonies that were presumptively identified as *Prototheca* species on wet mount. She received a trial of itraconazole, followed by voriconazole, but was unable to tolerate a prolonged treatment course. She eventually completed 4 months of doxycycline. Repeat bronchoscopy 7 years later grew *P. wickerhamii* and *Mycobacterium avium*.

DISCUSSION: These two cases present an opportunity to review the diagnosis of *Prototheca* in the laboratory. To our knowledge, these cases represent the second and third cases of human protothecosis in Canada. These cases also add to the evolving literature of human protothecosis, including its ability to cause hardware infections and colonize the lungs in immunocompetent patients.

CR15

Ureaplasma septic oligoarthritis and osteomyelitis in a pediatric patient after second renal transplant with hypogammaglobinemia secondary to rituximab therapy for Epstein–Barr virus viremia

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OBJECTIVES: The lower genital tract of sexually active women frequently harbors *Ureaplasma* species, which can be transmitted perinatally, leading to neonatal pneumonia. Immunocompromised children are at risk of developing *Ureaplasma* infections. Hypogammaglobulinemia is an important predisposing factor in cases of septic arthritis, and it has occurred in adults with history of renal transplant. We report a case of *Ureaplasma* septic oligoarthritis and osteomyelitis in a pediatric patient after second renal transplant and hypogammaglobulinemia secondary to rituximab therapy for Epstein-Barr virus (EBV) viremia.

CASE SUMMARY: A 16-year-old girl with a history of end-stage renal disease, a past failed renal transplant, and hypogammaglobulinemia secondary to rituximab therapy for EBV viremia presented with a 3-week history of left third metacarpophalangeal joint and left first metatarsophalangeal joint pain associated with swelling, erythema, and tenderness. She had a C-reactive protein level of 52 mg/L, white blood cell count of 8×10^9/L, and immunoglobulin level of immunoglobulin G 3.30 g/L (6.80–15.31). MRI showed findings consistent with osteomyelitis of the left first distal metatarsal bone. Joint fluid aspiration was performed along with multiple synovial biopsies and was sent for *Mycoplasma* and *Ureaplasma* polymerase chain reaction (PCR). *Ureaplasma* species PCR was positive on two synovial tissue samples from both affected joints. Treatment with oral moxifloxacin was begun, and her dosage of intravenous immunoglobulin adjusted given her low immunoglobulin level.

DISCUSSION: Anti-CD20 monoclonal antibodies are increasingly used in a wide range of indications. They are known to cause hypogammaglobulinemia. With the improvements in molecular diagnostic tests, physicians should consider

Mycoplasma and *Ureaplasma* septic arthritis in the differential diagnosis of arthritis with an indolent course and negative standard cultures in patients with hypogammaglobinemia. To our knowledge, this is the first case report of *Ureaplasma* septic oligoarthritis and osteomyelitis in a pediatric patient with second renal transplant and secondary hypogammaglobinemia.

CR16

Polyarthritis and disseminated skin lesions in a patient receiving eculizumab for treatment of atypical hemolytic uremic syndrome

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OBJECTIVES: Eculizumab is a monoclonal antibody targeting complement C5, and it is used for treatment of patients with atypical hemolytic uremic syndrome (aHUS). Patients receiving eculizumab are at increased risk for disseminated neisserial infections. We describe the diagnosis and management of a patient receiving eculizumab for aHUS presenting with a syndrome of polyarthritis and rash.

CASE SUMMARY: A 26-year-old woman presented with a 3-day history of malaise, myalgias, and polyarthritis. Past medical history was significant for treated hypertension and aHUS stabilized on eculizumab. She did not report being sexually active. Examination revealed acute arthritis of multiple large joints and bilateral flexor tenosynovitis of the wrists. There were widespread 5–10 mm pustular and non-blanchable, purpuric skin lesions. Blood cultures were negative; however, urine nucleic acid amplification testing and right knee synovial fluid culture both detected *Neisseria gonorrhoeae*, confirming a diagnosis of disseminated gonococcal infection (DGI). When subsequently approached in her mother's absence, she disclosed recent unprotected intercourse with a male partner. She was treated with 1g ceftriaxone intravenously for 7 days, and one dose of oral azithromycin was administered. Given the slow resolution of her joint swelling and limited mobility, adjuvant prednisone therapy was administered, resulting in rapid resolution of her symptoms.

DISCUSSION: This case provides several key learning points: (1) the need to consider both host susceptibility and epidemiological risk factors in the differential diagnosis and investigation of patients presenting with undifferentiated rash and polyarthritis; (2) appreciation that joint and skin disease in DGI is in part immunologically mediated and, therefore, administration of adjuvant anti-inflammatory therapy can assist in its resolution in patients receiving targeted antimicrobial therapy; (3) recognition of the importance of inquiring about sexual practices in a private, safe, and non-judgmental environment; and (4) identification of a gap in prevention, as the patient had not previously been immunized against meningococcal disease.

CR17

Suspicious gram-negative coccobacilli—laboratory exposure from an immunocompromised patient specimen co-infected with blastomycosis and suspected *Francisella tularensis:* A case report

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OBJECTIVES: *Francisella tularensis*, a gram-negative coccobacilli, is the causative agent of tularemia and a tier 1 select agent of the Centers for Disease Control and Prevention (CDC) Federal Select Agent Program. Appropriate laboratory practice, personal protective equipment, and testing algorithms are essential in minimizing laboratory-acquired infections. Here, we describe a case of a patient specimen presumptively identified as *F. tularensis* that included multiple laboratory personnel exposure, and we further discuss the significant biosafety issues that would have occurred as a result.

CASE SUMMARY: A 63-year-old man with a history of diabetes mellitus, temporal arteritis, inflammatory polymyopathy, and blastomycosis was admitted with acute pancreatitis. Serology confirmed active infection with blastomycosis, and multiple aerobic culture bottles grew unidentifiable tiny gram-negative rods. Subsequent culture bottles revealed presumptive *F. tularensis*, but only after multiple laboratory personnel exposures from benchtop testing. Reference testing was performed by the Indiana State lab, identifying the specimen as *F. tularensis* non-subsp. *tularensis*. Infection prevention and control was consulted, and affected individuals were given prophylactic doxycycline and monitored for 14 days. The patient was successfully treated with itraconazole for blastomycosis and gentamicin, followed by doxycycline for *Francisella* septicemia. Reflex testing performed by the CDC would later rule out *F. tularensis*.

DISCUSSION: This potential encounter with a high-risk pathogen presents the opportunity to review standard laboratory practice and to educate staff on rule-out algorithms for *F. tularensis*. Initial struggles with morphology and biochemical test result interpretation, combined with the use

of standard laboratory benchtop methods, created potential occupational hazardous incidents for lab personnel. Because of the highly infectious nature of *F. tularensis* (infectious dose ≤10 organisms), handling of suspected tularemia specimens should occur in biosafety level 3. In addition, the use of automated identification systems, such as matrix-assisted laser desorption/ionization time of flight mass spectrometry, may often misidentify due to the lack of available spectra within commercial or different RUO databases.

CR18

Prolonged shedding of severe acute respiratory syndrome coronavirus 2 with viral clearance post-vaccination in an asymptomatic renal transplant patient: A case report

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OBJECTIVES: Persistent viral shedding post-infection due to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) can occur in immunocompromised individuals. The clinical significance and potential infectivity of prolonged asymptomatic shedding after coronavirus disease 2019 (COVID-19) remain unclear. We describe a renal transplant patient with persistently positive SARS-CoV-2 detection by reverse transcription polymerase chain reaction (RT-PCR), with viral clearance after messenger RNA (mRNA) vaccination.

CASE SUMMARY: A 48-year-old renal transplant patient on tacrolimus, mycophenolate sodium, and prednisone tested positive for SARS-CoV-2 by nasopharyngeal swab (NPS) in April 2021. Lab-developed PCR assay confirmed variant of concern B.1.1.7 Pango lineage (N501Y S-gene mutation detected; E484K S-gene mutation undetected). The patient was unvaccinated against COVID-19 and asymptomatic at the time of positive NPS. Cycle threshold (Ct) values for E-gene and 5'-UTR were 11.86 and 13.81, respectively.

Three weeks later, he was hospitalized for hypoxemic respiratory failure with bilateral ground-glass opacities on chest radiograph. Repeat NPS was positive for SARS-CoV-2 (Ct values unchanged). Remaining septic workup including blood cultures was negative. He received tocilizumab (C-reactive protein 81.1 mg/L), remdesivir, and dexamethasone for COVID-19 pneumonia with clinical recovery. Despite remaining asymptomatic 3 months post-recovery, his repeat NPS tested positive (Ct values E-gene 21.74, 5'-UTR 22.61); reference lab testing confirmed B.1.1.7 lineage by whole-genome sequencing using Illumina COVIDSeq Test (Illumina, San Diego, California). At the time, nearly all sequenced variants in the province were B.1.617.2. One month after receiving two doses of mRNA vaccine (BNT162b2), his repeat NPS successfully converted negative for SARS-CoV-2.

DISCUSSION: To our knowledge, this represents the first case of use of an mRNA vaccine to facilitate clearance of prolonged asymptomatic shedding of SARS-CoV-2. Understanding the SARS-CoV-2 virological and antibody response in transplant recipients (literature review to follow) will help support not only the preventive role of vaccination but also potential treatment for asymptomatic COVID-19 infection in this population.

CR19

An unusual case of icteric leptospirosis after chinchilla bite, with rapid clinical response to plasma exchange

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OBJECTIVES: Leptopsirosis is reputedly the most common zoonosis worldwide but is uncommon in Canada. Maintenance hosts are typically rodents. Data regarding optimal management are equivocal, with unknown efficacy of antibiotics and non-pharmacologic interventions such as plasmapheresis. We describe a patient with classic features of icteric leptospirosis requiring critical care support who made a full recovery with plasmapheresis.

CASE SUMMARY: A 31-year-old previously healthy man presented to hospital after a chinchilla bite to his finger in a scrapyard, presumably a released pet. He was discharged home on oral antibiotics. He returned 11 days later, reporting 3 days of tactile fevers, sweats with worsening malaise, and voiding "foamy urine." He was visibly diaphoretic and mildly tachycardic (118 beats/min), but was otherwise well with no clear localizing symptoms. He had no recent travel history. Initial investigations showed low platelets (113×10^9/L), normal leukocytes and hemoglobin, and mildly elevated total bilirubin (19 µmol/L). Over the next 72 hours, he spiked fevers, developed frank hemoptysis with respiratory decompensation, and ultimately required intubation. He experienced an associated drop in platelets (15×10^9/L), rise in leukocytes (20.6×10^9cells/L), and rise in liver function tests and bilirubin (148 µmol/L), with visible jaundice. Serum creatinine rose to 296 µmol/L. He continued to deteriorate over 48 hours despite steroids, vasopressors, and supportive care. Plasmapheresis was initiated, and within 24 hours he experienced rapid improvement in

renal function and ventilation settings. Vasopressors were discontinued. He was extubated 48 hours later and made a full recovery. Urine *Leptospira* polymerase chain reaction later returned positive, as did serologies.

DISCUSSION: The optimal management of icteric leptospirosis is unknown. We describe a domestically acquired severe case with rapid response to plasmapheresis, adding to the body of literature supporting the efficacy of plasmapheresis. The case highlights that even in the absence of relevant travel, an index of suspicion for unusual zoonotic diseases should be maintained when clinical features are present.

CR20
WITHDRAWN

CR21
Extensive spinal osteomyelitis caused by *Blastomyces dermatiditis* in a previously healthy 12-year-old patient: A case report

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OBJECTIVES: Blastomycosis is a relatively uncommon condition, especially in the pediatric population. Generally, areas endemic for blastomycosis are warm, moist-soil environments in Canada and the United States. This case discusses the presentation of extensive spinal osteomyelitis caused by *Blastomyces dermatiditis* in a previously healthy 12-year-old patient without a history of travel to areas highly endemic for blastomycosis.

CASE SUMMARY: The patient was transferred from a community hospital for assessment of a new lump on the lower back. The patient first began experiencing lower back pain and right leg weakness a year before this admission to hospital. An ultrasound performed in the patient's home community revealed a loculated lesion in the left posterior flank, extending into subcutaneous and muscular plains. A follow-up MRI revealed osteomyelitis and discitis at L3–4 with areas of bone infection in L4 and L5. The suspected diagnosis at this point was tuberculosis, given that the patient had immigrated from a tuberculosis endemic country 4 years ago. Given the extensive nature of the infection, the patient was taken to the operating room for surgical debridement and washout of the spinal abscess on two separate occasions. Bone and tissue sampling confirmed spinal blastomycosis and osteomyelitis of L2–5. Post-operatively, the patient was treated with intravenous amphotericin B for 2 weeks and subsequently discharged home on oral itraconazole therapy for a minimum of 1 year.

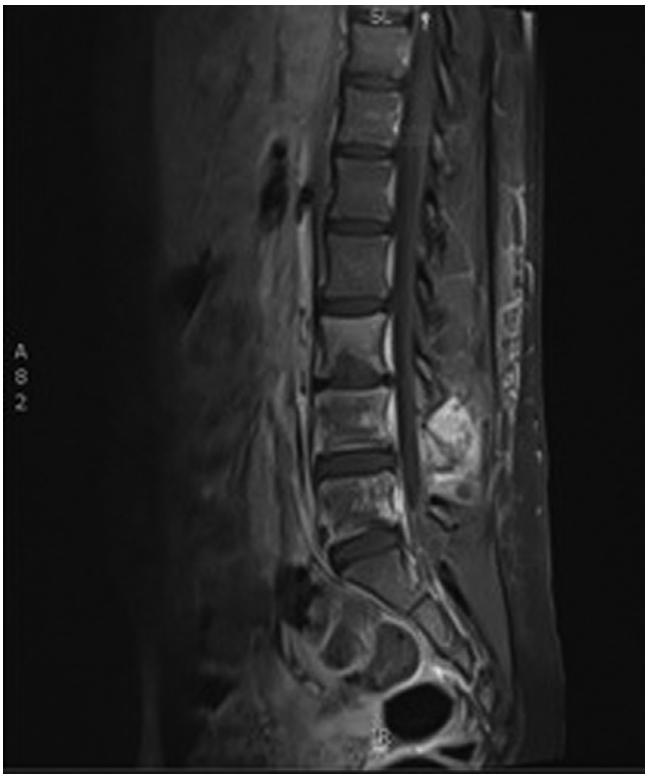

Figure CR21-1: MRI demonstrating destructive lumbar osteomyelitis (L3–4) with bone infection (L4–5)

DISCUSSION: In the pediatric population, there are few reported cases of spinal blastomycosis. The severity of the infection, its chronicity, and the absence of a history of travel or exposure to areas considered endemic for *B. dermatiditis* make this particular case unique. It also serves as a reminder to consider blastomycosis as a cause of spinal osteomyelitis, particularly when tuberculosis is included on the differential.

CR22
Fish out of water: A rare case report of *Lactococcus garvieae* bacteremia associated with osteomyelitis

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OBJECTIVES: *Lactococcus garvieae*, a gram-positive coccus, is a commonly found pathogen in certain types of fish but rarely causes infections in humans. The literature describing human pathogenicity is limited; however, it most often describes cases associated with endocarditis, frequently in the setting of marine life contact or immunocompromised status. Presented here is a rare case of *L. garvieae* bacteremia associated with sacral osteomyelitis.

CASE SUMMARY: A 77-year-old woman with end-stage renal disease on hemodialysis via left upper extremity arteriovenous (AV) fistula, hypertension, and type 2 diabetes mellitus presented with 1 week of worsening sharp, intermittent lower back pain. On initial presentation, the patient had a temperature of 100.4°F with otherwise stable vitals. No leukocytosis was present; however, sedimentation rate was 130 mm/hr and C-reactive protein was 17.5 mg/dL. Blood cultures were obtained before initiation of vancomycin. Physical exam revealed a systolic ejection murmur and a left AV fistula without warmth, erythema, or drainage. Blood cultures were positive in two out of two vials for *L. garvieae,* and vancomycin was switched to ampicillin–sulbactam on the basis of susceptibilities. A transthoracic echocardiogram showed no vegetations. MRI of spine and sacrum showed no evidence of osteomyelitis; however, given concern for the patient's continued symptoms and positive blood cultures, a tagged white blood cell scan was performed that showed moderate uptake along the bilateral sacroiliac joints. The patient was discharged with amoxicillin–clavulanate.

DISCUSSION: Although it is a rare cause of bacteremia, the patient in this case may have been at risk of *L. garvieae* infection given her dependence on dialysis. She remarked that she ate catfish but denied any other exposure to fishing or marine life. Further understanding and awareness of the pathogenicity of *L. garvieae* will help guide treatment options for physicians.

CR23

Disseminated *Mycobacterium marinum* in a patient on a tumour necrosis factor-alpha inhibitor

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OBJECTIVES: *Mycobacterium marinum* is a non-tuberculous mycobacterium commonly associated with skin and soft tissue infections, often acquired through contact with contaminated fresh or salt water, including fish tanks. Rarely, in immunocompromised patients, it is associated with multifocal disease. We describe a case of multifocal *M. marinum* infection in a patient who was receiving a tumour necrosis factor (TNF)-alpha inhibitor.

CASE SUMMARY: A 60-year-old woman who owned a fish tank and had a history of rheumatoid arthritis treated with certolizumab pegol presented with a 4-month history of a left-hand skin and soft tissue infection and transient left arm and axillary lymphadenopathy. She would initially respond to antimicrobials and relapse after their discontinuation. Her syndrome was associated with left-hand pain, reduced hand range of motion, and systemic symptoms, including fever and persistent nausea. She had concurrently developed a progressive, non-pruritic right forearm plaque consisting of grouped erythematous to violaceous, granulomatous papules with serous discharge. In the infectious diseases clinic, right forearm biopsies were taken and sent for histology and culture. Subsequent MRI of her left hand revealed tenosynovitis. The skin biopsy was reported with granulomatous inflammation, and *M. marinum* grew on culture. She was subsequently started on rifabutin, azithromycin, and ethambutol for disseminated *M. marinum,* with improvement in her skin lesions and wrist symptoms, although she required a switch from azithromycin and ethambutol to moxifloxacin and minocycline as a result of intractable nausea.

DISCUSSION: This case presents an opportunity to review disseminated *M. marinum* infections in patients on TNF-alpha inhibitors. Disseminated infections have been described in patients living with HIV or on biologics and in transplant recipients. Our case was unusual, with the presentation of tenosynovitis, itself a rare *M. marinum*–associated syndrome, along with contralateral skin findings. Susceptibility testing is not typically done for *M. marinum;* disseminated and deep infections are usually treated with a multi-drug regimen.

CR24

An unusual mimicker of recurrent bacterial sinusitis in a previously well child

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OBJECTIVES: Nodal natural killer T (NKT) cell, nasal type (ENKTL-NT), is a rare form of peripheral T-cell lymphoma that disproportionally affects men (2:1), with a median age of onset of 52 years. It is more common among Asian, Hispanic

White, and Native American populations. The diagnosis can initially be challenging to make because most patients present with localized disease leading to nasal obstruction and epistaxis, symptoms consistent with subacute bacterial sinusitis. Elevated lactate dehydrogenase (LDH) is commonly observed at presentation. The diagnosis is based on histopathology and immunophenotyping. We describe an otherwise healthy patient with recurrent bacterial sinusitis requiring multiple surgical interventions with a final diagnosis of ENTKL-NT lymphoma.

CASE SUMMARY: An 11-year-old boy of Native American descent was admitted for bacterial sinusitis with associated headache and neck pain. The initial investigation revealed elevated LDH, transaminase, and inflammatory markers. A brain MRI showed pansinusitis with bilateral cavernous sinus thrombosis and pachymeningeal enhancement, consistent with meningitis. A lumbar puncture was performed, showing a lymphocytic pleocytosis, elevated protein, and negative microbiological examination. He underwent sinus wash-out surgery followed by sinus rinses and broad-spectrum antibiotics with central nervous system penetration. Tissue cultures showed *Staphylococcus aureus* and *Arcanobacterium haemolyticum*. He had recrudescent fevers despite three additional sinus debridement surgeries and multiple broad-spectrum antibiotic changes. He eventually lost vision in his left eye and underwent urgent ophthalmology decompression. Tissue pathology unexpectedly revealed ENKTL-NT.

DISCUSSION: This case illustrates the importance of recognizing non-infectious causes of seemingly infectious clinical presentations to prevent premature closure and anchoring bias. In our case, the diagnosis was delayed because most of the pathological specimens were assessed for microbiology alone. On retrospective pathology review, the first nasal tissue specimen revealed a scant amount of NKT cell lymphoma. A high index of suspicion is necessary for the diagnosis of ENKTL-NT because delayed diagnosis is associated with a poor prognosis and high mortality.

CR25

Novel record of fungal eye infection caused by *Hanseniaspora uvarum* and associated with metal splinters

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OBJECTIVES: *Hanseniaspora uvarum* is commonly found on fresh fruit such as grapes plant, birds, and seafood, and it has an important role in alcoholic fermentation. The literature shows that *H. uvarum* infection among humans is very rare and unusual. However, we report a case of fungal eye infection caused by *H. uvarum* in an immunocompetent patient working in a forge.

CASE SUMMARY: A 42-year-old man visited the ophthalmology unit at Al-Sader Teaching Hospital, Basrah, Iraq, because of acute eye pain. He was working in a forge and, as a result of not wearing safety glasses, got a metal splinter. After 2 days, he developed a severe microbial eye infection in both eyes with redness, hard itching, and blurred vision. A swab sample was taken for microbial investigation. Molecular identification showed that *H. uvarum* was the only microbial colony recovered on plate cultures. Antifungal sensitivity test showed that *H. uvarum* was sensitive to clotrimazole, followed by posaconazole, and resistant to both fluconazole and colistin sulphate. Interleukin-17A (IL-17A) and lysozyme were used as immunotherapy in vitro. This microbe exhibited a notable resistance to IL-17A and lysozyme.

DISCUSSION: This case indicates the need to review and consider *H. uvarum* infections, from a common harmless microbe to a rare and serious causative fungal eye infection agent. To the best of our knowledge, this presentation is the first case of *H. uvarum* eye infection in humans because no studies have reported the isolation of *H. uvarum* from eye infection samples. In presenting this case alongside those previously reported, we add to the building literature suggesting that *Bacillus cereus* can cause severe, life-threatening illness in both immunocompetent and immunocompromised patients. Through this case presentation, we highlight and suggest considering the role of *H. uvarum* in severe and serious eye infections.

CR26

Disseminated cutaneous *Mycobacterium chelonae* infection in an adult immunocompetent host: A case report and literature review

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OBJECTIVES: *Mycobacterium chelonae* is a species of non-tuberculous mycobacteria that is known for causing disseminated

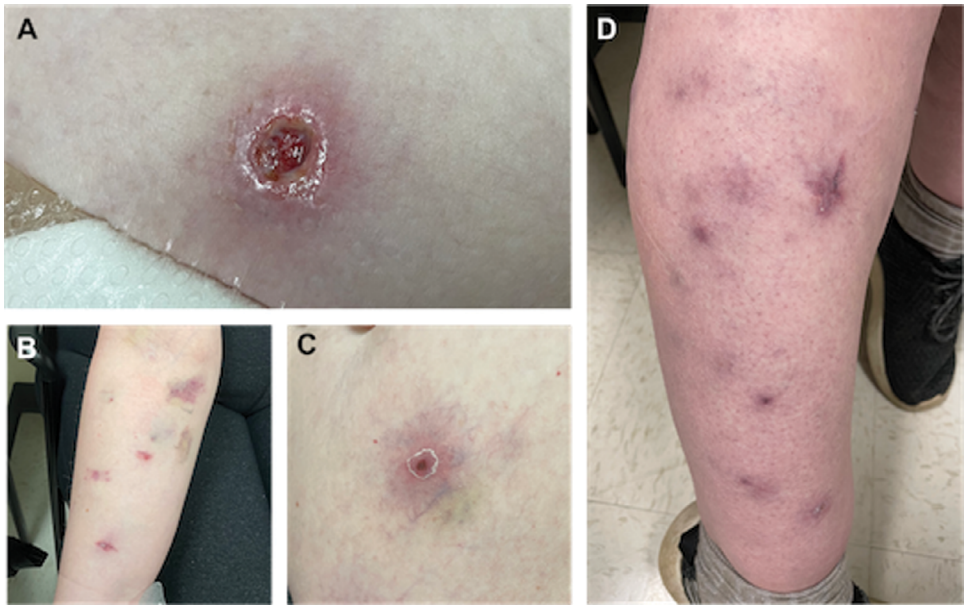

Figure CR26-1: Painful erythematous nodules, papules, erosions, and ulcerations in various stages located on the abdomen (A), right forearm (B), right thigh (C), and right calf (D). Consent obtained for image use

cutaneous infection in immunocompromised individuals or localized cutaneous disease in immunocompetent individuals. We describe a case of disseminated cutaneous *M. chelonae* infection in an immunocompetent woman with an infected implanted venous access device (IVAD) who presented with diffuse erythematous lesions. Disseminated cutaneous mycobacterial infections from rapidly growing mycobacteria (RGM) are rare but present with unique findings that can help clinicians narrow their differential diagnosis.

CASE SUMMARY: A 43-year-old woman with an IVAD presented to the emergency department with malaise, myalgias, intermittent fevers, and painful skin ulcerations increasing in size and frequency over the previous 5 months (Figure CR26-1). Skin biopsy revealed necrotizing granulomatous inflammation with acid-fast bacilli; however, mycobacterial culture was not initially sent. Multiple mycobacterial cultures from blood were negative, but a repeat skin biopsy yielded a positive mycobacterial culture for *M. chelonae.* An ultrasound of her breast revealed small hypoechoic lesions consistent with abscesses. She completed 8 weeks of parenteral amikacin, oral clarithromycin, and oral ciprofloxacin with transition to oral clarithromycin and ciprofloxacin for a planned 6-month course.

DISCUSSION: Clinicians should be aware that disseminated cutaneous *M. chelonae* infection in immunocompetent patients may occur after invasive procedures or in central line infections not responding to appropriate therapy. In patients with suspected RGM infections who are clinically stable, empiric therapy should be avoided, given the many susceptibility patterns present within this group of organisms. Instead, tissue biopsy for histopathological examination as well as mycobacterial culture should be sent early in the work-up to allow for faster diagnosis and improved management of these infections.

CR27

Fatal disseminated fungal infection due to *Blastoschizomyces capitatus:* First Canadian report of an emerging opportunistic yeast

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OBJECTIVES: Fungal infections complicate the courses of many patients with hematologic malignancies and hematopoietic stem cell transplants (HSCT). Although treatment of relatively common fungal infections is standardized, lack of evidence regarding rarer entities and their treatment contributes to poor outcomes. We describe a case of *Blastoschizomyces capitatus* (*Geotrichum capitatum*, *Saprochaete capitata*) fungemia in a Canadian patient with allogeneic HSCT.

CASE SUMMARY: A 39-year-old man with relapsed acute myeloid leukemia was admitted to hospital for haplo-identical HSCT. He developed profound mucositis, leading to oral posaconazole being changed to caspofungin for antifungal

prophylaxis. Five days after the insertion of a new peripherally inserted central catheter, he became febrile, and blood cultures were drawn. He developed new palpable papules on his extremities and new oxygen requirement. Blood cultures grew *B. capitatus*. Aggressive empiric therapy with liposomal amphotericin B and voriconazole was initiated. Two days later, susceptibility testing became available, confirming voriconazole minimum inhibitory concentration of 0.06, although no breakpoint interpretation was available. Despite treatment, he developed rapidly progressive disseminated disease with cutaneous lesions spreading to the whole body, escalating oxygen requirements with bilateral pulmonary nodules, ileus, and delirium. Ultimately, he developed intracerebral hemorrhage and died 13 days after initial fever.

DISCUSSION: This case presents an opportunity to review the burden of fungal disease complicating allogeneic HSCT and the indications for anti-fungal and especially anti-mold prophylaxis. To our knowledge, it also represents the first reported case of *Blastoschizomyces* infection in Canada. This emerging opportunistic yeast pathogen is well described in Mediterranean and subtropical climates, including Italy, Spain, Turkey, and Japan. Its emergence in Canada raises concern for pathogen shift due to global warming. *Blastoschizomyces* should be included in the differential diagnosis of fungal infections that can cause disseminated disease in patients with hematologic malignancy, particularly HSCT recipients.

CR28

A case of catalase-positive *Streptococcus*

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OBJECTIVES: To identify the emerging pathogen *Streptococcus halichoeri*, an unusual *Streptococcus* species that was found to be catalase-negative when grown on Mueller-Hinton agar but catalase-positive when grown on chocolate agar. It is known to cause bloodstream infections and cellulitis, as well as other infections.

CASE SUMMARY: A 53-year-old man from Atlantic Canada with multiple comorbidities including T10–11 level paraplegia, bilateral below-knee amputations, and chronic renal failure, with a chronic left greater trochanteric ulcer, presented to the emergency department in November 2021 with fever, chills, and night sweats. Bloodwork revealed an elevated white count and platelets and anaemia, as well as elevated creatinine and C-reactive protein. He was discharged home on amoxicillin–clavulanic acid, pending blood culture results. Both sets of blood culture returned with chaining and clustering gram-positive cocci suggestive of streptococci or enterococci seen in smears from both aerobic and anaerobic vials, and he was given ceftriaxone and metronidazole for possible mixed bacteremia. Growth from a single set of blood culture bottles was identified as *Streptococcus mitis*, and the other set grew tiny, whitish-grey, nonhemolytic colonies on sheep blood agar, chocolate agar, and anaerobic sheep blood agar but no growth on MacConkey agar. The isolate was initially reported as *Streptococcus* species because matrix-assisted laser desorption/ionization time of flight spectrometry identified it as 50/50 *Streptococcus equi*. Agglutination testing revealed group B antigen. Catalase from broth culture and Mueller-Hinton agar was negative, but from chocolate agar it was positive. The isolate failed to identify on the BD Phoenix (BD, Franklin Lakes, New Jersey). The sensitivity revealed susceptibility to penicillin, ceftriaxone, and vancomycin. Sequencing 16S revealed the identification as *S. halichoeri*.

DISCUSSION: *S. halichoeri* is an unusual *Streptococcus* species as it can be catalase positive. It has frequently been associated with canines and grey seals (*Halichoerus grypus*). Our patient has a pet dog and frequents waters that have grey seals. Such isolates can be dismissed as coagulase-negative *Staphylococcus*, especially from a non-sterile site. Thus, special attention should be applied when observing catalase-positive gram-positive cocci that fail to identify as staphylococci.

CR29

Case report: Recurrent multi-drug-resistant urinary tract infections and the process of obtaining bacteriophage therapy

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OBJECTIVES: Bacteriophage (phage) therapy predates the use of antibiotics and is gaining traction as a virus-like treatment for antibiotic-resistant infections. There are second-hand accounts of Canadian residents self-treating urinary tract infections using over-the-counter phage oral preparations as well as a few international single-patient case studies using intravenously administered phages.

CASE SUMMARY: A 70-year-old otherwise well woman had a 5-year history of recurrent urinary tract multi-drug-resistant *Escherichia coli* infections. She underwent several courses of antibiotic therapy, including up to 10 weeks total of ertapenem therapy. She initially presented with hydronephrosis and, after the use of stents, underwent a failed reconstruction of her ureter and ultimately had a nephrectomy. She continues to have recurrent "humiliating" urinary tract infections, including marked drug intolerances to fosfomycin and sulfa. She was seen in the chronic infection clinic and had her vaginal microbiota and estrogenization optimized. She remains on daily high-dose prophylaxis with 100 mg Macrobid® daily. Her *E. coli* isolate has been sent to two Canadian and one American centre in an attempt to isolate useful phages. Both Canadian centres have identified phages, but production is a hurdle. The patient is likely to be treated with a non-intravenous therapy protocol, and her case has undergone preliminary discussions with Health Canada. The proposed treatment protocol has been refined by a multi-city multi-disciplinary consortium and a national clinical research network.

DISCUSSION: This case illustrates the initial steps involved in acquiring phage therapy in Canada and highlights the lack of production capabilities in Canada. Health Canada was eager in assisting the design of an *N*-of-1 study, including working through the mandatory criteria of a serious life-threatening condition.

CR30

Periprosthetic joint infection of the knee secondary to the zoophilic yeast *Malassezia pachydermatis*: A case report

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OBJECTIVES: Although rare, fungal periprosthetic joint infections (PJI) are a highly morbid and challenging-to-treat complication of total joint arthroplasty. Limited information is available on the optimal management of fungal PJI, including preferred surgical procedure, initial antifungal choice and duration, and the utility of chronic suppressive therapy. This is particularly true for rarely encountered fungal pathogens, such as the case of *Malassezia pachydermatis* PJI we report here.

CASE SUMMARY: A 65-year-old man underwent primary right knee arthroplasty for osteoarthritis in May 2021, followed by revision arthroplasty in July 2021 for pain and stiffness. Post-operatively, he developed persistent drainage and underwent stage 1 revision arthroplasty for presumed PJI in August 2021, with intra-operative cultures positive for *Finegoldia magna* and *Micrococcus* species. He received 6 weeks of intravenous cefazolin and oral metronidazole, followed by oral cephalexin, but had ongoing pain and wound drainage that warranted repeat stage 1 revision arthroplasty in November 2021. *M. pachydermatis* was isolated from two of five intra-operative tissue cultures. No susceptibility testing could be performed. He was treated with intravenous AmBisome® for 10 days and then de-escalated to 200 mg oral voriconazole every 12 hours for 6 weeks, followed by 200 mg oral voriconazole daily as chronic suppressive therapy. Clinically, he is doing well, with plans to undergo stage 2 revision arthroplasty in the coming months.

DISCUSSION: To our knowledge, this is only the second reported case of a periprosthetic joint infection attributed to *M. pachydermatis*. Although a well-known cause of ear and skin infections in canines, the zoophilic yeast *M. pachydermatis* is considered a rare opportunistic pathogen in humans and can be part of the normal human skin flora, particularly among dog owners. Because our patient is immunocompetent, we theorize that the fungus may have been inoculated into the joint space via the draining sinus tract.

CR31

Acute HIV and spontaneously resolving HLH

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OBJECTIVES: To highlight a unique case of acute HIV with associated hemophagocytic lymphohistiocytosis (HLH) that resolved without intervention.

CASE SUMMARY: A 58-year-old man presented feeling generally unwell, with poor oral intake, weakness, and fever (38.3°C). His medical history was significant for hepatitis C, schizophrenia, and substance use disorder. He was found to have bicytopenia (white blood cell 1.47×10^9/L with ALC 0.42×10^9/L , platelets 41×10^9/L), elevated hepatocellular

liver enzymes (alanine transaminase 1,287 U/L, aspartate aminotransferase 1,767 U/L), elevated bilirubin (total 38.6 µmol/L, direct 25.4 µmol/L), ferritin 33,566 µg/L, and triglycerides 6.69 mmol/L. Abdominal ultrasound showed hepatosplenomegaly. His initial HIV enzyme immunoassay was positive, with confirmatory immunoblot being indeterminate. A workup for causes of acute liver injury and a complete infectious workup were otherwise negative. There was a high index of suspicion for HLH, and the patient met diagnostic criteria, which was later supported with an elevated interleukin-2 receptor alpha (soluble CD25) level of 3,897. He was seen by hematology early in his admission; by that time, his HLH was biochemically improving, so no HLH treatment was initiated. His HIV viral load then returned at >10,000,000 copies/mL, in keeping with acute HIV infection. The HLH lab parameters continued to improve until the time of discharge, and at that time he was started on antiretroviral therapy.

DISCUSSION: HLH has very rarely been reported in the literature to be associated with HIV. In the reported cases, the resolution of HLH was associated with either antiretroviral therapy or HLH-specific treatment. It is important to highlight acute HIV as a cause of HLH and that in the past, before fourth-generation HIV testing, this diagnosis and association may have been missed.

CR32

Hypercalcemia and osteomyelitis in an immunocompetent host with disseminated *Mycobacterium avium* cellulare: A case report

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OBJECTIVES: *Mycobacterium avium* cellulare (MAC) is a non-tuberculous mycobacterium that usually affects immunocompromised hosts. It rarely leads to systemic infections in immunocompetent patients. Hypercalcemia is rare metabolic phenomenon, associated with disseminated MAC, the mechanism of which remains controversial. We present a case of disseminated MAC infection in an immunocompetent host with recurrent respiratory infections, skin manifestation, osteomyelitis, and hypercalcemia.

CASE SUMMARY: A 65-year-old man presented with fever, weight loss, and a productive cough. He was treated as confirmed *Legionella* non-pneumophila and had non-specific sclerosis with lytic changes in the ribs and manubrium. Several months later, he developed generalized lymphadenopathy and a diffuse verrucous rash. An immunodeficiency work-up was negative. A lymph node excisional biopsy and skin biopsy both showed granulomatous inflammation with negative infectious work-up. He was noted to have mild but persistent hypercalcemia. Over the following 6 months, his lesions progressed, with worsening and symptomatic hypercalcemia. Parathyroid hormone level was suppressed, and angiotensin-converting enzyme level was not detected. His 25-hydroxy vitamin D level was normal. Polymerase chain reaction of a bone biopsy sample and matrix-assisted laser desorption/ionization time of flight spectrometry on pleural fluid eventually showed MAC, and he was treated accordingly. His hypercalcemia resolved as his MAC infection improved.

DISCUSSION: Granulomatous diseases such as mycobacterium tuberculosis are thought to cause hypercalcemia due to elevated vitamin D metabolites, mediated by extra-renal production of alpha-1 hydroxylase. However, the mechanism of hypercalcemia in MAC infections remains controversial among published cases. Our case showed a normal level of vitamin D, suggesting that there may be an alternative pathway. In addition, our patient had persistent hypercalcemia compared with transient levels in other cases. The degree of hypercalcemia in our patient paralleled his disease activity, suggesting a potential clinical correlation.

CR33

WITHDRAWN

CR34

Challenges in the treatment of infections due to gram-negatives with extensive drug resistance

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OBJECTIVES: The rise in infections due to resistant gram-negatives poses an ongoing threat worldwide. This case highlights the challenges related to susceptibility testing and access to non–Health Canada–approved antibiotics and phage therapy.

CASE SUMMARY: A 63-year-old woman with a history of hospitalization and antimicrobial treatment in Pakistan for painless obstructive jaundice travelled to Canada for further treatment and required endoscopic retrograde cholangiopancreatography (ERCP), stenting, and cholecystostomy tube insertion. Bile and drain cultures grew *Pseudomonas aeruginosa* that was susceptible only to aminoglycosides on first-line testing. Computed tomography, MRI, and repeated ERCP revealed

diffuse gallbladder wall thickening with sludge and significant pericholecystic fat stranding. Infectious diseases (ID) recommended 3 days of tobramycin given the apparent source control. The patient clinically improved and was discharged. She was readmitted 4 days later with fever, chills, generalized itching, and ankle edema. A blood culture grew *Enteroccous faecium* and New Delhi metallo-β-lactamase–positive, multi-drug-resistant *Klebsiella pneumoniae* that was initially only susceptible to doxycycline and tigecycline. Surgery for suspected cholangiocarcinoma with right hemi-hepatectomy and caudal excision was completed. Complications of cholangitis, liver abscesses, and acute kidney injury followed. The abscesses were drained percutaneously, and ID recommended vancomycin, doxycycline, tigecycline, tobramycin, and metronidazole. As a result of persistent positive cultures with *K. pneumoniae* with development of resistance to doxycycline and tigecycline, additional susceptibility testing was completed on a custom broth microdilution panel, revealing resistance to ceftobiprole, ceftolozane–tazobactam, ceftazidime–avibactam, meropenem–vaborbactam, imipenem–relebactam, plazomicin, and colistin with susceptibility only to cefiderocol. A request to the Special Access Program for cefiderocol was made, and phage searching was initiated. Access to cefiderocol was delayed, and despite treatment, the patient clinically worsened and died.

DISCUSSION: Overcoming the challenges related to susceptibility testing using validated methods and access to non–Health Canada–approved drugs and phage therapy with reasonable turn-around time will enhance efficiency in managing cases with extensive drug resistance.

CR35
Persistent infection with SARS-CoV-2 in a person with untreated HIV

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OBJECTIVES: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA can be detected in upper respiratory specimens of people with coronavirus disease 2019 (COVID-19) for prolonged periods of time, although the likelihood of recovering replication-competent virus beyond day 10 of illness (and day 20 among those with severe illness) is very low. Much greater variability has been observed with severely immunocompromised individuals, making it challenging to determine duration of transmission risk in this population. We present a case of persistent infection with SARS-CoV-2 for more than 20 weeks despite preceding vaccination in an individual with advanced HIV infection.

CASE SUMMARY: A 76-year-old man from a long-term-care facility tested positive for SARS-CoV-2 on a nasopharyngeal swab via reverse transcription polymerase chain reaction in May 2021, while asymptomatic. He was hospitalized for monitoring because of a history of significant immunocompromise related to untreated HIV infection with a CD4 count of 110 cells/mm^3. He had received two doses of the mRNA-1273 (Moderna) COVID-19 vaccine with the second dose administered 3 months before infection. He remained well throughout his admission without receiving COVID-19 directed therapies; however, he continued to have detectable SARS-CoV-2 RNA from upper respiratory tract samples until the time of his death from unrelated causes 142 days after the initial diagnosis. Because cycle threshold (Ct) values remained below 20, viral cultures were performed on nasopharyngeal swabs collected on post-diagnosis day 68 and 142, revealing the presence of infectious virus. SARS-CoV-2 serology was negative, and whole-genome sequencing confirmed persistent infection with the same virus.

DISCUSSION: Severely immunocompromised individuals, especially those with non-reversible immunosuppression, can have very prolonged SARS-CoV-2 infection. Ct values below 20 in this population should raise concern for persistence of replication-component virus. Measures that address reversible causes of immunodeficiency such as HIV infection are likely a critical component of a successful response to the COVID-19 pandemic.

CR36
WITHDRAWN

CR37
Pneumococcal serotype 22F bacteremia in a toddler

Praveen Kumar Saroey, Margaret S Moyo, Manjulata Rajguru

Cambridge Memorial Hospital, Cambridge, Ontario, Canada

OBJECTIVES: To describe the clinical presentation of bacteremia caused by pneumococcal serotype 22F.

CASE SUMMARY: A 15-month-old girl presented to the emergency department with a febrile convulsion after a 2-week history of a coryza illness and few days of high-grade temperature. The patient was systemically well and had no

clinical features of sepsis or meningo-encephalitis. She had features of a pneumonitis on assessment and radiology. On admission, she had a partial septic work up and a nasopharyngeal swab for extended viral panel. She was previously fit and healthy. Over the next 24 hours, she continued to spike high-grade temperatures with mild respiratory distress and no requirement for oxygen or respiratory support. Her initial complete blood count showed evidence of neutrophilia, and her C-reactive protein, initially <5, rose to 70.1 over 24 hours. Blood culture grew *Streptococcus pneumoniae* at 10 hours of incubation, and NPS panel was positive for parainfluenza III. The child was successfully treated with 48 hours of ceftriaxone followed by intravenous ampicillin. She was discharged on oral amoxicillin to complete a total of 2 weeks of antibiotics. Baseline immunoglobulins and CD4 subsets were within normal limits, and abdominal ultrasound confirmed the presence of a normal spleen. Serotype 22F was subsequently confirmed on sub-typing by the public health laboratory.

DISCUSSION: The clinical presentation of 22F serotype in children which is not well described. The strain is not part of PREVNAR 13® but is part of PREVNAR 15 (along with serotype 33F). Studies suggest that 22F may be responsible for as much as 10% of overall cases of pneumococcal disease. The case suggests a mild occult bacteremia–like presentation in children. Further studies are required to describe the clinical spectrum in different age groups and those with comorbidities. Future inclusion in immunization programs, and approval of PREVNAR 15 for children, is likely to further reduce pneumococcal disease.

CR38

Mycoplasma hominis mediastinitis after cardiac surgery: A case report

Mosaab E Alam[1], Jennifer Losie[1], Jennifer M Grant[2,3], Theodore S Steiner[2], Marthe K Charles[2,3], Valery Lavergne[3]

[1]Department of Infectious Diseases, University of British Columbia, Vancouver, British Columbia, Canada; [2]Division of Infectious Diseases, Vancouver Coastal Health, Vancouver, British Columbia, Canada; [3]Division of Medical Microbiology, Vancouver Coastal Health, Vancouver, British Columbia, Canada

OBJECTIVES: *Mycoplasma hominis* is a fastidious bacterium that usually colonizes humans' urogenital tract. This organism is rarely associated with disseminated infections, usually in immunocompromised adults. However, *M. hominis* cell wall composition can make its detection by routine microbiology diagnostically challenging. Here, we report a case of *M. hominis* mediastinitis in an immunocompetent patient after cardiac surgery.

CASE SUMMARY: A 54-year-old immunocompetent man, with a history of diabetes and dyslipidemia, was admitted with non-ST elevation myocardial infarction. He underwent coronary artery bypass graft and mechanical aortic valve replacement surgery. After multiple cardiothoracic interventions, the patient subsequently developed sepsis and sign of surgical site infection while on broad-spectrum antibiotics. As part of the initial septic workup, blood cultures were drawn, and the central venous catheter (CVC) was removed. The CVC culture showed >100 pinpoint colonies on blood agar, whereas the blood cultures were negative. The colonies isolated from the CVC were identified as *M. hominis* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF). This finding was initially interpreted as a possible contamination. Subsequently, a superficial swab of the sternotomy was collected; Gram stain showed abundant polymorphonuclears with no organisms seen and grew a pure culture of *M. hominis*. Mediastinitis was then suspected clinically and confirmed by imaging. A large retrosternal collection was drained and debrided and sent for microbiology testing. Once again, *M. hominis* was identified by MALDI-TOF and further confirmed by 16s polymerase chain reaction. After prolonged incubation, blood cultures were blindly sub-cultured and also grew *M. hominis*.

DISCUSSION: This is a rare case of postoperative mediastinitis complicated or caused by *M. hominis* bloodstream infection in an immunocompetent man. Detection of *M. hominis* as a cause of post-operative infection could be underestimated because of its fastidious nature and diagnostic limitations.

CASE REPORT SYMPOSIUM

Friday, April 8
11:45–12:45 PDT

CS01

A puzzling case of congenital syphilis

Amro Qaddoura, Alena Tse-Chang, Joan L Robinson

University of Alberta, Edmonton, Alberta, Canada

OBJECTIVES: To outline challenges in diagnosing congenital syphilis (CS).

CASE SUMMARY: An 11-month-old was diagnosed with CS when rapid plasmin regain (RPR) was unexpectedly reactive at 1,024 dilutions. His mother's syphilis serology

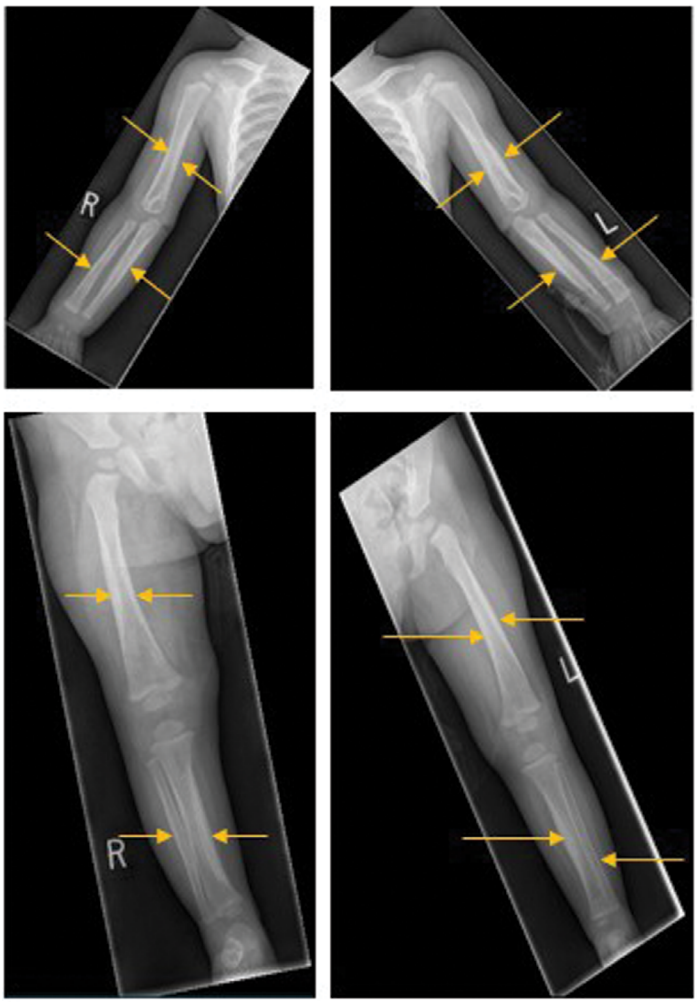

Figure CS01-1: X-rays demonstrating findings of chronic osteitis involving all long bones of the upper and lower extremities (yellow arrows) in keeping with congenital syphilis

was non-reactive at 19 weeks gestation. Despite routine testing of all women in our province at delivery, she was not retested. She was tested 27 days postpartum when named as a contact. RPR was 32 dilutions. At age 31 days, the infant had non-reactive enzyme immunoassay, *Treponema pallidum* particle agglutination assay, and RPR. At age 100 days, the infant was assessed for an erythematous rash involving the palms and soles and diagnosed with hand, foot, and mouth disease. Follow-up infant syphilis serology was done when his mother collected the requisition from a former address, revealing the result mentioned earlier. The infant then received 10 days of intravenous penicillin. Cerebrospinal fluid had normal leukocytes, protein, and glucose with non-reactive Venereal Disease Research Laboratory and negative syphilis polymerase chain reaction (PCR). Radiographs showed chronic osteitis of all extremity long bones (**Figure CS01-1**). PCR on the prior blood sample at age 31 days was negative.

DISCUSSION: This case emphasizes the importance of screening pregnant women for syphilis both during pregnancy and at delivery, especially with the ongoing outbreak in several provinces. However, it is possible that the mother became infected just before delivery and would have still been seronegative given that the infant did not have sufficient passive antibodies to be seropositive 31 days later. Perhaps the infant acquired syphilis after birth, but it seems unlikely that this would cause osteitis, although osteitis is also not expected from infection acquired at delivery. Manifestations of syphilis are under-recognized; the infant rash on day 100 was almost certainly due to syphilis. Syphilis can cause a rash of the palms and soles, even in an infant.

CS02

Concomitant serogroup B meningococcemia and rhinovirus/enterovirus upper respiratory tract infection in a meningococcal B–vaccinated patient on eculizumab: A case report

D Brody Duncan, Shariq Haider

McMaster University, Hamilton, Ontario, Canada

OBJECTIVES: We describe a case of serogroup B meningococcemia despite prior meningococcal B (MenB) vaccination in a patient on eculizumab to demonstrate the difficulties in diagnosing and preventing invasive meningococcal disease in immunocompromised patients.

CASE SUMMARY: A 68-year-old women presented to her outpatient oncologist with a 1-day history of chills, malaise, and myalgias. Her medical history included atypical hemolytic uremic syndrome, for which she had been on eculizumab since 2015, and she had received MenB vaccination. She had a recent household contact with upper respiratory tract infection. Blood cultures and a nasopharyngeal swab for multiplex polymerase chain reaction were sent. Two days later she developed a productive cough and rhinorrhea. Her blood cultures grew gram-negative diplococci, and her swab was positive for rhinovirus/enterovirus. She was admitted to hospital, found to have a fever and dusky toes suggestive of purpura fulminans, and started on empiric ceftriaxone. The culture subsequently speciated as *Neisseria meningitidis* serogroup B, with intermediate susceptibility to penicillin and full susceptibility to ceftriaxone. A lumbar puncture was done with normal cell count and no growth on culture.

The patient had rapid clinical improvement, follow-up blood cultures were negative, and she was discharged home to finish 14 days of ceftriaxone.

DISCUSSION: This case demonstrates the importance of a low threshold to suspect invasive meningococcal disease in patients on eculizumab. This patient also had a concomitant upper respiratory tract infection that could have confused the diagnosis if blood cultures had not been sent. There are recent reports of serogroup B meningococcemia despite vaccination in patients on eculizumab, likely a result of underlying impaired immune response. The issue of chemoprophylaxis is complex. Our patient had previously been on penicillin but stopped it because of intolerable gastrointestinal side effects, and her isolate was penicillin non-susceptible; there remains lack of clarity on the duration and choice of chemoprophylaxis in patients on eculizumab.

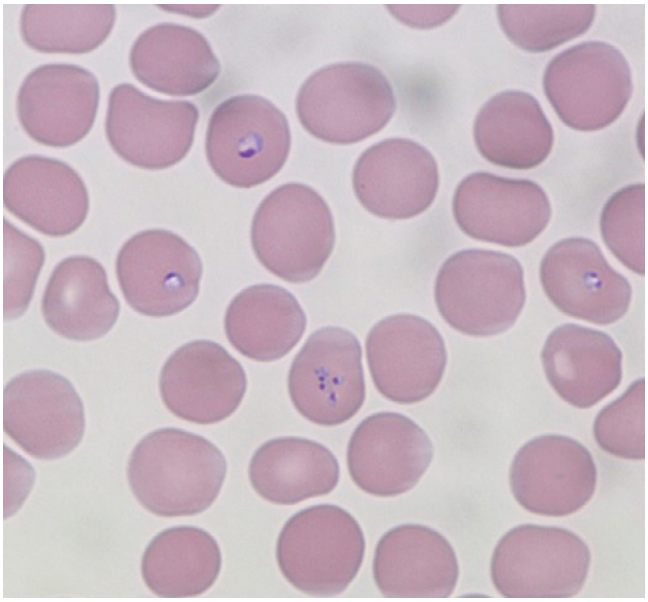

Figure CS03-1: Wright-stained peripheral blood smears showing Maltese cross

CS03

First case of human *Babesia microti* infection acquired in Atlantic Canada

Ziyad O Allehebi[1,2], Farhan M Khan[1,2], Mark Robbins[2], Elizabeth Simms[2], Richard Xiang[3], Allam Shawwa[3], L Robbin Lindsay[4], Antonia Dibernardo[4], Clarice d'Entremont[5], Alex Crowell[5], Jason J LeBlanc[1,2,6,7], David J Haldane[1,2,6,8]

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OBJECTIVES: Babesiosis is an emerging infectious disease caused by *Babesia*, a zoonotic hemoprotozoan parasite, with human disease in North America primarily attributed to *Babesia microti*. Clinical features range from asymptomatic infection to severe disease, and even death. To date, only rare cases of locally acquired human babesiosis have been described from Central and Western Canada. This report describes the first case of *B. microti* acquired in Atlantic Canada.

CASE SUMMARY: A 58-year-old immunocompetent man presented in July 2021 at a southwest Nova Scotia hospital with a history of headache, photophobia, fatigue, weakness, and fevers. He denied recent travel or tick bites. Since 2019, he has received three courses of doxycycline for Lyme disease. Initial investigations revealed a normal white blood cell count, hemoglobin, and low platelets. Wright-stained peripheral blood smears to investigate his new-onset thrombocytopenia revealed intra-erythrocytic ring forms and extracellular merozoites suspicious for parasitic infection (Figure CS03-1). Parasitemia was estimated at 2.3%. The National Microbiology Laboratory confirmed *B. microti* on whole-blood polymerase chain reaction. Clinical improvement was seen after starting treatment with 10 days of atovaquone and azithromycin and 14 days of doxycycline for possible Lyme co-infection. Parasitemia became undetectable by day 7.

DISCUSSION: In Nova Scotia, the *B. microti* reservoir white-footed mouse and vector *Ixodes scapularis* is the same as for *Borrelia burgdorferi*, the causative agent of Lyme disease, which is endemic in the province. Seroprevalence studies from the Canadian Blood Services found rare human cases of *B. microti*, and other surveillance studies identified *B. microti*–infected *Ixodes* ticks and animals in Manitoba, Ontario, Quebec, New Brunswick, and Nova Scotia. We report the first confirmed locally acquired *B. microti* infection in Atlantic Canada. Surveillance and health care provider education are required as the epidemiology of tick-borne diseases changes in Canada.

CS04

Redefining endemicity: A case of presumed isolated ocular coccidioidomycosis in a patient on anti-tumour necrosis factor therapy who has never left Ontario

Danielle Ouellette[1], Mohammadreza Rahimi Shahmirzadi[1], Lise Bondy[1], Jeffrey Fuller[1,2]

[1]Western University, London, Ontario, Canada; [2]London Health Sciences Centre, London, Ontario, Canada

OBJECTIVES: Over the past decade, reports of infections due to the so-called endemic fungi have been increasing in patients without travel to previously defined endemic regions. Here we describe a case of presumed isolated ocular coccidioidomycosis in a patient who has never lived in or visited a region where *Coccidioides* species are endemic.

CASE SUMMARY: A 40-year-old woman presented with acute-onset left eye blurry vision. On fundoscopy, there were two cream-coloured macular lesions without significant vitreitis or anterior segment inflammation. Her history was pertinent for right-eye blindness from childhood trauma, hidradenitis suppurativa on adalimumab, and previous intravenous use of methamphetamines, although she reported complete abstinence for more than 2 years. She had no travel history and in fact has never left the province of Ontario, although she had been homeless for a period of time several years back. An extensive infectious work-up was non-contributory except for *Coccidioides immitis* serology, which returned immunoglobulin (Ig) G reactive and IgM non-reactive by enzyme immunoassay (EIA). Serologies for *Blastomyces* and *Histoplasma* were non-reactive. Given the lack of compatible travel history, Coccidioides antigen EIA (Miravista Diagnostics, Indianapolis, Indiana) was sent as a confirmatory test and returned positive at 0.15 ng/mL; *Blastomyces* and *Histoplasma* antigen EIA were negative. Unfortunately, intraocular tissue cultures could not be obtained without further risking her remaining vision. Lumbar puncture, head computed tomography (CT), and chest and abdomen CT were unremarkable. She was treated with intravitreal voriconazole and fluconazole 800 mg oral daily for 4 months, with a plan to complete an additional 8 months of fluconazole 400 mg oral daily and likely lifelong suppressive therapy thereafter.

DISCUSSION: This case highlights the importance of considering the endemic mycoses in patients presenting with a compatible clinical syndrome, even in the absence of traditional epidemiologic risk factors. This is particularly true for immunocompromised patients and those with additional risk factors such as anti-tumour necrosis factor therapy.

CS05

Cytomegalovirus retinitis in a pre-transplant patient with relapsed acute lymphoblastic leukemia on salvage chemotherapy: A case report

Maude Paquette[1], Sonia Cellot[1], Josette Champagne[1], Thai Hoa Tran[1], Henrique Bittencourt[1], Jessica McMahon[1], Cynthia Qian[1], Marie-Lyne Bélair[2], Rosanne Superstein[1], Ana C Blanchard[1]

[1]Centre Hospitalier Universitaire Sainte-Justine, Montreal, Quebec, Canada; [2]Hôpital Maisonneuve-Rosemont, Montreal, Quebec, Canada

OBJECTIVES: Retinitis is a rare manifestation of cytomegalovirus (CMV) disease. It has been mostly described in patients with AIDS or after transplant. We describe the case of a pre-transplant patient with relapsed/refractory acute lymphoblastic leukemia (ALL) on salvage chemotherapy who developed CMV retinitis.

CASE SUMMARY: A 20-year-old man with relapsed T-cell ALL presented to the oncology clinic with a 7-day history of blurry vision and increased right eye pain. His leukemia was refractory to an initial chemotherapy regimen that included nelarabine, and he was receiving hyper-CVAD chemotherapy associated with daratumumab, venetoclax, and steroids as a bridge to hematopoietic cell transplant.

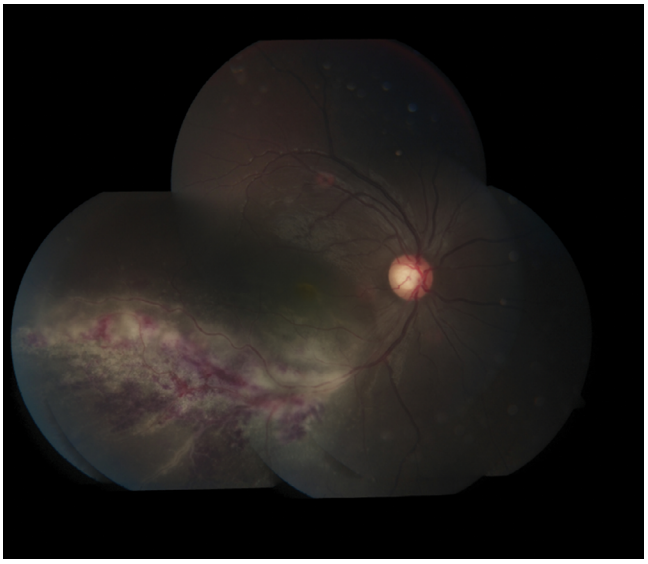

Figure CS05-1: Pre-treatment examination of right eye retinal lesion

Ophthalmologic examination showed a decreased visual acuity at 20/400, macular edema and retinitis in the right eye (Figure CS05-1), and a macular lesion in the left eye. CMV polymerase chain reaction (PCR) in the blood was positive at 5.5 log (316,228 copies/mL), and CMV PCR in the vitreous fluid was at 4.8 log (66,069 copies/mL). He was profoundly lymphopenic at 0.03×10^9/L. The patient was treated with intra-vitreous foscarnet, CMV intravenous immunoglobulin, and intravenous ganciclovir for 7 weeks with significant improvement of the lesions and of his visual acuity. He was transitioned to maintenance therapy with valganciclovir until he succumbed from disease progression 2 months later.

DISCUSSION: CMV retinitis is rare in non-AIDS and non-transplant patients. Daratumumab is an anti-CD38 monoclonal antibody causing potent cellular immunosuppression, which is increasingly used in salvage chemotherapy for T-cell ALL. This case illustrates that CMV should be suspected as a cause of retinitis in patients who are on regimens containing daratumumab, especially if given in association with other agents affecting cellular immunity. Moreover, although CMV monitoring is not currently recommended in pre-transplant settings, this case adds evidence to question whether the use of biologic therapies such as daratumumab may warrant viral surveillance.

POSTER PRESENTATIONS

P01

Anosmia-related Internet search and the course of the first wave of the COVID-19 pandemic in the United States

Kenneth M Madden[1,2,3], Boris Feldman[1,3]

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OBJECTIVES: The current pandemic of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first reported in Wuhan, China. Although the first case in the United States was reported on January 20, 2020, in Washington State, the early pandemic time course is uncertain. One approach with the potential to provide more insight into this time course is the examination of search activity. This study analyzed US search data before the first press release indicating anosmia as an early symptom (March 20, 2020).

METHOD: Daily Internet search query data were obtained from Google Trends (September 20–March 20 for 2015–2020, weeks 1–26) both for the United States and on a state-by-state basis. Normalized anosmia-related search activity for the years before the pandemic was averaged to obtain a baseline level. Cross-correlations were performed to determine the time lag between changes in search activity and SARS-CoV-2 cases or deaths.

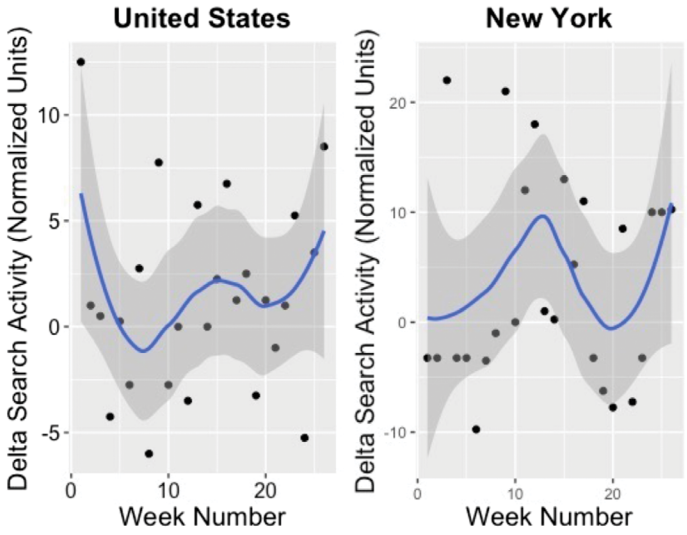

Figure P01-1: Delta Search Activity from September 20th, 2019 to March 20th, 2020: Change in anosmia-related search activity during the pandemic first wave (Delta, Normalized Units) for both national data, and the state of New York

RESULTS: Only New York showed both significant increases in anosmia-related terms during the pandemic year (September 20–March 20 for 2015–2020; weeks 1–26; Figure P01-1; $F = 4.711$, $p = 0.039$) as well as a significant lag (6 d) between increases in search activity for anosmia-related terms and increases in the number of cases or deaths attributed to SARS-CoV-2.

CONCLUSION: There is no evidence from search activity to suggest earlier spread of SARS-CoV-2 than has previously been reported. The increase in anosmia-related searches preceded increases in SARS-CoV-2 cases and deaths by 6 days, but this was only significant over the background noise of searches for other reasons in the setting of a very large outbreak (New York, spring 2020).

P02

Estimating SARS-CoV-2 seroprevalence in Canadian blood donors, April 2020–March 2021: Improving accuracy with multiple assays

Ashleigh Tuite[1], David Fisman[1], Kento T Abe[2,3], Bhavisha Rathod[2], Adrian Pasculescu[2], Karen Colwill[2], Anne-Claude Gingras[2,3], Qi-Long Yi[4], Sheila F O'Brien[4,5], Steven J Drews[6,7]

[1]Dalla Lana School of Public Health, University of Toronto, Toronto, Ontario, Canada; [2]Lunenfeld-Tanenbaum Research Institute at Mt. Sinai Hospital, Sinai Health, Toronto, Ontario, Canada; [3]Department of Molecular Genetics, University of Toronto, Toronto, Ontario, Canada; [4]Canadian Blood Services, Epidemiology and Surveillance, Ottawa, Ontario, Canada; [5]School of Epidemiology and Public Health, University of Ottawa, Ottawa, Ontario, Canada; [6]Canadian Blood Services, Microbiology, Edmonton, Alberta, Canada; [7]Department of Laboratory Medicine and Pathology, University of Alberta, Edmonton, Alberta, Canada

OBJECTIVES: We have previously used composite reference standards and latent class analysis (LCA) to evaluate the performance of laboratory assays in the presence of tarnished gold standards. Here we apply these techniques to repeated, cross-sectional study of Canadian blood donors, whose sera underwent parallel testing with four separate severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) antibody assays.

METHOD: We designed a repeated cross-sectional design with random cross-sectional sampling of all available retention samples (n = 1,500/month) for a 12 -month period from April 2020 until March 2021. Each sample was evaluated for SARS-CoV-2 immunoglobulin G (IgG) antibodies using four assays: an Abbott Architect assay targeting the nucleocapsid antigen (Abbott-NP, Abbott, Chicago, Illinois) and three in-house IgG enzyme-linked immunosorbent assays recognizing distinct recombinant viral antigens: full-length spike glycoprotein (Spike), spike glycoprotein receptor binding domain, and nucleocapsid. We used two analytic approaches to estimate SARS-CoV-2 seroprevalence: a composite reference standard and LCA.

RESULTS: Using LCA to estimate true seropositivity status on the basis of the results of the four antibody tests, we estimated that seroprevalence increased from 0.8% (95% CI 0.5% to 1.4%) in April 2020 to 6.3% (95% CI 5.1% to 7.6%) in March 2021. Despite regions of the country experiencing very different epidemic trajectories, seroprevalence estimates at the final study time point (March 2021) were not substantially different across the country, ranging from a low of 4.2% (2.5%–7.0%) in Alberta to a high of 7.0% (4.4%–11.1%) in British Columbia. After adjustment for age, sex, province, ethnicity, vaccination status, and rural location, the odds of SARS-CoV-2 seropositivity increased during the January–March 2021 period, relative to April–June 2020 (adjusted odds ratio 3.18, 95% CI 2.33 to 4.43).

CONCLUSION: Our study provides further support for the use of LCA in upcoming public health crises, epidemics, and pandemics when a gold-standard assay may not be available or identifiable.

P03

Urban and rural trench fever in Manitoba associated with culture-negative endocarditis and systemic embolization: A retrospective case series of *Bartonella* serologies, 2010–2020

Carl Boodman[1], Terence Wuerz[1], Philippe Lagacé-Wiens[1], L Robbin Lindsay[2], Antonia Dibernardo[2], Jared Bullard[1,3], Derek R Stein[3], Yoav Keynan[1]

[1]University of Manitoba, Winnipeg, Manitoba, Canada; [2]National Microbiology Laboratory, Winnipeg, Manitoba, Canada; [3]Cadham Provincial Laboratory, Winnipeg, Manitoba, Canada

OBJECTIVES: *Bartonella* are gram-negative bacilli not identified by routine bacterial culture. Human disease resulting from *Bartonella* in North America is primarily caused by two species: *B. henselae* (cat scratch disease) and *B. quintana* (trench fever). *B. quintana* is transmitted by body lice and is associated with inadequate access to housing and running water. The objective of this study is to review adult cases with positive *Bartonella* serologies ordered in Manitoba to assess speciation, risk factors, clinical manifestations, and outcomes.

METHOD: This retrospective case series includes all *Bartonella* serologies ordered on adults in Manitoba from January 1, 2010, until December 31, 2020. We reviewed the charts of adult patients with positive *Bartonella* serologies to extract clinical and demographic data. Descriptive statistics were performed.

RESULTS: A total of 1,014 *Bartonella* serologies were ordered (adult and pediatric patients). Of 1,014, 24 were positive (2.4%). Eight pediatric cases were excluded from, and 16 adults with positive *Bartonella* serologies underwent chart review. Molecular identification occurred on explanted cardiac valves in 5 cases (31.3%); *B. quintana* was identified in all 5. Six (37.5%) individuals were diagnosed with probable *B. quintana* infection, leading to a total of 11 *B. quintana* cases (68.8%). Of these, 8 (72.7%) were associated with endocarditis. Four cases of *B. quintana* (36.4%) were associated with rural geography. Four (25.0%) cases of probable *B. henselae* were identified. Of these, 2 (50%) had fever and lymphadenopathy, and 2 had endocarditis (50%). One low-titre positive serology was deemed to be a false positive.

CONCLUSION: *B. quintana* is a common cause of *Bartonella* serologic positivity among adults in Manitoba. Positive *Bartonella* serology is associated with endocarditis and systemic

embolization. *B. quintana* endocarditis occurs in both urban and rural settings and reflects a lack of suitable housing in both inner-city Winnipeg and remote communities.

P04

Evaluation of a new chromogenic medium for screening of *Burkholderia cepacia* complex from respiratory specimens

Tanisha Bharara[1], Rajesh Kumar[2], Deeksha Bhardwaj[2], Vikas Gautam[2]

[1]North Delhi Municipal Corporation Medical College and Hindu Rao Hospital, New Delhi, India; [2]Postgraduate Institute of Medical Education and Research, Chandigarh, India

OBJECTIVES: To evaluate CHROMagar™ (DRG International, Springfield, New Jersey) *Burkholderia cepacia* medium for screening of *B. cepacia* complex from respiratory specimens

METHOD: A hospital based observational study was carried out in the Department of Microbiology in two different cities. A total of 100 respiratory specimens (including specimens from patients with cystic fibrosis) were tested. Thirty pure *B. cepacia* complex (BCC) isolates and 60 non-fermenting gram-negative bacilli (NFGNB) other than BCC were also plated on the media. Ethical clearance was provided by both institutional ethical committees. Specimens and pure laboratory confirmed matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF) isolates were plated on MacConkey agar as well as CHROMagar *B. cepacia* medium as per standard guidelines and incubated for 48 hours at a mean 36°C (SD 1) under aerobic conditions. BCC isolates were identified using Gram staining, biochemical tests, and MALDI-TOF. Antimicrobial susceptibility was done by Kirby-Bauer disc diffusion method and VITEK 2 AST card. *B. cepacia* ATCC 25416 was used for quality control. Results were statistically analyzed, and sensitivity, specificity, positive predictive value, negative predictive value, and *p* value were calculated.

RESULTS: Of the 100 respiratory specimens tested, 17 grew BCC on CHROMagar *B. cepacia,* and only 9 specimens grew BCC on McConkey agar (positive predictive value = 100%, $p = 0.013$). Four false-positive results were found on CHROMagar *B. cepacia;* however, the growth characteristics were morphologically distinct from that of BCC. Thirty pure isolates of BCC were inoculated on CHROMagar *B. cepacia,* all formed bluish-green colonies with a blue halo, whereas 78% of NFGNB other than BCC were inhibited on the medium. Overall sensitivity, specificity, positive predictive value, and negative predictive value of CHROMagar *B. cepacia* were found to be 100%, 78%, 100%, and 96%, respectively.

CONCLUSION: The study concludes that CHROMagar *B. cepacia* medium is a highly sensitive and specific medium for isolation of BCC from respiratory specimens.

P05

SARS-CoV-2 virus-like particle neutralizing capacity in blood donors depends on donor serological profile and SARS-CoV-2 vaccination history

Steven J Drews[1,2], Queenie Hu[3], Kento T Abe[3,4], Anne-Claude Gingras[3,4], Karen Colwill[3], Bhavisha Rathod[3], Qi-Long Yi[5,6], Sheila F O'Brien[5,6]

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OBJECTIVES: The first 3 months of 2021 saw a changing landscape of circulating severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants and the early stages of a mass coronavirus disease 2019 (COVID-19) vaccination campaign. This study was undertaken to characterize the neutralizing capacity of plasma from Canadian blood donors against wild-type (Wuhan-1) and variant (eg, Alpha [B.1.1.7], Beta [B.1.351], Gamma [P1] and Delta [B.1.617.2]) SARS-CoV-2 from January to March 2021.

METHOD: A repeated cross-sectional design was used, and a random cross-sectional sample of all available retention samples ($n = 1{,}500$/month) was drawn monthly for January, February, and March 2021. Qualitative immunoglobulin G analysis was undertaken for anti-spike (anti-S), anti-receptor binding domain (anti-RBD), and anti-nucleocapsid protein (anti-N). A tiered testing approach of specimens with any potential evidence of a signal for anti-S or anti-RBD (with or without anti-N) was used to select specimens for further analysis by neutralization methods. Spike-pseudotyped virus-like particle (VLP) neutralization assays were undertaken for wild-type (Wuhan-1) and variants.

RESULTS: Specimens were stratified on the basis of donor-declared vaccination history and then stratified on the presence or absence of anti-N as follows: group 1, vaccinated plus anti-N ($n = 5$); group 2, vaccinated and no anti-N ($n = 20$); group 3, unvaccinated plus anti-N ($n = 20$); and group

4, unvaccinated and no anti-N (n = 20). No wild-type or variant VLP neutralization capacity was identified in group 4. In groups 1–3, neutralization of beta VLPs was constantly lower than neutralization of wild-type VLPs ($p < 0.05$). Group 2 presented with additional reduced neutralization capacity against Alpha, Gamma, and Delta variants ($p < 0.05$).

CONCLUSION: In the first 3 months of 2021, Canadian blood donors had varying levels of humoral protection against wild-type and variant SARS-CoV-2. Neutralizing capacity was highest in vaccinated blood donors. Even in the presence of anti-S or anti-RBD antibodies, some unvaccinated blood donors had no neutralizing antibodies against wild-type or variant VLPs.

P06

Decreasing parvovirus B19 and hepatitis A nucleic acid test positivity rates in Canadian plasma donors after the initiation of COVID-19 restrictions in March 2020

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OBJECTIVES: This study compares the rates of parvovirus B19 (B19) and hepatitis A virus (HAV) nucleic acid test (NAT) positivity in predominantly Canadian plasma samples for the pre–coronavirus disease 2019 (COVID-19) restriction era (2015 through first quarter [Q1] 2020) and the post–COVID-19 restriction era (Q2 2020– Q3 2021).

METHOD: Plasma specimens were collected by the blood operator and sent with a larger volume plasma to a plasma fractionator. Samples were pooled (16 per pool) for parvovirus B19/HAV testing using the Procleix Panther System (Grifols Diagnostic Solutions Inc, San Diego, California). Any HAV positive (reactive = above assay cut-off) and B19 nucleic acid testing (NAT) positive (reactive ≥10,000 IU/mL) pools were resolved by individual specimen testing (reactive = above assay cut-off for both targets). These pools were predominantly from Canada but included a small number of donations (eg, <5%) from the United States. Data were collated using Excel (Microsoft Corp, Seattle, Washington). Chi-square analysis utilized Vassar Stats (http://vassarstats.net/newcs.html).

RESULTS

Table P06-1: Incidence rate for B19 and HAV in plasma samples from 2015-2021

	n (%)	
Year	**B19**	**HAV**
2015	82/568217 (0.01)	2/568217 (0.0004)
2016	35/469820 (0.007)	8/469820 (0.002)
2017	42/481834 (0.009)	6/479583(0.001)
2018	46/501695 (0.009)	3/501695 (0.0006)
2019	34/482057 (0.007)	6/482059 (0.001)
2020 Q1	12/136108 (0.009)	1/136108 (0.0007)
2020 Q2–Q4	14/358669 (0.004)	0/358669 (0)
2021 Q1–Q3	0/388604 (0)	0/388603 (0)

B19 = Parvovirus B19; HAV = hepatitis A virus; Q = Quarter

There was a significant difference in the proportion of B19 from the pre–COVID-19 restriction period to the post–COVID-19 restriction period (Yates $\chi^2[1]$, $p = 0.03$). There was a significant difference in the proportion of HAV from the pre–COVID-19 restriction period to the post–COVID-19 restriction period (Yates $\chi^2[1]$, $p = 0.01$).

CONCLUSION: This study indicates that both B19 and HAV NAT positivity rates decreased significantly in plasma specimens after the implementation of COVID-19 restrictions in Canada.

P07

Comparison of matrix-assisted laser desorption-ionization time-of-flight mass spectrometry with internal transcribed spacer sequencing for identification of filamentous molds

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OBJECTIVES: Identification of molds using matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry has been explored as a supplement to microscopic identification. We aimed to compare the performance of MALDI-TOF for mold identification with that of internal transcribed spacer (ITS) polymerase chain reaction and sequencing.

METHOD: A total of 40 clinical and proficiency testing fungal isolates (9 *Aspergillus* species, 10 other hyaline molds, 8 dematiaceous fungi, 11 dermatophytes, and 2 *Mucorales*

species) were tested on the Bruker Biotyper instrument at 2–3 days of growth, using direct transfer, tube extraction, and liquid culture extraction methods. Mold identification to species was accepted if a score of ≥1.7 was obtained using the Bruker MBT Filamentous Fungal Library 2.0 database or if a score of ≥20 was obtained on the mass spectrometry identification online platform. All isolates were sequenced using an in-house developed ITS sequencing protocol. The final identifications obtained by MALDI-TOF and ITS sequencing were compared. Isolates that gave discrepant results were re-cultured and re-identified morphologically.

RESULTS: There was one case of discrepant identification to the genus level between different MALDI-TOF extraction method–analysis library combinations (an isolate of *Epidermophyton floccosum* that identified as *Tricophyton tonsurans* on the Bruker database). Of 40 isolates, 27 had an acceptable identification to at least the genus level using a MALDI-TOF method; of these, 24 had agreement with the ITS sequencing method to at least the genus level. For the three cases of discrepant results between MALDI-TOF and ITS sequencing, repeat culture and morphological examination confirmed all of the MALDI-TOF results, with the ITS sequencing results being suspicious for contamination.

CONCLUSION: In this study, MALDI-TOF identification of molds had ≥89% agreement with ITS sequencing and was faster and technically simpler. A potential workflow for mold identification could include MALDI-TOF identification followed by ITS sequencing if no acceptable MALDI-TOF result is obtained.

P08

Use of MassARRAY system for the detection of SARS-CoV-2

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OBJECTIVES: The key to preventing the spread and propagation of this coronavirus disease 2019 (COVID-19) pandemic is the early identification and isolation of infectious patients. Various methodologies and diagnostic platforms are available. The current gold standard for COVID-19 diagnosis is real-time reverse transcriptase polymerase chain reaction (RT-PCR). To overcome the limitations posed by short supply experienced early during the pandemic and to increase our capacity, we assessed the performance the MassARRAY System (Agena Bioscience, San Diego, California).

METHOD: The MassARRAY System combines RT-PCR with high-throughput mass spectrometry processing. We compared the MassARRAY performance with a research-use-only E-gene/EAV assay (catalogue no. 40-0776-96; TIB Molbiol, Berlin, Germany) and RNA Virus Master (catalogue no. 06754155001; Roche) PCR. Discordant results were tested with a laboratory-developed assay using the Corman et al. E-gene primers and probes.

RESULTS: One hundred eighty-six patient specimens were analyzed using the MassARRAY severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Panel. The performance characteristics were as follows: positive agreement was 85.71% (95% CI 78.12% to 91.45%) and negative agreement was 96.67% (95% CI 88.47% to 99.59%). Of 186 results, 19 (10.2%) were found to be discordant and assessed by a different assay, with the exception of 1 for which the sample was not available for repeat testing. Of 18, 14 agreed with the MassARRAY after testing with the secondary assay. The overall performance after discordance testing was as follows: positive agreement was 97.3% (95% CI 90.58% to 99.67%) and negative agreement was 97.14% (95% CI 91.88% to 99.41%).

CONCLUSION: Our study demonstrates that the MassARRAY System is an accurate and sensitive method of SARS-CoV-2 detection. After discordant agreement with an alternate RT-PCR test, the performance was found to have sensitivity, specificity, and accuracy exceeding 97%, making it a viable diagnostic tool. It can be used as an alternative method during periods when real-time RT-PCR reagent supply chains are disrupted.

P09

Evaluation of the 2018–2019 influenza vaccine effectiveness against medically attended influenza using electronic medical records and claims data

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OBJECTIVES: Health administrative databases are a rich source of information that can be leveraged to estimate real-world influenza vaccine effectiveness (VE). We aimed

to evaluate the VE of standard egg-based influenza vaccines compared with no vaccination.

METHOD: This retrospective cohort study was conducted during the 2018–2019 influenza season. All individuals aged ≥3 years who had at least one relevant record per year between 2015 and 2019 in their primary care electronic medical record were included. Individuals were considered protected 14 days after receiving a standard egg-based influenza vaccine. The outcome was the first occurrence of medically attended influenza defined by clinical diagnostic codes (J09, J10, J11) in primary care or hospital settings. Adjusted odds ratios (aORs) were derived from multivariate logistic regression, and adjusted VE (aVEs) were calculated using 100 × (1-aORs).

RESULTS: A total of 5,066,980 individuals were included, with 1,307,702 (25.8%) vaccinated individuals. Median age was 54 (interquartile range 32–66), and 58.1% were female. Moderate vaccine protection was observed in children with aVEs of 28.9% (99% CI 26.2% to 31.5%) and 13.6% (99% CI 10.0% to 17.1%) in 3–8 years and 9–17 years, respectively. Negative aVEs were observed in adults: –16.8% (99% CI –22.3% to -11.5%) in 18–49 years, –8.5% (99% CI –13.8% to –3.4%) in 50–64 years, –18.5% (99% CI -29.4% to -8.5%) in 65–74 years, and –21.3% (99% CI –34.5% to –9.3%) in ≥75 years. When stratified by the number of primary care visits, aVE estimates increased, resulting in significant positive vaccine protection in frequent health care users.

CONCLUSION: Although analysis found that adult vaccines were at higher risk of medically attended influenza during the 2018–2019 season, this was likely due to detection bias and misclassification of exposure status, correlated with health care–seeking behaviour. This might have affected the results leading to an underestimation of the 2018–2019 influenza VE.

P10

SARS-CoV-2 seroprevalence in the vaccine era: The Canadian Blood Services Serosurvey, January–September 2021

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OBJECTIVES: Seroprevalence studies bridge the gap left from case detection and vaccination records. Using residual blood from healthy blood donors, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seroprevalence was evaluated Canada-wide over vaccine deployment.

METHOD: Between January and September 2021, serial cross-sectional samples from blood donors at all Canadian Blood Services locations were included. The Roche Elecsys anti–SARS-CoV-2 antibody assays detect total antibodies to spike (S) and nucleocapsid (N) proteins. Anti-S was analyzed neat and 1:10 dilution until August; in September, the dilution changed to 1:400. Seroprevalence was standardized to population-level demographics and assay characteristics adjusted using the Rogan-Gladen equation.

RESULTS: Of 128,018 samples, the percentage anti-S positive increased from 2.78% (95% CI 2.6% to 3.0%) to 97.0% (95% CI 96.6% to 97.4%), and anti-N increased from 2.24% (95% CI 2.2% to 2.4%) to 4.4% (95% CI 4.0% to 4.8%). The percentage anti-N positive peaked highest in Alberta (8.3%; 95% CI 6.8% to 9.7%) and the Prairies (5.9%; 95% CI 4.7% to 7.2%); was lowest in Atlantic region (0.7%; 95% CI 0% to 1.3%); was higher among those aged 17–24 years (9.3%; 95% CI 8.0% to 10.6%) and racialized donors (8.9%; 95% CI 7.5% to 10.4%). The percentage anti-S positive increased first in donors aged older than 60 years; all peaked by July. By September, the median anti-S concentration was as follows: 17–24 years, 5,005 U/mL (interquartile range [IQR] 2,902 to 8,227); 30–39 years, 4,059 (IQR 1,871 to 5,507); 40–59 years, 3,077 (IQR 1,344 to 5,365); 60–69 years, 2,818 (IQR 1,195 to 5,202), and 70 years and older, 2,597 (IQR 989 to 4,587).

CONCLUSION: SARS-CoV-2 seroprevalence due to natural infection was below 5% in 2021, but cumulative seroprevalence was likely higher because waning antibody was not considered. Anti-S seroprevalence was largely due to vaccination. The early increase in older donors is consistent with vaccine roll-out policies prioritized by age. Lower anti-S concentrations in older individuals are likely related to waning antibody with longer time since second vaccine dose; a muted response with older age has not been ruled out. Ongoing monitoring of seroprevalence continues to be important for public health policies, including a potential third dose of vaccine.

P11

A qualitative study evaluating barriers and enablers to improving antimicrobial use for bacteriuria in hospitalized adults

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OBJECTIVES: Inappropriate use of antimicrobial agents for treatment of bacteriuria is commonly reported. The objective of this study was to explore barriers and enablers to improving management of urinary tract infections (UTIs) and asymptomatic bacteriuria (ASB) in hospitalized adults.

METHOD: A multidisciplinary group of health care providers was recruited to participate in focus groups between May and July 2019. Nurses, nurse practitioners, physicians, and pharmacists involved in the assessment, diagnosis, and treatment of UTIs and ASB in hospitalized patients were included. Each focus group lasted 60–90 minutes and consisted of five to eight participants. Focus group discussions were facilitated by a research coordinator using an interview guide that consisted of open-ended questions coded to the theoretical domains framework (TDF) V2. Discussions were transcribed verbatim. Data were coded to the TDF independently by two members of the research team, then compared. Thematic analysis was used to identify themes.

RESULTS: Five semi-structured focus groups were conducted. Thirty-three health care providers from five hospitals participated — 15 pharmacists, 11 nurses or nurse practitioners, and 7 physicians. Diagnostic challenges, organizational structure, and education were the main themes discussed. Barriers and enablers to improving management of bacteriuria were mapped to 12 of the 14 theoretical domains. Barriers identified by participants that were most extensively discussed included workload and documentation (*environmental context and resources*), confidence in diagnosing UTIs and ASB (*belief about capabilities*), ordering of urine cultures (*social/professional role and identity*), and influence of patients, caregivers, or both (*social influences*). Key enablers highlighted by participants included education (*environmental context and resources*) and feedback or collaboration with colleagues (*social influences*).

CONCLUSION: Health care providers highlighted barriers and recognized facilitators that may improve delivery of care to patients with bacteriuria. A wide range of barriers at the individual and organization levels should be addressed to improve management of bacteriuria.

P12

Universal pre-operative SARS-CoV-2 screening by RT-PCR in Manitoba: Results and cost analysis

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OBJECTIVES: The utility of universal pre-surgical screening for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is not established. Although detection of positive cases before intubation may reduce exposure for health care workers and patients, prevalence is low, and detection of post-infectious cases may result in unnecessary delay of surgery and poor patient outcomes. We report on the results and cost efficiency of universal pre-operative screening in Manitoba during both inter-epidemic and epidemic periods of the coronavirus disease 2019 (COVID-19) pandemic.

METHOD: All pre-operative SARS-CoV-2 reverse transcription polymerase chain reaction tests in Manitoba between January 1, 2021, and October 24, 2021, were analyzed using the laboratory information system. Positive counts and proportions in pre-operative tests were compared with provincial counts and proportions. Where available, cycle thresholds (Cts) for positive tests were reviewed to determine likelihood of infectious case detections, defined as Ct value <30. Cost analysis was performed using actual reagent costs and labour costs of $0.83 per workload unit.

RESULTS: Two hundred nine pre-operative SARS-CoV-2-positive samples were identified province-wide, accounting for 0.55% of 38,062 total provincial cases and 0.43% of 48,231 pre-operative tests. Pre-operative tests accounted for 27.2% of all SARS-CoV-2 testing by the hospital laboratories. Of 37,451 pre-operative tests with an available Ct value, only 37 (0.1%) had Ct values <30 potentially corresponding with an infectious case, and 105 detections had Ct values >30. During the study period, each potentially infectious case cost ~$12,150 in materials and ~$25,300 in labour. Cost efficiency was even lower during inter-epidemic periods and after widespread availability of vaccines.

CONCLUSION: Despite epidemic activity, screening asymptomatic pre-operative patients for SARS-CoV-2 has a low yield (number needed to test >1,000 per infectious case) and utilizes laboratory resources inefficiently. Moreover, 74% of positive pre-operative tests have Ct values >30, possibly suggesting remote infection that may delay surgery. This practice should be re-evaluated, and alternative approaches considered.

P13

A 60-minute turnaround time for influenza and respiratory syncytial virus PCR at emergency triage leads to a significant reduction in investigations and hospitalisations

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OBJECTIVES: To evaluate the impact of a reduced turnaround time by implanting influenza–respiratory syncytial virus (RSV) screening at emergency triage on clinical investigations and hospitalisations.

METHOD: During the 2019–2020 flu season, a protocol of influenza–RSV screening was implanted at emergency triage in Rimouski Regional Hospital for patients with flu-like symptoms, and rapid testing was done using the Cobas Liat platform. The resulting turnaround times, number of patients with antibiotic prescriptions, additional testing (imaging) or laboratory analyses (serology, hematology, microbiology), and number of hospitalisations were compared with those of the previous season (2018–2019), where no emergency triage screening was present and where testing was done using the Simplexa Focus platform. Results were collected with electronic medical records and analysed using Epi Info 7.2.3 (https://www.cdc.gov/epiinfo/support/downloads.html). This study was approved by the CISSS ethics committee.

RESULTS: A total of 576 tests were done at the emergency room during the first season (2018–2019), and 1,161 were done during the second season (2019–2020). The positive rates were 44% (flu 27%, RSV 17%) during the first season, and 50% (flu 43%, RSV 9%) during the second season. The median turnaround time was reduced from 7.1 hours to 0.9 hours ($p < 0.001$). A reduction in investigations was observed, particularly in positive patients. Namely, hemocultures went from 31% to 13% ($p < 0.001$); urine analyses, from 15% to 7% ($p < 0.001$); urine cultures, from 14% to 7% ($p < 0.001$); blood pictures from 44% to 23% ($p < 0.001$); and chest X-ray from 68% to 35% ($p < 0.001$). Antibiotics administration in the emergency room went from 33% to 18% ($p < 0.001$), and hospitalisations were also reduced from 23% to 11% ($p < 0.001$).

CONCLUSION: A reduced turnaround time in influenza–RSV detection allows a faster diagnosis of patients with flu-like symptoms, leading to reduced additional investigations, hospitalisations, and antibiotics prescription.

P14

Antibiotic prescription rates in long-term-care facilities during the SARS-CoV-2 pandemic in British Columbia and Ontario

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OBJECTIVES: To determine the impact of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus and resulting control measures on antibiotic prescribing in long-term-care facilities (LTCFs) in British Columbia and Ontario during the first wave of the pandemic.

METHOD: Antibiotic prescription data were collected for LCTF patients aged 65 years and older in British Columbia and Ontario from epidemiological week 10 to 27 (~March–June) for 2017–2020. Weekly prescription rates per 1,000 residents, stratified by sex and antibiotic class, were calculated. Rates during 2020 were compared with historical averages. Interrupted time series analyses are currently being undertaken to quantify the change in prescription rates.

RESULTS: In total, 18,785 LTCF residents from British Columbia and 73,228 from Ontario were prescribed an antibiotic, of whom 65% (British Columbia) and 68% (Ontario) were female. In total 57,441 (British Columbia) and 163,921 (Ontario) antibiotic courses were prescribed during the period studied.

Overall rates in 2020 were below historical values for both provinces, although more pronounced for Ontario (–11.1%) compared with British Columbia (–4.8%; see Figure P14-1). Prescription rates in British Columbia were mostly below historical values for men, but not for women. In Ontario, prescription rates were below historical values for both sexes. In both provinces, a decrease in antibiotic prescriptions was observed for beta-lactams, quinolones, and sulfonamides–trimethoprim. In Ontario, a decrease was also observed in prescriptions for macrolides, lincosamides, and streptogramins, and prescription rates in British Columbia for this class were above historical values. Prescription rates for tetracycline were above historical values in Ontario.

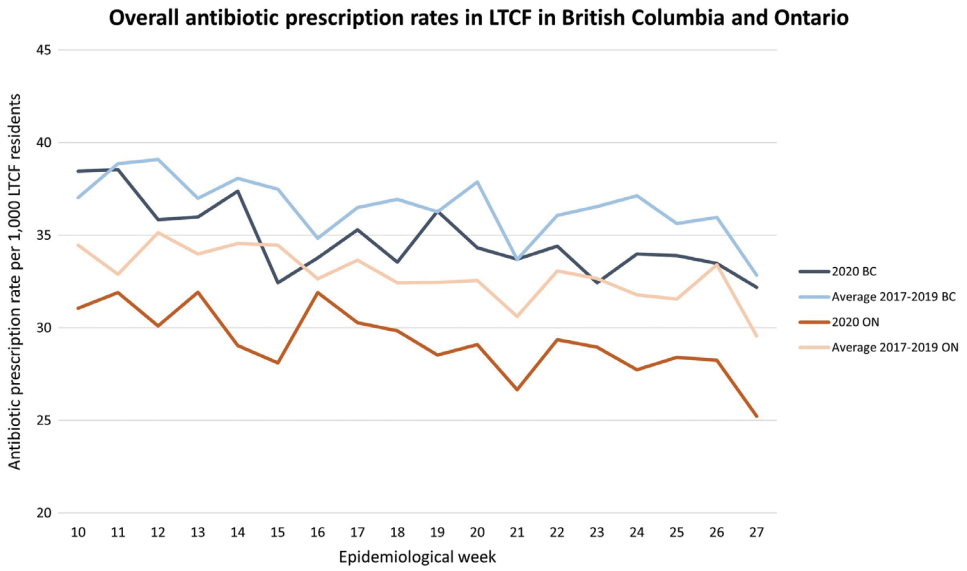

Figure P14-1: Overall antibiotic prescription rates in LTCF in British Columbia and Ontario

CONCLUSION: Antibiotic prescription rates in LTCFs during the first wave of the SARS-CoV-2 pandemic were below historical values for both provinces, although more pronounced for Ontario. This difference might be related to lower physician visits or fewer respiratory tract infections in Ontario compared with British Columbia and should be seen in the light of differences in LTCF systems and response to the pandemic between both provinces.

P15

Implementation of a prospective audit and feedback pilot project among medical and radiation oncology inpatients

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OBJECTIVES: Patients with cancer are more vulnerable to infections and tend to be complex from an infectious diseases perspective. A two-phase approach was taken to implement an antimicrobial stewardship (AMS) service pilot project. Phase 1 of the initiative was a point prevalence assessment to review antimicrobial use and identify the potential scope for AMS in the target inpatient populations. Phase 2 was implementation of a pilot prospective audit and feedback (PAF) service for these patients.

METHOD: In phase 1, two assessors conducted monthly prospective point prevalence surveys on all antimicrobial therapy for medical and radiation oncology inpatients admitted to a tertiary care centre from September to December 2020, assessing each regimen for concordance with guidelines and general AMS principles. In phase 2, PAF was conducted for these inpatients twice weekly, from February to May 2021, by AMS pharmacists. An infectious diseases physician was available for consultation as needed. The primary outcomes were percentage of AMS-concordant regimens and acceptance rate of AMS recommendations.

RESULTS: During the point prevalence assessment, 38 cases were reviewed, and of these, 11 (29%) were AMS concordant, whereas 27 (71%) warranted AMS recommendations. During the PAF pilot, 306 patients were reviewed, 94 were on prophylactic therapy only, and 42 already had a formal infectious diseases consultation. Seventy-five recommendations were made for 50 of 170 patients with a full or partial acceptance rate of 76%.

CONCLUSION: A PAF pilot service was effectively implemented in medical and radiation oncology inpatients at a tertiary care centre that did not have a pre-existing AMS or PAF service for this area. Acceptance rates for recommendations were similar to those in other patient populations within the same institution.

P16

In the era of universal coverage of direct-acting antiviral agents, which barriers to and facilitators of HCV treatment initiation persist among people who inject drugs?

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OBJECTIVES: Barriers to hepatitis C virus (HCV) treatment initiation, such as incarceration and cocaine use, were previously identified among people who inject drugs (PWID). Whether these barriers persist since the universal coverage of direct-acting antivirals (DAAs) has not been documented. We assessed the temporal evolution of HCV treatment initiation and associated factors, comparing eras of interferon-based regimens (2011–2013), restricted access to DAAs (2014–2018), and universal DAA coverage (2018–2020).

METHOD: We included chronically HCV-infected participants followed in a community-based PWID cohort between 2011 and 2020 in a Canadian city. Socio-demographic, drug use behaviour, incarceration, and health services utilization data were collected at 3-month intervals. Self-reported treatment initiation was validated in medical charts. A time-updated multivariable Cox regression was conducted to examine factors associated with treatment initiation in the three eras.

RESULTS: Of 276 participants (84% male, median age 39), 126 (45.7%) initiated treatment during follow-up. Yearly initiation increased over time, from 3% (95% CI 1% to 8%) in 2011 to 19% (95% CI 13% to 25%) in 2016 and 54% (95% CI 41% to 66%) in 2018. Under universal DAA coverage, odds of treatment initiation were lower for male gender (aHR = 0.34, 95% CI 0.12 to 0.93) relative to previous periods. Cocaine use and recent incarceration were negatively associated with initiation throughout all periods. High-injection frequency as a barrier seems to have improved since DAA introduction (0.33 [95% CI 0.10 to 1.14] versus 0.88 [95% CI 0.52 to 1.51] in 2014–2018 and 0.94 [95% CI 0.46 to 1.93] in 2018–2020). Age >40 years was positively associated with treatment initiation in 2014–2018 (1.97 [95% CI 1.21 to3.21]), but not in other periods. Contact with a primary care provider (PCP) was positively associated with treatment initiation, although estimates were attenuated under universal coverage (1.64 [95% CI 0.79 to 3.41]) relative to 2011–2013 and 2014–2018.

CONCLUSION: Treatment initiation has increased since introduction of universal DAA coverage, including treatment of younger PWID, who did not previously meet liver damage criteria. Barriers such as male gender, incarceration, and cocaine use remain, whereas contact with a PCP appears less effective in reaching those still untreated.

P17

Development and validation of a whole-cell biosensor-based platform for the study of β-lactamase activity and inhibition

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OBJECTIVES: The clinical utility of β-lactam antibiotics has been endangered by the production of β-lactamase enzymes by bacterial pathogens. Administration of β-lactamase inhibitors alongside β-lactams has been effective in overcoming resistance conferred by serine β-lactamases; however, no such inhibitors have been approved for clinical use against metallo-β-lactamases (MBLs). Our aim was to develop and validate a whole-cell biosensor assay that can be used to assess β-lactamase inhibition. We aim to use this assay as a primary screen to identify new MBL inhibitors.

METHOD: The biosensor plasmid was constructed by HiFi assembly, containing *ampR*–P*ampC* and a luminescent reporter (*lux* operon). AmpR detects the accumulation of peptidoglycan catabolites in the bacterial cytoplasm after β-lactam treatment and regulates the expression of the luminescent reporter. *Escherichia coli* BW25113 cells were transformed with the construct for use in β-lactamase inhibition assays. Biosensor cells were co-incubated with β-lactamase–producing *E. coli* and treated with a series of antibiotic–inhibitor combinations. Luminescence readings were taken 2 hours post-treatment and used to determine extent of enzyme inhibition.

RESULTS: Detection of β-lactamase inhibition has been evaluated using three enzymes: TEM-116 (SBL, class A), New Delhi metallo-β-lactamase 1 (NDM-1; MBL, class B), and OXA-48 (SBL, class D). Tazobactam and clavulanic acid–based inhibition of TEM-116 were detectable at levels as low as 25 μM and avibactam at levels as low as 10 μM when administered along with amoxicillin (20 μM). Similar results were observed for avibactam against OXA-48–producing bacteria. A series of reported NDM-1 inhibitors were tested, including ethylenediaminetetraacetic acid, which was detected to inhibit NDM-1 at concentrations as low as 2 μM in combination with 2 μM meropenem.

CONCLUSION: We report a rapid and sensitive cell-based biosensor for the evaluation of β-lactamase activity. This assay will be used as a primary screen with the aim of identifying

novel β-lactamase inhibitors, with a focus on clinically relevant MBLs such as NDM-1, IMP-1, and VIM-2.

P18

Evaluation of the Seegene Allplex™ SARS-CoV-2/FluA/FluB/RSV assay

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OBJECTIVES: As pandemic control measures ease and seasonal incidences of influenza A, influenza B, and respiratory syncytial virus (RSV) increase to pre-pandemic rates, having ready ability to detect severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) simultaneously with these targets is important. This study evaluates the clinical and analytical performance of the combined Seegene Allplex™ SARS-CoV-2/FluA/FluB/RSV assay (Seegene, Seoul, South Korea).

METHOD: Clinical performance was evaluated using archived specimens, including 255 nasopharyngeal (NP) swabs and 151 saline gargles (SGs). NP and SG specimens were originally run on the Allplex 2019-nCoV assay for detection of SARS-CoV-2, and NP swabs were run on the Allplex Respiratory Virus Essential Assay for detection of influenza A and B and RSV. Positive predictive agreement (PPA) and negative predictive agreement (NPA) with the combined assay was calculated for each target. Analytical performance was assessed by determining the limit of detection (LOD), stability, the reproducibility, and response to heat treatment. Samples were extracted on the STARlet in vitro diagnostic (IVD) liquid handler (Seegene, Seoul, South Korea), then were set up for polymerase chain reaction (PCR) using the Allplex SARS-CoV-2/FluA/FluB/RSV assay on the STARlet. PCR was run on the CFX96TM IVD thermocycler (BioRad, Hercules, California).

RESULTS: The clinical evaluation of NP specimens resulted in a PPA of 98.9% for SARS-CoV-2, 98.0% for influenza A, 100.0% for influenza B, and 95% for RSV. The NPA was 100.0% for all targets. For SGs, PPA and NPA were 100.0% for all targets. Heat inactivation had minimal impact on performance for both specimen types. A 5-day stability at 22°C and 4°C presented acceptable variations. NP LOD for all targets varied between 137 to 1,286 copies/mL, and SG LOD varied between 329 to 2,506 copies/mL.

CONCLUSION: The Allplex SARS-CoV-2/FluA/FluB/RSV assay is suitable for the detection of SARS-CoV-2, influenza A and B and RSV from NP swabs, and SARS-CoV-2 from SGs.

P19

Comparison of the GeneXpert® Xpress Strep A and ID NOW A2 molecular assays with throat culture for diagnosis of group A *Streptococcus* pharyngitis

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OBJECTIVES: The gold standard for diagnosis of group A *Streptococcus* (GAS) pharyngitis is throat cultures (TCs), which take 1–2 days to complete and may contribute to inappropriate antibiotic utilization. This study evaluated the performance of the ID NOW A2 (Abbott Diagnostics, Mississauga, Ontario) and GeneXpert® Xpress Strep A (Cepheid, Sunnyville, California) molecular assays to diagnose GAS

METHOD: One hundred throat ESwabs™ (COPAN, Murrieta, California) collected during routine clinical care were cultured. Of these, 50 were GAS positive and 50 were GAS negative, with 23 positive for other oropharyngeal bacteria. Blood agar plates (Oxoid, Nepean, Ontario) were incubated at 35°C anaerobically for up to 48 hours. Any beta-hemolytic colonies were identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (Bruker, Bremen, Germany). Specimens were frozen at –80°C after inoculation for further molecular testing. Three experimental conditions were evaluated on ID NOW to determine the most accurate testing method using ESwabs. The study proceeded with the proprietary swabs being instilled into the ESwab liquid Amies fluid, then being placed into the sample receiver and run as per manufacturer's recommendations. The Xpress Strep A was run as per manufacturer's recommendations. The time to run the molecular tests was compared.

RESULTS: Both molecular assays demonstrated 100% (95% CI 92.9% to 100%) sensitivity and specificity compared with TC. For ID NOW A2 assay, positive results were available within 1:49–2:30 minutes for a positive and 6:09 minutes for a negative. For Xpert Strep A assay, results were available within 17:22–22:44 minutes, and negative results were available within 33:45 minutes.

CONCLUSION: Both the ID NOW A2 and Xpress Strep A assays performed comparably to TC in diagnosis of GAS pharyngitis but provided results 1–2 days sooner than would be expected with culture. Implementation of these assays would improve patient care and assist in appropriate antibiotic use.

P20

Hepatitis B rates are lower among Canadian blood donors born in hepatitis B vaccine–eligible years, 2005–2020

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OBJECTIVES: Blood donors without hepatitis B virus (HBV) sexual and percutaneous risks are tested for HBV. We aimed to measure the prevalence of HBV among first-time Canadian Blood Services (CBS) blood donors across Canada from 2005 to 2020 and determine whether being born in a cohort eligible for HBV vaccination in Canada was associated with testing positive for hepatitis B.

METHOD: We calculated the HBV-positive rate among first-time blood donor samples collected from 2005 to 2020. Samples were tested for HBV surface antigen (HbsAg; Abbott PRISM analyzer, Abbott, Chicago, Illinois); HBV nucleic acid testing (NAT; Roche 6800/8800 System, Roche Molecular Systems, Pleasonton, California). HbsAg was confirmed by neutralization; anti-HBc and NAT were unconfirmed. First-time donors from 2005 to 2020 in all provinces except Quebec were stratified by provincial HBV vaccine eligibility by year of birth and residing province. Logistic regression models adjusted for sex assessed the association between HBV positivity and birth cohort and residing province.

RESULTS: The HBV positive rate (HbsAg or HBV NAT) was 61.5 per 100,000 (pht) donors in 2005; 46.5 pht in 2020; highest in males at 85 pht and ages 30–49 years (79 pht) in 2020. From 2005 to 2020, the odds of testing HBV positive were higher for males (odds ratio [OR] 2.1, 95% CI 2.7 to 3.6), being in a vaccine-ineligible birth cohort (OR 1.9, 95% CI 1.6 to 2.2), and residing in British Columbia (OR 1.3, 95% CI 1.05 to 1.5) but lower if residing in Manitoba (OR 0.7, 95% CI 0.5 to 0.99) or the Atlantic region (OR 0.3, 95% CI 0.2 to 0.4).

CONCLUSION: Among first-time blood donors from 2005 to 2020, being born in an HBV vaccination–eligible year was protective against HBV infection. This supports the continued use of HBV vaccination programs across Canada.

P21

Hepatitis B virus genotype surveillance among Canadian blood donors and the referred patient population, 2016–2021

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OBJECTIVES: More than 250,000 individuals chronically infected with hepatitis B virus (HBV) are estimated to live in Canada. HBV genotypes have a distinct geographic distribution and are highly associated with country of birth. Canada has experienced increased immigration over the past 10 years, primarily from regions that include HBV-endemic countries. This study aimed to investigate the proportions and trends of HBV genotypes within blood donor and clinical populations of Canada over the past 6 years (2016–2021).

METHOD: Study samples involved two cohorts: (1) Canadian blood donors (n = 234) deferred from donation because of HBV surface antigen , HBV DNA, or anti-hepatitis B core antibody positivity and (2) HBV DNA positive patients from across Canada (clinical referred population, n = 3,539). Plasma or serum was extracted, the HbsAg or polymerase coding region amplified, and Sanger or next generation sequenced to allow genotype determination by phylogenetic analysis.

RESULTS: Six HBV genotypes were detected among deferred blood donors (A–E, G), and eight genotypes were detected among the clinical referred population (A–H and C/D), with the highest proportion among genotypes D and A, respectively.

Differences in HBV genotype proportions among the two cohorts were observed across most provinces. Males made up most of the referred population among genotypes A–E ($p < 0.0001$), except for genotypes B and C. The mean age was 43.5 years (95% CI 43.02 to 43.98), with significant mean age differences observed among genotypes A to E ($p < 0.0001$). Distinct trends of increasing (D+E, referred; A+B, blood donor) and decreasing (C, referred; D, blood donor) genotype prevalence were observed over the study period.

CONCLUSION: HBV genotypes in Canada are highly diverse and represent a large immigrant population. Observed trends in genotype prevalence imply shifts among the HBV-infected population of Canada that warrants continued surveillance. Proportional differences in HBV genotypes between blood donors and the clinical referred population require further study.

P22

Increasing SARS-CoV-2 testing capacity through specimen pooling: An acute care centre experience

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OBJECTIVES: Innovation in laboratory testing algorithms to address seemingly uncontrollable global supply chain shortages in plastics and other consumables during emergencies such as the current coronavirus disease 2019 (COVID-19) pandemic are urgently needed. We report our experience with specimen pooling on severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing in an acute-care hospital microbiology laboratory during a high testing demand period that exceeded available processing capacity.

METHOD: Fifty-five positive COVID-19 nasopharyngeal specimens were pooled one in four with previously tested negative specimens. A Hamilton STARline liquid handler was programmed to prepare and track each pool. Correlation and agreement were calculated. A custom Excel (Microsoft Corp., Redmond, Washington) tool was designed for use by the technologists to aid interpretation, verification, and result entry. The primary specimens from the positive pools were returned to the individual testing stream. Using the Excel tool, individual results were reported directly into the electronic medical record from negative pools by the laboratory technologist. Cost-per-test impact for pooling was measured in reference to the consumable cost only and was denoted as the percentage reduction in cost versus the baseline cost-per-test of the individual testing stream.

RESULTS: Validation showed a strong correlation between the signals observed when testing specimens individually versus those that were pooled. Average crossing point difference was 1.352 cycles (95% CI –0.235 to 2.940). Overall agreement observed between individually and pooled tested specimens was 96.8%. Stratified agreement showed an expected decreased performance of pooling for weakly positive specimens dropping below 60% after Cp 35.

CONCLUSION: Post-implementation data showed the consumable cost -savings achieved through this algorithm was 85.5% after 8 months, creating both testing and resource capacity. The clinical significance of the observed decreased performance with lower viral loads is questionable. Pooling is an effective method to use for SARS-CoV-2 testing during the current pandemic to address resource shortages and provide quick turnaround time for high test volumes without compromising performance.

P23

Real-life experience with intravenous fosfomycin in Canada: Results from the CLEAR (Canadian Leadership on Antimicrobial Real-life usage) registry

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OBJECTIVES: Intravenous (IV) fosfomycin is Health Canada approved to treat a variety of infections. We report on the use of IV fosfomycin in Canada

METHOD: An IV Fosfomycin usage questionnaire was developed and received approval from the University Ethics Committee (April 2019). The Canadian Leadership on Antimicrobial Real-life usage (CLEAR) registry uses the web-based research data management program, REDCap® (Research Electronic Data Capture; Vanderbilt University, Nashville, Tennessee) (https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=F7JXNDFXEF) to facilitate clinicians voluntarily entering details associated with their clinical experiences using IV fosfomycin.

RESULTS: As of December 13, 2021, data were available for 18 patients. Infections treated were bacteremia–sepsis ($n = 5$), hospital-acquired bacterial pneumonia ($n = 3$), complicated urinary tract infection (cUTI) ($n = 2$), ventilator-associated pneumonia ($n = 2$), community-acquired pneumonia ($n = 2$), bone and joint infection ($n = 2$), central nervous system infection ($n = 1$), and complicated intra-abdominal infection ($n = 1$). IV fosfomycin was used as directed therapy to treat *Escherichia coli* (one extended spectrum beta-lactamase [ESBL] and two carbapenem-resistant Enterobacterales [CRE]), *Klebsiella* spp (one ESBL and two CRE), *Pseudomonas aeruginosa* ($n = 6$), vancomycin-resistant *Enterococcus faecium* ($n = 2$), methicillin-resistant *Staphylococcus aureus* ($n = 2$). and *Klebsiella pneumoniae* carbapenemase–producing *Citrobacter* spp. IV fosfomycin susceptibility testing was performed on 77.8% of isolates. IV fosfomycin was primarily used in combination with other antimicrobials (88.8%). IV fosfomycin was used because of resistance to ($n = 13$) and failure of ($n = 5$) previously prescribed antimicrobials. Dosage regimen was customized in all patients on the basis of creatinine clearance. Most common treatment duration was >10 days ($n = 10$). Microbiological success was 87.5% (eradicated or presumed eradicated); clinical success was 88.2% (cured or improved). Thirty-day mortality was 5.6%. Six patients had adverse effects (hypokalemia [$n = 4$], gastrointestinal upset [$n = 1$], and elevated alanine transaminase [$n = 1$]; none resulted in discontinuation).

CONCLUSION: In Canada, IV fosfomycin is used to treat a variety of severe infections caused by pathogens resistant to other antimicrobials. Other than for cUTI, it is used in combination with other antimicrobials with high microbiological and clinical cure rates. More data are needed to fully elucidate the efficacy and safety of IV fosfomycin in Canada.

P24

Rapid and accurate detection of hepatitis B antiviral drug resistance mutations using next-generation sequencing with R10.4 flow cells on the Oxford GridION

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OBJECTIVES: Antiviral drugs (AVD) such as lamivudine, entecavir, or tenofovir, which inhibit the viral polymerase enzyme, have been used for the treatment of chronic hepatitis B (HBV). With long-term AVD use, resistance mutations may occur in the *pol* gene. Detection of these resistance mutations is crucial for proper patient management. We investigated next-generation sequencing of the *pol* gene using GridION and the recently introduced R10.4 flow cells (Oxford Nanopore Technologies, Oxford, United Kingdom), designed to improve homopolymer reading and consensus accuracy.

METHOD: The procedure consisted of DNA extraction from plasma samples (MagNA Pure 24, Roche Molecular Systems, Branchburg, New Jersey), polymerase chain reaction to amplify an 820 bp region of *pol* gene covering the most common resistance mutations, library preparation using the Q20+ kit, sequencing to >8,000X coverage on the R10.4 flow cell, and bioinformatic analysis using Geneious (Biomatters, Auckland, New Zealand) and ABL TherapyEdge (Luxembourg). Patient samples were previously sequenced using a comparator method (laboratory-developed Illumina Miseq assay).

Table P24-1: Basecalling accuracy for codons associated with HBVDR

Amino acid	Basecalling accuracy (%)
M204	
A	99.7
T	99.6
G	99.3
N236	
A	99.5
A	99.1
C	99.1
L180	
T	99.5
T	99.3
G	99.3
M250	
A	99.3
T	99.2
G	99.3

RESULTS: The basecalling and codon calling accuracy were determined for the HBV World Health Organization international standard for the most common AVD resistance (AVDR) mutations. False positive AVDR mutations were called at <0.2% for these codons. One known positive patient sample with six mutations ranging from 4% to 50% of the viral load was sequenced. All six mutations were detected with similar mutation loads as our comparator method. The procedure could be performed in a single day.

CONCLUSION: The R10.4 flow cells and Q20+ library kit show promise in sequencing HBV for detection of AVDR mutations. Basecalling error rates in the order of 1% should enable AVDR calling at >5% mutation load with confidence, although further validation is required.

P25

Optimizing recovery of Shiga toxin-producing *Escherichia coli* from PCR-positive feces

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OBJECTIVES: When using polymerase chain reaction (PCR) to detect Shiga toxin–producing *Escherichia coli* (STEC), subsequent culture is critical for public health and clinical management. We therefore examined the ability of different culture methods to recover from PCR-positive feces.

METHOD: Clinical fecal specimens submitted for diagnosis of bacterial gastroenteritis were tested using the BD MAX™ Enteric Bacterial Panel PCR (BD, Franklin Lakes, New Jersey). During the study period, all specimens positive by PCR for STEC were cultured in gram-negative broth (GNB), in trypticase soy broth (TSB), and on STEC CHROMAgar™ (DRG International, Springfield, New Jersey). The Shiga Toxin QuikChek™ assay, which detects Shiga toxin 1 and 2 proteins, was performed from GNB, TSB, and suspect STEC colonies on the CHROMAgar. Laboratory technologists recorded the QuikChek results and the ease of interpretation for each culture method. The public health laboratory attempted to recover an isolate in all new QuikChek-positive cases.

RESULTS: From July 8 to October 20, 2021, 40 of 59 PCR-positive feces were positive by any culture method. All methods had similar sensitivities when compared with the composite culture result (83% for CHROMAgar, 80% for TSB, and 83% for GNB). The sensitivities of TSB and GNB compared with CHROMagar were 85% and 82%, respectively. The combination of GNB and chromogenic media was 98% sensitive compared with composite. One sample was positive by TSB only, three by GNB only, and four by CHROMagar only. The QuikChek bands from positive cultures were faint in 56% of samples from TSB, 18% from GNB, and 0% from the CHROMagar. An isolate was recovered for serotyping in all new QuikChek-positive cases (n = 36; four repeat cases).

CONCLUSION: A combination of a broth (preferably GNB) and chromogenic media provide optimal recovery of STEC from PCR-positive fecal specimens, with little added benefit of a second broth. New methods are needed to enhance recovery rate of culture or perform molecular typing without an isolate.

P26

Verification of the Xpert® Xpress SARS-CoV-2 assay for the detection of SARS-CoV-2 from nasopharyngeal specimens in transport media and saliva specimens collected in Spectrum™ kits

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OBJECTIVES: To verify the performance of Xpert® Xpress severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) assay and the GeneXpert Dx system for the detection of SARS-CoV-2 virus from nasopharyngeal (NP) specimens in transport media as well as from saliva specimens collected in Spectrum™ SDNA-1000 collection kits. The Xpert Xpress SARS-CoV-2 assay is a rapid, multiplexed real-time polymerase chain reaction test that offers detection of SARS-CoV-2 E gene and N2 gene. Results are interpreted automatically by the GeneXpert System and are based on the detection of respective gene targets and specimen controls. There has been limited yet promising data for the system's utilization with saliva specimens, which may offer a valuable alternate to nasopharyngeal specimens.

METHOD: Sixty-four archived clinical specimens previously tested at our microbiology laboratory were used in this study. Thirty-four specimens were NP specimens and 30 were saliva specimens. Thirty-four specimens were positive for SARS-CoV-2 and 30 specimens were negative. Of the positive specimens, 14 were NP swabs and 20 were saliva

specimens in Spectrum. Four specimens with S gene target failure were included in this study. AccuPlex™ SARS-CoV-2 reference material (LGC Clinical Diagnostics) containing 5,000 copies/mL of recombinant SARS-CoV-2 was used for a limit-of-detection study using serial dilutions of the reference material, each run in triplicate. For precision studies, two positive samples were run each in triplicate over 3 days.

RESULTS: The Xpert Xpress SARS-CoV-2 assay had 100% sensitivity and specificity for the detection of SARS-CoV-2 virus in NP and saliva specimens. The limit of detection was found to be 20 copies per reaction. The coefficient of variation was less than 1% for E and N2 genes.

CONCLUSION: The Xpert Xpress SARS-CoV-2 assay is an accurate, rapid test for the detection of SARS-CoV-2 from NP and saliva specimens

P27

Determining COVID-19 community incidence threshold for pre-operative testing

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OBJECTIVES: Pre-operative severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) testing is primarily being used to identify pre- and asymptomatic patients and postpone surgeries if positive to reduce patient risk of developing a potentially severe coronavirus disease 2019 infection postoperatively. This study aimed to analyze the yield of pre-operative testing and to determine an incidence-threshold at which pre-operative testing would prove beneficial.

METHOD: This was a retrospective chart review analyzing data between December 2020 and June 2021 (second and third wave) at an academic health centre. Patients awaiting surgical or other procedures (likely) requiring intubation were included if tested as per protocol within 48 hours of their scheduled procedure by nasopharyngeal swab and polymerase chain reaction analysis. On the basis of cycle threshold (Ct) and availability of repeat tests, we categorized positive cases as follows: A Ct value >30 in single test or >25 followed by negative test or test with higher Ct value was considered remote infection, Ct <25 in first positive or negative repeat test was considered an active infection. Cases with a Ct value of 25–30 and no second test were considered indeterminate. Weekly unlinked cases (ie, no travel history, close contact, or outbreak exposures) were used to calculate the 7-day community incidence rate.

RESULTS: A total of 10,884 pre-operative tests were conducted; 86 (0.79%) returned positive. Among positive specimens, 18 (20.9%) were active, 59 (69.9%) were remote, and 9 (9.2%) were indeterminate infections. Yield with weekly community incidence of <20/100,000 was two active cases (0.05%; 9.1% of the 22 positives) and increased to eight cases (0.21%; 28.57% of the 28 positives) between 20/100,000 and 35/100,000 and eight cases (0.25%; 22.22% of the 36 positives) above 35/100,000.

CONCLUSION: The majority of positive tests were among patients with remote SARS-CoV-2 infection. However, with increased community transmission, the proportion of active infections among positive specimens increased substantially. Thus, we propose a rate of 20/100,000/week of unlinked cases as a cut-off to discontinue pre-operative testing.

P28

Epidemiology of cytomegalovirus antiviral resistance testing for solid organ and bone marrow transplant patients, 2011–2018

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OBJECTIVES: To characterize cytomegalovirus (CMV) antiviral resistance risk factors and mutations in transplant or other severely immunocompromised patients in British Columbia.

METHOD: Genotyping of resistant mutations occurred at the national reference laboratory. Retrospective review of patients with CMV antiviral resistance testing was conducted for the following: patient demographics, transplant type, viral load, antiviral prophylaxis, treatment, and 12-month mortality. Mann–Whitney *U*, *t*, or Fisher exact tests examined differences between patients with and without resistance detection.

RESULTS: Fifty-eight plasma and three tissue or fluid specimens were submitted for antiviral resistance testing. A

total of 27/58 samples (47%) had resistant mutations detected, which occurred more frequently among solid organ (than in haematopoietic stem cell) transplant patients and made up 64% (versus 26%; $p = 0.05$). Significant risk factors for CMV resistance were time from transplant to testing ($p = 0.001$) and previous resistance testing ($p = 0.002$). Patients with resistant CMV had approximately 50 more days of antiviral therapy ($p = 0.03$) and took 44 days longer to clear viremia ($p = 0.006$). The commonest resistance mutations were on the following UL97 loci: A594 (20%), H596 (12%), and L595 (12%). Three samples had mutations on both UL97 and UL54.

CONCLUSION: Longer time out from transplant and previous resistance testing were significantly associated with CMV resistance. Those with resistant CMV received longer antiviral therapy and had longer times to viremia clearance than those without resistant CMV. Most mutations were on UL97, conferring ganciclovir resistance.

P29

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

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OBJECTIVES: Ceftobiprole is an intravenous cephalosporin with broad-spectrum activity and 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 Canadian Leadership on Antimicrobial Real-life usage (CLEAR) registry.

METHOD: A ceftobiprole usage questionnaire was developed using the input of infectious diseases and medical microbiology specialists (physicians and pharmacists) across Canada. The CLEAR registry protocol and 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® (Research Electronic Data Capture) (https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=A8EHM8JJRF) to facilitate clinicians voluntarily entering details associated with their experiences using ceftobiprole.

RESULTS: Data were available for 54 patients (as of December 13, 2021). The most common infections treated with ceftobiprole were endocarditis (40.7% of patients), bone and joint infection (29.6%), and hospital-acquired bacterial pneumonia (11.1%). Of patients, 94.4% had bacteremia and 27.8% were in the intensive care unit. Ceftobiprole was primarily used as directed therapy for methicillin-resistant *Staphylococcus aureus* (MRSA) infections (96.3% of patients). Ceftobiprole susceptibility testing was performed on isolates from 51.9% of patients. It was used concomitantly with daptomycin in 51.9% of patients and with vancomycin in 22.2%. Ceftobiprole was used because of failure of (64.8%), resistance to (16.7%), or adverse effects from or intolerance of (16.7%) previously prescribed antimicrobial agents. The dosage regimen was customized in 98.1% of patients on the basis of their creatinine clearance. Treatment duration was primarily >10 days (66.7% of patients) with microbiological success in 95.8% of patients and clinical success in 85.4%. The 30-day mortality was 7.4%, and 3.8% of patients reported an adverse effect.

CONCLUSION: 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 has an excellent safety profile.

P30

Impact of the Xpert® norovirus assay on laboratory workflow and turnaround time

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OBJECTIVES: Noroviruses commonly cause acute gastroenteritis outbreaks in communal settings, including long-term care facilities and hospitals. Timely identification of positives is crucial for confirmation of active cases and management of potential outbreaks, as well as for diagnostic purposes. Previously, our laboratory utilized a lab-developed real-time

norovirus polymerase chain reaction (PCR) laboratory-developed test (LDT) detecting ORF1–ORF2 sequences in norovirus genogroup I (GI) and genogroup II (GII), which required batching of samples and significant hands-on processing time. We assessed the positive and negative percentage agreement between the Xpert® norovirus assay and LDT. After implementation of the Xpert, we evaluated its impact on laboratory workflow and turnaround time (TAT).

METHOD: Twenty retrospective clinical and proficiency-testing specimens were included in the verification. Of these, 12 (60%) were known positive for GI or GII by the LDT, of which 10 (83%) were stool and 2 (20%) were vomitus. Another 8 stool specimens were known negative for norovirus but positive for other enteric pathogens. After implementation of the Xpert, the workflow of laboratory technologists was surveyed, and TAT was calculated for all clinical specimens from October to December 2021.

RESULTS: The positive and negative percentage agreement was 100% (12/12) and 100% (8/8), respectively. No invalid results occurred during the verification. Cycle threshold (Ct) values of the samples ranged from 16 to 31 and were comparable to the LDT with a Pearson's coefficient of 0.907 (95% CI 0.681 to 0.961). The average hands-on processing time required by laboratory technologists was 3.4 minutes for the Xpert versus 40 minutes for the LDT ($p = 0.0001$). The average TAT was 3.9 hours for the Xpert versus 18.8 hours for the LDT ($p = 0.0337$).

CONCLUSION: The Xpert norovirus assay demonstrated excellent performance compared with the LDT with significantly improved TAT and reduced laboratory workload. This improved TAT can have important implications in outbreak management and initiation of infection control measures to prevent further disease spread.

P31

Evaluation of ng carba 5 and bioMérieux CarbaNP kits for carbapenamase detection

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OBJECTIVES: Carbapenem-resistant Enterobacterales (CPE) are a major public health concern, identified by the World Health Organization as one of the 10 greatest threats to global health. Rapid reporting of the type of gene can affect infection control and treatment. The objective was to assess the performance of the NG Carba5 lateral flow assay and the BioMérieux CarbaNP for the detection of carbapenemase genes.

METHOD: Sixty known polymerase chain reaction–confirmed reference isolates of CPE were subcultured from a –70° freezer. These isolates were then subcultured three times onto blood agar and then 100 µL of 0.5 McFarland suspensions were added to ESwab™ containers and run on the WASP™ and WASPLab (COPAN Diagnostics, Murrieta, California) using Colorex™ Supercarba (CHROMagar™; DRG International, Springfield, New Jersey). Cultures were used for the CarbaNP and Carba5 tests. If negative, they were also tested from SBA.

RESULTS: Of the 60 reference strains, 60 tested positive with the Carba5 kit compared with 57 of 60 with the CarbaNP kit, where 3 OXA strains tested negative.

Table P31-1: Carbapenemase assay results

	CarbaNP+	Carba5+
OXA/NDM	8	8
OXA	11+/3–	14
NDM	8	8
KPC	16	16
IMP	4	4
VIM	10	10

CONCLUSION: Surveillance testing for CPE requires a sensitive method to detect low amounts of organism and low levels of resistance and be timely and cost effective. Results showed the Carba5 kit had a greater sensitivity (100%) than the CarbaNP kit (95%) for detecting carbapenemase genes. The Carba5 kit can delineate between the actual type of carbapenemase gene, is better at detecting OXA genes, and takes 15 minutes to perform.

P32

Microbiology laboratory role in an outbreak with a multi-drug-resistant *Enterobacter cloacae* in a neonatal intensive care unit

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OBJECTIVES: Hospital-acquired infection with antibiotic-resistant organisms (AROs) increases morbidity and health care costs. Early recognition of ARO outbreaks is essential to minimize harm and reduce ongoing transmission. This study illustrates the importance of the microbiology

laboratory in investigation of an outbreak of a novel multidrug resistant Enterobacter (MDRE) in a neonatal intensive care unit (NICU).

METHOD: In May 2019, three neonates at McMaster Children's Hospital developed septicemia with a novel MDRE. An outbreak was declared, and rectal surveillance of all infants and hypothesized environmental sources (eg, sink drains) was organized by a multidisciplinary team. Methods were developed to detect MDRE from swabs: urine chromogenic agar with a gentamicin disk and Colorex™ C3GR (CHROMagar™). The VITEK2 GNI and AST N390 cards were used for identification and susceptibility.

RESULTS: More than 1,000 swabs were tested from May to August 2019. The Colorex C3GR media improved detection and eased workflow as the WASP/WASPLab™ system (COPAN Diagnostics, Murrieta, California) was used for processing. In total, 92 MDRE isolates were detected (from two sink drains and 12 rectal swabs). During the outbreak, eight infections were identified (six bacteremias, one urinary tract infection, one endotracheal aspirate). The molecular laboratory performed 10 pulsed-field gel electrophoresis runs. An additional 40 shifts for MLT were added and 500 VITEK IDS cards were set up. Weekly point prevalence, NICU closure, cohorted nursing and pump rooms, extra cleaning, and facilitated weekly meetings and communications occurred throughout the outbreak.

CONCLUSION: This case study of a novel MDRE outbreak in an NICU illustrates key aspects of outbreak management and highlights the significant increased workload and costs to the microbiology lab to efficiently assist in outbreak management. The microbiology laboratory is an essential member of the outbreak management team and plays a critical role in identifying and understanding the transmission dynamics of ARO outbreaks.

P33

Genetic and phenotypic characterization of the first Canadian case of Ambler class A carbapenemase FRI-8, isolated in Quebec in 2021

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OBJECTIVES: To determine the mechanism of carbapenem resistance in a phenotypically carbapenemase-positive *Enterobacter cloacae* complex (N21-01785) that was negative by polymerase chain reaction (PCR) for common carbapenemase genes.

METHOD: An 87-year-old patient with no known travel history was hospitalized in medicine–palliative care with complaints of increasing low back pain. A rectal swab was taken in the context of an ongoing *Klebsiella pneumoniae* carbapenemase (KPC) outbreak. N21-01785 was isolated from the patient on ChromID CARBA medium and found to be carbapenem resistant and positive for potential carbapenemase production using the modified carbapenem inactivation method. Screening with known carbapenemase genes (KPC, New Delhi metallo-β-lactamase, OXA-48, IMP, VIM, GES, and IMI/NMC) was negative. Whole-genome sequencing (WGS) using the NextSeq Illumina and Oxford Nanopore MinION platform was used to determine mechanism of resistance. Susceptibilities were conducted using microbroth dilution (Sensititre, CAN1MSTF; ThermoFisher Scientific, Waltham, Massachusetts) and standard broth microdilution (BMD).

RESULTS: When tested using BMD, the isolate was resistant to IMI, MEM, and ERT. Sensititre data showed N21-01785 was resistant to ERT, imipenem–relebactam, and colistin; intermediate to MEM; and susceptible to all other antimicrobials tested. Although positive for the modified carbapenem inactivation method test, N21-01785 was negative for carbapenemase production by Rosco (Taastrup, Denmark) Neo-Rapid Carba and Beta-carba testing. Using WGS data, we confirmed the identification of *Enterobacter asburiae* (ST1639) and the presence of $bla_{\text{FRI-8}}$ located on a 148 kb IncFII plasmid. The only other resistance gene found on this plasmid was a truncated *mcr-10*.

CONCLUSION: This is the second occurrence in Quebec of the rare carbapenemase FRI. It is concerning that this clinical isolate was recovered from a patient who did not receive any invasive or antibiotic treatment preceding or during her hospitalization and had no known history of travel. This work highlights the need to use WGS methods for the screening of carbapenemase-producing strains if one considers the growing diversity of carbapenemases missed by conventional PCR.

P34

Implementation of next-generation sequencing workflow for SARS-CoV-2 genomic surveillance in a large acute-care teaching hospital

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OBJECTIVES: The emergence of new severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOC) is a major public health threat. Next-generation sequencing (NGS) has emerged as a powerful and feasible means of surveillance for the emergence of new VOCs. We describe the implementation of an NGS workflow for sequencing SARS-CoV-2–positive specimens, aimed at expediting hospital outbreak investigations and for timely detection of potential novel VOCs.

METHOD: A room dedicated to NGS work was set up and equipped with a thermal cycler, a polymerase chain reaction hood, a mini-centrifuge, a vortex mixer, a magnetic separation rack, a fridge, pipettes, and tips. A validation panel of SARS-CoV-2–positive specimens (E-gene Cp ~19-22; $n = 8$) was used. Sequencing libraries were prepared using NEBNext ARTIC SARS-CoV-2 Companion kit–Oxford Nanopore Technologies (ONT; New England Biolabs, Ipswich, Massachusetts), Ligation Sequencing kit SQK-LSK109, and Native Barcoding Expansion EXP-NBD104 (ONT, Oxford, England) following manufacturer's protocols. SARS-CoV-2 whole-genome sequencing (WGS) was performed on a MinION (ONT) and basecalled by MinIT (ONT). Data were uploaded to the cloud EPI2ME (ONT), where they were further analyzed using the Fastq ARTIC + NextClade workflow.

RESULTS: The NGS program implementation required 5 months for room setup and personnel training. Turnaround time from sample receipt to result verification was 5 days. The reagent cost for each sample was CAD$56.89. All virus strains were 21A (Delta) variant, including AY.4 (4/8 samples), AY.9 (2/8 samples), AY.12 (1/8 samples), and B.1.617.2 (1/8 samples). These were concordant with Public Health Ontario data on variant trends. We also found a complete dropout of amplicon 72 (ARTIC primers V.3) in all sequences.

CONCLUSION: Implementing SARS-CoV-2 WGS workflow in a hospital molecular microbiology laboratory is possible. However, several enhancements are necessary, including cost reduction, sequencing primer improvement, and the need for a bioinformatic pipeline.

P35

Stability characteristics of SARS-CoV-2 virus stored and transported under ambient conditions in various transport media

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OBJECTIVES: Availability of diagnostic testing for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection is a critical component of the pandemic control strategy. However, access to testing can be limited as a result of inadequate health care resources for collection and logistical networks for specimen transport to testing laboratories. One approach to improve community access to SARS-CoV-2 testing includes simplified, decentralized sample collection and reduced reliance on cold chain during specimen transport. The objective of this study was to assess stability of SARS-CoV-2 RNA from self-collected bi-lateral anterior nasal swabs (BLANS) in various commercial viral transport media under various storage conditions using three SARS-CoV-2 molecular detection assays.

METHOD: We evaluated BLANS stability for the detection of SARS-CoV-2 with contrived positive specimens stored at –20°C to 4°C and 18°C to 42°C in the following media types: VTM/UTM, buffered/saline-based media, and inactivating media (guanidine/guanidinium).

RESULTS: Specimens collected in saline (0.85% NaCl), Copan, Yocon, or Mantaac preserved SARS-CoV-2 detection over various temperatures (18°C–42°C) at 5 days (cycle threshold differences of ≤3 compared with baseline) and then a reduction in stability at 7 days was noted. In contrast, a significant impact on SARS-CoV-2 detection was observed for specimens collected in Beaver (buffered saline) and Cobas (guanidine/guanidinium) over the various conditions assayed. When specimens were subjected to temperature excursion studies including freeze–thaw cycles (–20°C to 4°C), we obtained equivalent detection of SARS-CoV-2 across all

transport media with no greater than a 3 Ct value difference compared with baseline.

CONCLUSION: Our study demonstrating extended stability of SARS-CoV-2 virus in BLANS sample matrix in various transport media under various ambient transport conditions supports a promising decentralized collection strategy to improve access to coronavirus disease 2019 diagnostic testing in under-served communities. However, media type must be considered because not all media were found to be acceptable.

P36

Evaluating the impact of incorporating clinical practice guidelines for management of infectious syndromes into an electronic application

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OBJECTIVES: To improve optimal antimicrobial prescribing at our institution, guidelines for infectious syndromes were incorporated into an electronic application (e-app) in 2017. The objective of this study was to assess the impact of the e-app on antimicrobial prescribing.

METHOD: A retrospective chart review assessing antimicrobial prescribing patterns before and after implementation of the e-app using an interrupted time series was performed. Admitted pediatric patients who received empiric antimicrobials for an infectious syndrome listed in the e-app were considered for inclusion. Prescribing was independently assessed by two reviewers using a standardized checklist that accounted for patient characteristics. Assessment of optimal antimicrobial prescribing was compared, and discrepancies were resolved through discussion.

RESULTS: A total of 237 patients were included in the pre-implementation arm and 243 patients were included in the post-implementation arm. Pneumonia or pleural effusions (23.8%), appendicitis (19.2%), and sepsis (15.2%) were the most common indications for antimicrobial use. Empiric antimicrobial use was optimal in 81.9% of patients pre-implementation compared with 93.0% of patients post-implementation. We assessed for level (change immediately after the intervention) and trend changes in the outcome. A statistically significant level change of 15.5 percentage points (95% CI 2.77% to 28.3%; $p = 0.019$) was observed in optimal antimicrobial prescribing after implementation of the e-app. The trend change was a 1.22 percentage point improvement per month relative to the pre-intervention trend, but it was statistically insignificant (95% CI –0.2 to 2.68; $p = 0.10$). The combined results suggest that the e-app had a large immediate impact that was sustained over the following year.

CONCLUSION: Empiric antimicrobial prescribing for pediatric patients with infectious syndromes improved after implementation of an e-app for dissemination of clinical practice guidelines. Use of e-apps may also be an effective antimicrobial stewardship strategy to improve antimicrobial use and ensure optimal prescribing in other patient populations.

P37

Ten years of central line–associated bloodstream infection surveillance in Canadian pediatric and neonatal intensive care units, 2011–2020

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OBJECTIVES: To determine the frequency of central line–associated bloodstream infections (CLABSIs) in Canadian pediatric and neonatal intensive care units (PICUs and NICUs, respectively) and identify trends over 10 years.

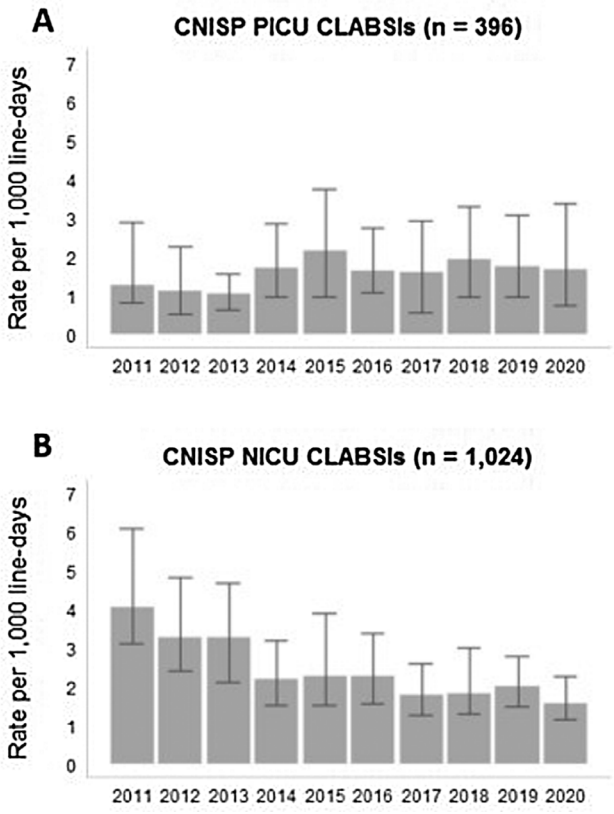

Figure P37-1: Canadian Nosocomial Infection Surveillance Program (CNISP) central line-associated bloodstream infections (CLABSI) rate per 1,000 line-days among participating Canadian acute care hospitals. (A) pediatric intensive care unit (PICU): (B) neonatal intensive care unit (NICU)
Note: NICU CLABSIs with missing associated denominator data were excluded from rate calculations (n = 21)

METHOD: The Canadian Nosocomial Infection Surveillance Program (CNISP) conducts hospital-based sentinel surveillance of health care–associated infections. Each year from 2011 to 2020, 9–12 PICUs and 15–19 NICUs participated in CLABSI surveillance. Data including line-day denominators were collected using standardized definitions and forms. Negative-binomial regression was used to test for linear trends, with robust standard errors to account for clustering by hospital.

RESULTS: CLABSI rates in PICUs were relatively stable from 2011 to 2020 (1.0–1.9 per 1,000 line-days, test for trend $p = 0.26$) (Figure P37-1A). Among the 396 PICU CLABSIs, 44% were female, and the median age was 6 months (interquartile ratio [IQR] 2–26 mo). Median days from PICU admission to infection was 20 days (IQR 8–54 d). Thirty-day all-cause mortality was 9.6%. In NICUs, CLABSI rates decreased from 2011 to 2020 (4.0 to 1.6 per 1,000 line-days; test for trend $p < 0.0001$; Figure P37-1B). Among the 1,045 NICU CLABSIs, 41% were female. Median age was 18 days (IQR 10–46 d). Median days from NICU admission to infection was 16 days (IQR 9–35 d). Thirty-day all-cause mortality was higher in 2017–2020 than in 2011–2016 (13% versus 7%, $p = 0.002$). In 2020, the most common microorganisms identified in PICU and NICU CLABSIs were coagulase-negative staphylococci (CONS; 29%, $n = 18/63$, and 27%, $n = 25/92$, respectively) and *Staphylococcus aureus* (18%, $n = 11/63$, and 27%, $n = 25/92$, respectively). In NICUs, the percentage of identified microorganisms that were *S. aureus* increased (from 8% to 27%, $p = 0.010$) between 2011 and 2020, whereas CONS decreased (from 50% to 27%, $p = 0.016$); in PICUs, no significant trends were observed.

CONCLUSION: NICU CLABSI rates have decreased significantly over the 10-year period, whereas PICU CLABSI rates have remained relatively stable. Continued efforts on CLABSI prevention are needed.

P38
Rapid identification of methicillin-resistant *Staphylococcus aureus* from positive blood cultures

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OBJECTIVES: *Staphylococcus aureus* is a common and serious cause of bacteremia. Timely initiation of appropriate therapy has implications for patient morbidity and mortality, infection control practices, and antimicrobial stewardship. Methicillin resistance is conferred by altered penicillin binding protein, PBP2a, which can be detected by latex agglutination, immunochromatography, or polymerase chain reaction of the *mecA* gene. Conventional differentiation between methicillin-susceptible *S. aureus* (MSSA) and methicillin-resistant *S. aureus* (MRSA) from blood cultures typically takes 2–3 days after susceptibility testing is performed on colonies isolated on solid media. We evaluated the feasibility of a rapid identification method for methicillin resistance from positive blood cultures using bacteria grown in broth, followed by immunochromatographic PBP2a testing.

METHOD: Simulated blood culture bottles were spiked with clinical isolates of *S. aureus* and incubated in the BD BACTEC™ Automated Blood Culture System (BD, Franklin Lakes, New Jersey) until positivity followed by pelleting (lysis centrifugation). A 10 µL loop of the bacterial pellet was inoculated into brain heart infusion broth containing a

quarter piece of a 30 ug cefoxitin disk. The broth was then incubated at 35°C for 1 hour, and the bacteria grown was tested using the Alere PBP2a SA Culture Colony Test (Abbott, Chicago, Illinois). The pellet was also inoculated onto sheep blood agar and incubated 18–20 hours at 35°C, followed by susceptibility testing by cefoxitin disk diffusion.

RESULTS: PBP2a tests performed on *S. aureus* isolates (26 MSSA, 28 MRSA) after broth incubation of blood culture pellet showed complete concordance with standard cefoxitin disk diffusion performed on isolates from SBA.

CONCLUSION: Broth incubation of *S. aureus* bacterial pellet from positive blood cultures with cefoxitin disk induction, followed by PBP2a testing, is a reliable and convenient method for rapid identification of methicillin resistance in *S. aureus* within 2–3 hours of blood culture positivity.

P39

Evaluation of a new chromogenic agar for identification of *Candida* species, including *Candida auris*

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OBJECTIVES: *Candida auris* is unlike other pathogenic *Candida* species in that it has been associated with hospital outbreaks around the world. In addition to being associated with higher morbidity and mortality than other pathogenic yeast, it has also proven to be difficult to identify. In this study, we evaluated a new chromogenic medium that can identify and differentiate clinically significant *Candida* species, including *C. auris*.

METHOD: Fifty-one pathogenic yeast isolates, including *C. auris* ($n = 11$), *C. albicans* ($n = 6$), *C. glabrata* ($n = 6$), *C. dubliniensis* ($n = 6$), *C. tropicalis* ($n = 6$), *C. krusei* ($n = 6$), *C. parapsilosis* ($n = 1$), *C. lusitaniae* ($n = 1$), *Saccharomyces cerevisiae* ($n = 2$), and *C. guilliermondii* ($n = 1$), were inoculated to CHROMagar™ Candida Plus medium (DRG International, Springfield, New Jersey). Species closely related to *C. auris* were also tested; *C. haemulonii* ($n = 2$) and *C. duobushaemulonnii* ($n = 3$). Plates were incubated at 35°C for 36–48 hours aerobically. Colour interpretation was documented per manufacturer's instructions.

RESULTS: *C. auris* (light blue, blue halo), *C. albicans and C. dubliniensis* (blue-green), *C. glabrata* (mauve), *C. tropicalis* (metallic blue, pink halo), and *C. krusei* (dry pink) isolates all gave 100% concordance (41/41) with their expected colours according to manufacturer's specifications. The other 10 yeast isolates produced white, light pink, or light blue colonies with no halos. Both *C. haemulonnii* (white, no halo) and *C. duobushaemulonnii* (very pale blue, no halo) could be easily differentiated from *C. auris*.

CONCLUSION: CHROMagar Candida Plus performs accurately in the identification and differentiation of common pathogenic *Candida* species, including *C. auris*. It has utility in being the primary *Candida* chromogenic agar in clinical microbiology laboratories with the advantage of also producing a distinct colour for *C. auris*. Although not specifically studied here, this media could be useful for *C. auris* screening but also for use in routine clinical testing, such as for mixed yeast cultures or identification of yeast directly from clinical specimens.

P40

Investigational microbiota-based live biotherapeutic RBX2660 for reduction of recurrent *Clostridioides difficile* infection: What do Canadian infectious diseases specialists think?

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OBJECTIVES: Fecal microbial transplantation (FMT) is recommended for treatment of recurrent *Clostridioides difficile* (rCDI) after failure of antibiotic treatment. RBX2660 (Rebiotix, Roseville, Minnesota) is an investigational microbiota-based live biotherapeutic in development for treating rCDI. In this survey, Canadian CDI experts discussed the properties and potential uses of FMT and RBX2660 in Canada.

METHOD: A group of Canadian infectious diseases (ID)–FMT practitioners were convened virtually in April 2021 to review FMT availability in Canada and to assess the potential role of RBX2660 in the Canadian marketplace, taking into consideration composition, manufacture, administration, safety, and efficacy.

RESULTS: Participants commented that in Canada, of the approximately 38,000 cases of primary CDI, an estimated

2,000–2,500 have multiple rCDI (>3) and could benefit from FMT. In Canada, ID and gastrointestinal specialists are primarily responsible for FMT and believe it has a high success rate, although it is not standardized in terms of collection and manufacture, donor and stool testing, and administration (eg, colonoscopy and enema, oral capsules). Donor screening, manufacture of FMT product, and wide availability are major barriers for clinicians. RBX2660 is a single-dose, 150 ml, donor-derived, intensively screened intestinal microbiota preparation that is rectally administered and has been investigated across six clinical studies for the treatment of rCDI. ID specialists identified advantages of RBX2660, including standardized manufacture, donor and stool testing, ease of administration, and good safety and efficacy in preventing rCDI. ID specialists found the microbiome data supportive; they showed that after RBX2660 treatment patient microbiomes significantly converged toward a "healthy microbiome" profile, along with positive metabolomic changes, notably an increase in secondary bile acids that suppress *C. difficile* spore germination.

CONCLUSION: Canadian CDI experts agreed that RBX2660 strengths include a standardized GMP manufacturing process, ease of administration, good safety, and efficacy data. Participants concluded that RBX2660 can be considered a candidate rCDI therapy in Canada.

P41

Recalibrated estimates of non-bacteremic and bacteremic pneumococcal community-acquired pneumonia in hospitalized Canadian adults from 2010 to 2017 with the addition of an extended-spectrum serotype-specific urine antigen detection assay

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OBJECTIVES: In the context of age- and risk-based pneumococcal vaccine recommendations in Canada, this study presents updated data from active surveillance of pneumococcal community-acquired pneumonia (pCAP) and invasive pneumococcal disease (IPD) in hospitalized adults from 2010 to 2017.

METHOD: *Streptococcus pneumoniae* was detected using culture (blood and sputum) and urine antigen detection (UAD). Serotyping was performed with Quellung, polymerase chain reaction, or the PCV13- and PPV23 (non-PCV13)-specific UADs. Laboratory results, demographic, and outcome data were categorized by age (16–49, 50–64, and ≥65) and by disease (non-bacteremic pCAP, bacteremic pCAP, and IPD [non-CAP]).

RESULTS: A total of 11,129 CAP cases and 216 cases of IPD (non-CAP) were identified. Laboratory testing for *S. pneumoniae* was performed in 8,912 CAP cases, identifying 1,264 (14.2%) as pCAP. Of pCAP cases, 805 (63.7%) were non-bacteremic and 459 (36.3%) were bacteremic. Adults aged 65 years and older represented 54.5% of non-bacteremic pCAP, 41.4% of bacteremic pCAP, and 48.6% of IPD cases. Adults aged 50–64 years contributed 30.3%, 33.1%, and 29.9%, respectively. In pCAP, PCV13 serotypes declined between 2010 and 2014 as a result of declines in serotypes 7F and 19A, then plateaued from 2015 to 2017 with persistence of serotype 3. In later study years, non-bacteremic pCAP was predominant, and PPV23 (non-PCV13) serotypes increased from 2015 to 2017, with serotypes 22F, 11A, and 9N being most frequently identified. Compared with non-pCAP, pCAP cases were more likely to be admitted to intensive care units and require mechanical ventilation. These outcomes and mortality were more common in bacteremic pCAP and IPD than in non-bacteremic pCAP.

CONCLUSION: Along with IPD, pCAP surveillance (bacteremic and non-bacteremic) is important because their trends may differ over time. With insufficient herd protection from PCV13 childhood immunization or use of PPV23 in adults, this study supports direct adult immunization with PCV13 or higher valency conjugate vaccines to reduce the residual burden of pCAP and IPD.

P42

Emergence of a mutation in the nucleocapsid gene of SARS-CoV-2 interferes with PCR detection in Canada: A call for industry to release primer and probe sequences for global monitoring

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OBJECTIVES: The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was met with rapid development of robust molecular-based detection assays. Despite the relatively moderate mutational rate of SARS-CoV-2, numerous mutations with known negative impact on diagnostic assays have been identified. In early 2021, we identified four samples positive for SARS-CoV-2 with a nucleocapsid (N) gene dropout on Cepheid (Sunnyvale, California) Xpert® Xpress SARS-CoV-2 assay. Using whole-genome sequencing, we sought to identify the causative mutation and evaluate the distribution of this mutation among Canadian SARS-CoV-2 sequences.

METHOD: The SARS-CoV-2 genomes of each of the four samples displaying N gene dropout were sequenced using the ARTIC protocol. Analyses of the suspected mutation were conducted on 41,712 SARS-CoV-2 genomes from Canada obtained from GISAID (Munich, Germany). Distribution of the mutation in Canada was visualized using the geographic information system QGIS. A maximum likelihood tree was created with IQ tree.

RESULTS: Sequencing revealed a single common mutation in the N gene (C29200T) in each of the four samples with N gene dropout. Spatiotemporal analysis showed that the mutation was found in 0.6% of sequences and in at least six different Canadian provinces from spring 2020 to May 2021. Phylogenetic analyses showed that this mutation arose multiple times in Canadian samples and is present in five different variants being monitored and of concern.

CONCLUSION: The Cepheid testing platform is commonly used in Canada, including in remote regions. As such, the existence of N gene mutation dropouts required further investigation. Although commercial SARS-CoV-2 molecular detection assays have contributed immensely to the response effort, many vendors are reluctant to make primer–probe sequences publicly available. We hope that our industry partners will seriously consider making primer–probe sequences available so that diagnostic escape mutants can be identified promptly and responded to appropriately to maintain diagnostic accuracy.

P43

Appropriateness of antibiotics prescribed by residents on call: A retrospective cross-sectional study

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OBJECTIVES: There are few data on appropriateness of antimicrobial prescriptions by learners during regular work hours compared with on-call hours. We aimed to describe the appropriateness of antimicrobials prescribed by learners among hospitalized patients on the basis of timing of prescription, as well as to identify any potential factors that correlated with appropriateness.

METHOD: We conducted a retrospective cross-sectional study of 350 inpatient charts at two academic centers in St. John's, Newfoundland. Sample size was calculated on the basis of data from a preliminary review of 100 charts. Eligible antimicrobial prescriptions started overnight in adult inpatients were compared with those prescribed during daytime hours over a 1-year period. Routine pre-operative antimicrobials were excluded. Standardized chart review was performed with an infectious diseases specialist to determine appropriateness, categorized according to the National Antimicrobial Prescribing Survey worksheet, which was compared with a χ^2 test. Variables hypothesized to predict appropriateness of treatment were analyzed via logistic regression.

RESULTS: Of initial antimicrobials regimens started overnight, 74.7% (52.2% optimal, 22.4% adequate) were deemed appropriate compared with 59.6% (34.6% optimal, 25.0% adequate) of initial prescriptions during the day

(p = 0.002). Overall appropriateness after accounting for reassessment and final duration of antimicrobials was 62.6% (35.0% optimal, 27.6% adequate) for the overnight group compared with 57.4% (33.0% optimal, 24.4% adequate) in the daytime group (p = 0.024). Of the variables tested, having a documented assessment and indication and having a stop date or duration written with the initial prescription were associated with a higher rate of appropriate prescriptions.

CONCLUSION: Interestingly, our study found that for learners, antimicrobials started overnight were overall more appropriate than those started during the day, suggesting that final decisions on antimicrobials made during the day had more influence on overall regimen appropriateness. Ensuring appropriate assessment and workup at time of prescription and flagging antimicrobials for reassessment would likely be most meaningful in improving appropriateness.

P44

Development of a luminescence assay for monitoring antibiotic sheltering resulting from bacterial outer membrane vesicle formation

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OBJECTIVES: Outer membrane vesicles (OMVs) secreted by gram-negative bacteria can contain proteins responsible for antibiotic resistance, including β-lactamases such as New Delhi metallo-β-lactamase 1 (NDM-1). The release of β-lactamase-containing OMVs by antibiotic-resistant bacteria can have a sheltering effect, protecting bacteria that are otherwise susceptible to antibiotics. A rapid inexpensive luminescence-based assay was developed to study factors contributing to OMV formation and antibiotic sheltering.

METHOD: The antibiotic sheltering effect of an *Escherichia coli* strain that produces NDM-1 was investigated using a luminescence-based *E. coli* biosensor. This biosensor allows the impact of β-lactam antibiotics on peptidoglycan catabolism to be monitored, triggering an easily detected luminescence signal. Strong luminescence is observed when a β-lactam is present, whereas luminescence decreases if the antibiotic is degraded. Using this assay, degradation of a carbapenem antibiotic by NDM-1–containing OMVs was evaluated by measuring luminescent output of the biosensor strain.

RESULTS: Degradation of meropenem by NDM-1 was detected by the biosensor. Optimization of assay conditions was carried out to ensure that the antibiotic degrading activity detected was from OMVs containing NDM-1, eliminating the possibility of degradation by free β-lactamases. The assay was then applied to assess how factors known to promote hypervesiculation relate to antibiotic sheltering. Factors studied include carbapenems and D-amino acids.

CONCLUSION: The assay can be used to monitor the formation of β-lactamase–containing OMVs, using the luminescence output as an indicator of β-lactam degradation. This approach will continue to be applied to assess how factors that promote hypervesiculation affect antibiotic sheltering of susceptible bacteria in a multi-infection context and how can this lead to antibiotic treatment failure.

P45

Enhancing tick-borne disease surveillance in British Columbia with inclusion of two new qPCR targets for *Rickettsia rickettsii* and *Babesia microti*

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OBJECTIVES: As climate change creates favourable environmental conditions for tick abundance in Canada, the spread of tick-borne diseases (TBDs) into British Columbia is a major concern. The current tick surveillance quantitative polymerase chain reaction (qPCR) assay at British Columbia Center for Disease Control Public Health Laboratory can detect *Borrelia, Anaplasma,* and *Ehrlichia* species. This study aims to add two new targets for detection of *Rickettsia rickettsii* and *Babesia microti,* causative agents of Rocky Mountain spotted fever and babesiosis, to the current tick surveillance qPCR assay.

METHOD: qPCR primers and probes targeting the *R. rickettsii* hypothetical protein (Rri6) and *B. microti* CCTη gene for T-complex protein 1 subunit (BmCCT) were assessed for specificity, sensitivity, PCR efficiency, precision, ruggedness, and accuracy. qPCR was performed on an Applied Biosystems™ 7500 Fast Real-Time PCR System using the TaqMan™ Fast Advanced Master Mix (ThermoFisher Scientific, Waltham, Massachusetts). Synthetic gBlock™ Gene Fragments (Integrated DNA Technologies, Coralville, Iowa) and clinical specimens were used for analytical and clinical validation. DNA was extracted using the Qiagen Dneasy® Blood & Tissue Kit Qiagen (Germantown, Maryland). Positive *B. microti* samples were confirmed using 18S rRNA Sanger sequencing.

RESULTS: The detection limit for *B. microti* and *R. rickettsii* targets were 10 and 100 copies/reaction, respectively. Both targets had acceptable linearity ($R^2 > 0.99$) and PCR efficiency (99.3% BmCCT; 93.5% Rri6). Precision, measured by % coefficient of variation, was <0.692 and <0.751 for BmCCT and RRi6 targets. Accuracy was 100% for both targets, as measured by clinical *B. microti* specimen and simulated gBlock strains of *R. rickettsii*.

CONCLUSION: Both detection targets performed satisfactorily for all the assessed validation parameters; thus, the proposed qPCR assay may be a reliable method for screening *B. microti* and *R. rickettsii,* in addition to *Borrelia, Anaplasma,* and *Ehrlichia* species. Overall, this addition will help improve TBD surveillance in British Columbia and may provide helpful insight on the spread of emerging TBDs in British Columbia.

P46

A comparative study of air purification between the nano-confined catalytic oxidation technology and two other conventional technologies

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OBJECTIVES: Nano-confined catalytic oxidation (NCCO) is an air purification technology that is likely to be the most effective, sustainable, and environmentally friendly method to sanitize the air by reducing odor, removing airborne chemicals, and destroying bacteria as well as viruses. NCCO combines the oxidizing strength of active oxygen with a very low concentration of ozone and the catalytic properties of zeolites to absorb and oxidize pollutants, including airborne bacteria and viruses. Environmental smoke from tobacco and likely cannabis causes adverse health effects because of the mixture of compounds found in the smoke. In this study, the performance of NCCO air purifiers is compared with two other commonly used air purifiers using different technologies. The experimental method is designed to test the odor removing ability of cigarette smoke by all three types of air purifiers under similar conditions

METHOD: The study involves 20 consenting volunteers who are asked to evaluate the odor of cigarette smoke before and after air purification in a controlled environment. The experimental apparatus consists of two airtight chambers, one containing a cigarette on a stand and the other containing an air purifier with a vent for sampling. Particulate matters are prevented from entering the odor sampling chamber. Odor evaluations are assessed by the volunteers using a numerical scale ranging from 1 (*no smell*) to 5 (*overpowering smell*). The volunteers are not aware of which air purifier is being used in the chamber.

RESULTS: The NCCO air purifier reduced the odor level by 70%. The other two commercially available air purifiers achieved only 28% to 34% reduction.

CONCLUSION: The NCCO air purification technology outperforms two other conventional air purification technologies by more than 100%.

P47

Performance of the Cue COVID-19 point-of-care test: Prospective clinical verification and operational insights from a multi-centre clinic service delivery model

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OBJECTIVES: The coronavirus disease 2019 (COVID-19) pandemic highlighted the critical need for rapid and accurate molecular diagnostic testing. Access to laboratory reverse transcription polymerase chain reaction (RT-PCR) is challenged by delays in specimen delivery, longer process time, and limited access. The utility for decentralized point-of-care testing (POCT) was evaluated. The Cue COVID-19, a Health Canada– and Food and Drug Administration–authorized molecular POCT for severe acute respiratory syndrome coronavirus 2 detection, was deployed at a network of clinics in Ontario. The analytical verification of Cue POCT before implementation, the clinical performance (prospectively verified against a Health Canada–approved lab RT-PCR assay), and operational experience were examined.

METHOD: Verification of analytical sensitivity, accuracy, and precision was performed with contrived specimens. Prospective clinical verification over a 3-month period consisted of paired testing by Cue COVID-19 POCT and RT-PCR for all clients of a clinic POCT service (n = 3,037). Evaluation of POCT implementation included metrics on error rates (operator, mechanical device, and reporting software app) on the fleet of 25 Cue devices across seven clinics.

RESULTS: Prospective verification demonstrated clinical sensitivity of 100% and clinical specificity of 99.4% for Cue

COVID-19 POCT. A false-positive rate of 0.57%, although still acceptable under Health Canada standards, indicates a role for confirmation with RT-PCR on the basis of local epidemiology (when positive predictive value is low). A low device error rate (1.04%) indicated stable mechanical performance. An invalid rate of 3.44% was observed, suggesting sample inadequacy due to potential errors in specimen collection or testing procedure.

CONCLUSION: Our findings reveal the value of COVID-19 POCT and service delivery in a decentralized model to rapidly detect cases and curb transmission in travellers, workplaces, and congregate events. The insights gleaned on quality assurance and operational experience are readily transferable to other POCT diagnostic services in the future.

P48

SARS-CoV-2 multiplexing PCR to enhance sensitivity and prevent impacts of single-target gene failure

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OBJECTIVES: Real-time reverse transcription polymerase chain reaction (RT-PCR) has been widely used for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) detection because of its high sensitivity and specificity. With an RNA genome prone to mutation, a multi-target approach for SAS-CoV-2 detection should be used to prevent loss of sensitivity or target gene failure. Ensuring adequate sensitivity is particularly important in the early stage of infection to reduce transmission events and ensure proper management of vulnerable populations. We sought to evaluate whether a real-time multiplex RT-PCR using multiple SARS-CoV-2 targets detected in the same fluorescent channel, or use of digital droplet PCR (ddPCR), could improve sensitivity compared with a clinical laboratory-developed test (LDT).

METHOD: A multiplex RT-PCR consisting of three SARS-CoV-2 targets (E, RdRp, and N1) detected with the same fluorophore were compared with reactions using individual targets. Testing was performed on serially diluted samples and a panel of 80 nasopharyngeal samples (40 negative, 34 positive, and 6 indeterminate). A similar series of experiments was performed to evaluate benefits of the RainDance ddPCR compared with the LDT.

RESULTS: The multiplex RT-PCR assay correctly identified 33/34 (97%) of the positives, 40/40 (100%) of negatives, and 4/6 (64%) of the indeterminate, showing high concordance with the LDT. The limit of detection for ddPCR was 3.2 copies/μL, representing a 10-fold increase in analytical sensitivity compared with the LDT. Comparing RT-PCRs for individual targets with the single-channel multiplex showed an additive effect for each target.

CONCLUSION: The multiplexed RT-PCR is an accurate assay with performance similar to the LDT but adds value by ensuring detection if one or two targets fail to be detected with SARS-CoV-2 PCR target site mutations. The increase in sensitivity of ddPCR multiplex RT-PCR may be useful for confirming low-level detections and might be better suited for SARS-CoV-2 detection in early infection.

P49

Impact of using phlebotomy team on blood culture contamination and vancomycin prescribing: A cross-sectional study by antimicrobial stewardship program and microbiology and clinical laboratories in a community hospital

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OBJECTIVES: Contaminated blood cultures (BLCX) often lead to a cascade of unnecessary antibiotic prescribing, particularly vancomycin; avoidable antibiotic toxicity; resistance; increased length of stay; and costs. We describe the outcome of implementing a plebotomy team (PhlT) on BLCX contamination rates and vancomycin use and the prevalence of BLCX contamination in specimens collected by nursing staff compared with those collected by the PhlT.

METHOD: The trained PhlT was deployed to collect BLCX daily from 9:00 a.m. to 9:00 p.m. starting February 2021. A retrospective chart review of positive blood cultures in the months of July–Sept. 2020 and 2021 was performed to determine the percentage of contaminated BLCX and vancomycin use, before and after PhlT deployment, respectively. Further analysis of positive BLCX collected from July to September 2021 was done to determine the prevalence of BLCX contamination in specimens collected by nursing staff compared with PhlT.

RESULTS: There was a significant decline in the average percentage of contaminated BLCX by 43% (from 5.3% before PhlT to 3% after PhlT). This was associated with a 60% decline in vancomycin use (16 versus 6.3/1,000 patient days in July–September 2020 and 2021, respectively). The relative prevalence of BLCX contamination in specimens collected by nursing staff was 2.5 times those collected by PhlT (July–September 2021).

CONCLUSION: We demonstrate that employment of PhlT significantly reduces BLCX contamination and unnecessary vancomycin prescribing. Wider adoption of PhlT in community hospitals can assist in minimizing the evolution of antimicrobial resistance and improve patient safety

P50

Simple, rapid, cost-effective loop-mediated isothermal amplification method for detection of *Ureaplasma* spp from endotracheal aspirates of intubated neonates

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OBJECTIVES: *Ureaplasma* spp are commonly found in the microbiome of the female genital tract and are transmitted to the newborn. An association between *Ureaplasma* respiratory tract colonization and bronchopulmonary dysplasia and chronic lung disease has been observed in premature infants; consequently, some have advocated for treatment to prevent poor pulmonary outcomes. However, it has been suggested that to be effective, treatment should be started soon after birth. Empiric antibiotic treatment of all premature babies, unfortunately, runs counter to antimicrobial stewardship. Culture results take days and requires complex media. The objective of this study was to develop a simple, rapid, and cost-effective loop-mediated isothermal amplification method (LAMP) method for the detection of *Ureaplasma* spp to enable targeted treatment.

METHOD: Sixty-one endotracheal aspirates from 53 premature infants with gestational age less than 26 weeks and collected within 72 hours were used. The specimens were sent to a reference laboratory for culture. A 100 µL aliquot of the specimen was mixed with 100 µL of lysis buffer and boiled for 10 minutes. After mixing and centrifugation, 5 µL of the supernatant was used for LAMP. LAMP primers were designed using Primer Explorer V5 software (Eiken Co., Tokyo, Japan). A 213 bp fragment of ureaplasma-specific 16S rDNA was used as the target. LAMP was done using WarmStart® LAMP Kit (NEB Inc., Ipswich, Massachusetts) according to manufacturer's instructions. All specimens were also tested with a confirmatory polymerase chain reaction (PCR). A commercial supply of ureaplasma DNA was used as positive control.

RESULTS: Twelve specimens were positive for *Ureaplasma* spp by culture and LAMP. Three specimens were LAMP positive and culture negative. Forty-six specimens were negative by both culture and LAMP. All LAMP positive specimens were also PCR positive. The test performance values for LAMP compared with culture were as follows: sensitivity, 100%; specificity, 93%; negative predictive value, 100%; and positive predictive value, 80%.

CONCLUSION: The LAMP method developed for detection of *Ureaplasma* spp from endotracheal aspirates of premature infants was efficient, rapid, and correlated well with culture.

P51

Determination of HCV genotypes and sub-genotypes from Canadian serum and plasma samples sent to a reference laboratory, 2016–2021

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OBJECTIVES: Here we present the results of hepatitis C virus (HCV) genotyping for samples from provincial and other laboratories sent to a reference laboratory over the 5-year period from 2016 to 2021.

METHOD: HCV-positive serum/plasma samples were initially assessed for HCV genotype (GT) and sub-genotype (sub-GT) at provincial or national laboratories. Partial or complete virus genome sequences were determined for each sample at the reference laboratory using established Sanger or next-generation sequencing methodologies. Sequences were evaluated by phylogenetic placement in Mega 7 software compared with a reference list of HCV GTs and sub-GTs (ICTV Reference, May 2019). When phylogenetic analysis was unable to place the sequence into a defined HCV sub-GT, the sample was classified as "other sub-GT." Data were stored and queried in a COGNOS database (IBM Corporation, Armonk, New York).

RESULTS: A total of 3,587 HCV-positive samples were processed, and all known HCV GTs (GT 1–8) were detected. Some GTs (eg, GT 1, 53%; GT 3, 28%; GT 2, 6%; and GT6, 6%) were more abundant than others (eg, GT 4, 2%; GT 5, 0.1%; GT 7, 0.1%; and GT 8, 0.1%). HCV recombinant forms were present in 0.7%, and mixed infections represented 4.5%. Undefined (novel) sub-GTs represented 2% of samples. Over the 5-year period, the relative percentages for GT1 and GT2 remained relatively consistent, GT6 samples showed a decline (2016 = 9%, 2021 = 4%), and increased numbers were seen for GT 3 (2016 = 21%, 2021 = 30%) and for mixed infections (2016 = 2%, 2021 = 5%).

CONCLUSION: Sequence analysis of viral genomes from HCV-positive samples has confirmed the presence of all known genotypes in Canadian serum/plasma samples sent to an HCV Reference Laboratory. The order of abundance for HCV genotypes (GT 1 > GT3 > GT2/GT6) is consistent over the 5-year period.

P52

Validation of Colorex chromogenic agar on WASPLab in screening for *Serratia marcescens* in neonatal intensive care units

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OBJECTIVES: *Serratia marcescens* is commonly associated with outbreaks in neonatal intensive care units. Investigations of outbreaks require efficient recovery of clinical and environmental isolates to prevent potentially fatal sepsis, meningitis, or pneumonia. The objective of this study was to validate a new Colorex™ (CHROMagar™) *Serratia* agar for neonatal *Serratia* screening using the WASP™ and WASPLab™ (COPAN Diagnostics, Murrieta, California).

METHOD: This study used 579 *Serratia* surveillance specimens collected with ESwab™ kits (COPAN) processed on the WASP. Known reference strains ($N = 105$) of *S. marcescens* were also tested. Cultures were analyzed using WASPLab™ imaging analysis (COPAN Diagnostics, Murrieta, California). Results were compared with the current testing method, which uses MacConkey agar. Positive results were confirmed with VITEK MS (bioMérieux, Marcy-l'Étoile, France).

RESULTS: Of the 579 samples tested, 6 were positive for *S. marcescens* by the current method using MacConkey plates, versus 24 positives for *Serratia* species with Colorex *Serratia* agar and the WASP and WASPLab imaging analysis. Twenty-two were identified as *S. marcescens,* 1 as *S. liquifaciens,* and 1 as *S. odifera.* All 24 isolates were blue in colour and grew heavy on the Colorex *Serratia* agar. Eighteen specimens showed very light growth of target colour blue colonies that identified as *Klebsiella oxytoca, Citrobacter freundii,* and *Enterobacter cloacae.* Eleven specimens showed a light growth of non-target clear colonies that identified as *Proteus, Morganella,* and *Pseudomonas* species. One hundred two known *Serratia* isolates grew well on Colorex *Serratia* agar with varying blue to blue-green colour. Colorex *Serratia* agar sensitivity was 100% (95% CI 0.61 to 1) and specificity was 97% (95% CI 0.95 to 0.98).

CONCLUSION: Results showed Colorex *Serratia* agar had a significantly greater sensitivity than MacConkey agar in isolating *S. marcescens* from neonatal surveillance specimens. The use of the WASP for set up provides efficient and consistent processing, and WASPLab imaging allows for high-resolution digital imaging analysis. WASPLab also has the capability to use segregation software to analyze images and rapidly result negatives.

P53

Detection of SARS-CoV-2 RNA in stool samples from the patients associated with acute gastroenteritis

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OBJECTIVES: Although severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is primarily a respiratory virus pathogen, gastrointestinal symptoms such as diarrhea, vomiting, loss of appetite, and nausea have been reported in coronavirus disease 2019 (COVID-19) cases, with the prevalence of diarrhea and vomiting ranging from 1.25% to 61.3%. The objective of our study is to look at the prevalence

of COVID-19 in patients with stool samples submitted for suspect viral gastroenteritis and the frequency of respiratory samples submitted for COVID-19 testing among those tested positive for SARS-CoV-2 in the stool samples.

METHOD: The Public Health Lab of Alberta Precision Laboratory provides a molecular panel for viral gastroenteritis (GEV) including norovirus, rotavirus, sapovirus, astrovirus, and adenovirus for stool specimens submitted from children aged <5 years, hospitalized patients, and outbreak investigations in Alberta. Stool samples submitted for GEV from May 29, 2020, to December 15, 2020, were tested for SARS-CoV-2 using a one-step quantitative reverse transcription polymerase chain reaction targeting the E gene.

RESULTS: Among the 1,684 stool samples received for GEV, SARS-CoV-2 was detected in 48 (2.9%) collected from 47 patients. Three patients also tested positive for norovirus GII. The median age of the 47 patients was 62 years (interquartile ratio [IQR] 22–74) with a F:M ratio of 1:1.2. Of these 47 patients, 19 had a positive COVID-19 respiratory sample: 16 were collected before the positive stool samples (median 6, IQR 3–9 d) and 3 were collected 19–404 days after the positive stool samples. For the 26 patients with no positive COVID-19 respiratory samples, only 8 had a respiratory sample submitted for COVID-19 testing within 6 days of the positive stool samples.

CONCLUSION: Although COVID-19 is known to present with gastroenteritis symptoms, many were not tested for COVID-19, with collection of respiratory samples representing missed opportunities to make a diagnosis, but the prevalence of SARS-CoV-2 RNA detected in stool samples during the first 12 months of the pandemic in Alberta was low.

P54

Performance of an automated 16S Sanger sequencing pipeline using analysis packages in R

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OBJECTIVES: Sanger 16S rRNA sequencing is routinely performed using traditional protocols that can be labour intensive and require specialized expertise. We developed a fast, simplified, and largely automated workflow for 16S Sanger sequencing combining real-time polymerase chain reaction (PCR), sequencing on a cartridge-based genetic analyser, and fast data interpretation with an R-based script. The accuracy of the automated method for identifying bacterial isolates was assessed in comparison with routine bacterial identification.

METHOD: The first 500 base pairs of the bacterial 16S rRNA gene were amplified from 99 previously characterized bacterial isolates using real-time PCR. Amplicons were sequenced using the SeqStudio Genetic Analyzer (ThermoFisher Scientific, Waltham, Massachusetts). Sequence analysis, National Center for Biotechnology Information Basic Local Alignment Search Tool (BLAST) searches, and result interpretation were performed using an analysis pipeline utilizing packages in R (R Foundation for Statistical Computing, Vienna, Austria). All sequences were also analyzed using manual alignment and BLAST search interpretation. Results of the R-based protocol were compared with manual sequence analysis and results determined by routine methods in the laboratory.

RESULTS: The automated workflow produced results equivalent to manual analysis with an agreement of greater than 98% with conventional identification methods to the genus or species level. The automated workflow generated longer consensus reads, resulting in a 3% increase in reads passing quality control cut-offs and 6% more sequences with a valid identification compared with manual analysis. In addition, sequencing using the automated pipeline can be completed in about 6.5 hours, which reduces hands-on time of conventional analysis procedures by approximately 10 minutes per sample.

CONCLUSION: Automated R-based 16S Sanger sequencing analysis performs at least as well as manual analysis methods with some improvements in sequence quality and identification. By using the script-based analysis, sequences can be generated and interpreted with a fast turnaround time and very little hands-on manipulation. This simplified protocol can be readily implemented by front-line microbiology laboratories with minimal expertise.

P55

Comparison of the Allplex™ vaginitis screening assay and conventional methods for diagnosis of vaginitis

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OBJECTIVES: This study evaluates the clinical performance of the Allplex™ Vaginitis Screening assay (Seegene, Seoul, South Korea) compared with conventional testing for vaginitis.

METHOD: Specimens were stored at −80°C and chosen retrospectively from patients who had a vaginal Aptima® Multitest swab specimen performed for Aptima Combo 2 testing during the same visit as a vaginal Eswab™ or gel swab (COPAN, Murrieta, California) for Gram smear evaluation for bacterial vaginosis (BV) using modified Nugent criteria, and for presence of yeast by Gram smear, culture, or both. Conventional trichomonas vaginalis (TV) testing was performed on Multitest swabs on the Aptima TV assay. For BV, specimens with Nugent scores of 0–3 and of 4–6 without clue cells were considered negative, whereas scores of 4–6 with clue cells or of 7–10 were considered positive. For study purposes, Allplex BV normal or indeterminate results were considered negative results. Specimens in which *Candida* species were positive by molecular tests were considered in agreement if *Candida* species were isolated in culture.

RESULTS: Close to 700 multitest swabs were extracted on the STARlet in vitro diagnostic liquid handler (Seegene, Seoul, South Korea), then were set up for polymerase chain reaction using the Allplex Vaginitis Screening assay on the STARlet. PCR was run on the CFX96 IVD thermocycler (BioRad, Hercules, California). Sensitivity and specificity of the *Candida albicans* (CA), *Candida* others (CO), TV, and BV were calculated using a modified gold standard, with the Aptima CT/TV or BV molecular assays used to resolve discrepancies. Sensitivity and specificity were 97.6% and 99.5% for CA, 96.7% and 98.6% for CO, 100% and 100% for TV, and 98.1% and 86.3% for BV.

CONCLUSION: Clinical performance of the Allplex Vaginitis Screening assay appear to be a suitable alternative to conventional testing, which may allow more efficient use of existing human resources

P56

Syphilis positivity rates in Alberta during the first two waves of the COVID-19 pandemic

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OBJECTIVES: The steep increase to more than 2,000 syphilis cases in 2019 resulted in the declaration of a syphilis outbreak in Alberta. Since the first case of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection was identified on March 5, 2020, Alberta has undergone five waves of coronavirus disease 2019 (COVID-19) when all non-urgent medical appointments were cancelled, including the diagnosis and treatment of sexually transmitted infections. In this descriptive study, we aimed to assess the difference in syphilis positivity and testing metrics to 2019 data, during the first two waves (March 1–May 31, 2020, and October 1, 2020–February 10, 2021).

METHOD: Serological confirmatory syphilis tests and syphilis polymerase chain reaction (PCR) on genital lesion swabs are performed at the Public Health Laboratory of Alberta. These test data were retrospectively extracted from the laboratory information system. Test volumes and positivity rates from January 2019 to April 2021 were compared with those for the first two waves of COVID-19 in the province. Prenatal results were also compared with general population data.

RESULTS: In the first wave, of the 798 samples tested, 585 were *Treponema pallidium* particle agglutination positive. During the same period in 2019, 1,104 samples were tested with 702 positive results. In the second wave, 1,597 samples were tested with 1,180 positive results. In the corresponding period in 2019 through early 2020, 1,380 of 1,879 samples were positive. The positivity rate of syphilis in the first COVID-19 wave was significantly higher compared with the same period in 2019 (73.3% versus 63.6%; $p < 0.05$). Syphilis PCR from genital swabs showed significantly higher positivity during the pandemic waves compared with the same periods in 2019 (18.2% versus 11.9%; $p < 0.05$). There was no significant change in the prenatal syphilis serology positivity rates.

CONCLUSION: The syphilis positivity rate was higher during the first two waves of the COVID-19 pandemic, most likely as a result of the pre-selection of patients for testing and clinical visits.

P57

Comparison of the Aptima® CV/TV and BV assays with conventional methods for diagnosis of vaginitis

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OBJECTIVES: This study evaluates the performance of the Aptima® *Candida* vaginitis (CV)/*Trichomonas* vaginalis (TV), and bacterial vaginosis (BV) assays (Hologic, San Diego, California) compared with conventional testing for vaginitis.

METHOD: Specimens were stored at −80°C and chosen retrospectively from patients who had a vaginal Aptima Multitest swab specimen collected for Aptima Combo 2 testing during the same visit as a vaginal Eswab™ or gel swab (Copan, Murrieta, California) for Gram smear evaluation for BV using modified Nugent criteria and for presence of yeast by Gram smear, culture, or both. TV testing was performed on Multitest swabs on the Aptima TV assay. For BV, Nugent scores of 0–3 and 4–6 without clue cells were considered negative, and scores of 4–6 with clue cells or of 7–10 were considered positive. Two hundred seventy-seven multitest swabs were run on the Aptima CV/TV and 388 were run on the BV assay on the Panther system (Hologic, San Diego, California). Sensitivity and specificity of the *Candida glabrata* (CG), *Candida* spp (CS), TV, and BV were calculated using a modified gold standard, with re-review of Gram smear and a second molecular assay, the Allplex™ Vaginitis Screening Assay (Seegene, Seoul, South Korea) used to resolve discrepancies. The estimated technologist error rate in Nugent score interpretation was also calculated.

RESULTS: Sensitivity and specificity were 100% and 99.2% for CG, 93.3% and 95.6% for CS, 100% and 100% for TV, and 98.1% and 97.5% for BV between Panther assays and modified gold-standard results. The positive percentage agreement and negative percentage agreement between the Panther BV assay and the conventional method were 98.9 % and 87.0%, respectively, with an estimated Nugent score interpretation error rate of 4.6%.

CONCLUSION: The Aptima CV/TV and BV assays performed well and appear to be a suitable alternative to conventional testing, which may result in more consistent results.

P58

Surface and air contamination with severe acute respiratory syndrome coronavirus 2 from hospitalized coronavirus disease 2019 patients in Toronto, March–May 2020

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OBJECTIVES: We aimed to determine the burden of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in air and on surfaces in rooms of patients hospitalized with coronavirus disease 2019 (COVID-19) and investigate patient characteristics associated with SARS-CoV-2 environmental contamination.

METHOD: Nasopharyngeal swabs and surface and air samples were collected from the rooms of 78 inpatients with COVID-19 at six acute-care hospitals in Toronto from March to May 2020. Samples were tested for SARS-CoV-2 RNA and cultured to determine potential infectivity, and whole viral genomes were sequenced. The association between patient factors and detection of SARS-CoV-2 RNA in surface samples was investigated by constructing mixed-effects logistic regression models.

RESULTS: SARS-CoV-2 RNA was detected from surfaces (125/474 samples; 42/78 patients) and air (3/146 samples; 3/45 patients); 17% (6/36) of surface samples from 3 patients yielded viable virus. Viral sequences from nasopharyngeal and surface samples clustered by patient. Multivariable analysis indicated that hypoxia at admission, polymerase chain reaction–positive nasopharyngeal swab (cycle threshold

of ≤30) on or after surface sampling date, higher Charlson comorbidity score, and shorter time from onset of illness to sampling date were significantly associated with detection of SARS-CoV-2 RNA in surface samples.

CONCLUSION: The infrequent recovery of infectious SARS-CoV-2 virus from the environment suggests that the risk to health care workers from air and near-patient surfaces in acute-care hospital wards is likely limited. Nonetheless, early detection and isolation of COVID-19 patients is important to ensure minimization of exposure risk to health care workers, particularly when patients are admitted shortly after onset of symptoms.

P59

Implementation of hepatitis C virus reflex RNA testing in a provincial public health laboratory

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OBJECTIVES: Reflex hepatitis C virus (HCV) RNA testing of anti-HCV–positive specimens is a client-centred approach to improve engagement in care by increasing the proportion of confirmatory tests, while decreasing the time to test result. However, validated protocols and guidance available to support laboratories in implementing reflex testing are limited. We sought to implement HCV RNA reflex testing in a provincial public health lab and to describe its impact on active HCV diagnosis.

METHOD: A validation was conducted to determine concordance of HCV RNA NAT results on the Abbott m2000 (Abbott, Chicago, Illinois) between serum and plasma, using 27 anti-HCV reactive (25 RNA-positive, 2 RNA-negative) specimens (1 ethylenediaminetetraacetic acid [EDTA] plasma and 2 serum separator tubes [SSTs] per case, collected same day). One SST was held for 10 days after collection at 4°C. An algorithm for reflex HCV RNA testing was developed on the basis of the validation results and implemented in January 2020. We then determined the number of anti-HCV–positive serum specimens RNA tested up to November 2021.

RESULTS: We found 100% concordance of HCV RNA nucleic acid test (NAT) results between serum and plasma for serum specimens with high screen anti-HCV index value (>11 on Siemens Centaur) and reactive on confirmatory testing (Abbott Architect). Results were still 100% concordant after 10 days storage. The reflex HCV RNA testing algorithm implemented selects serum samples with anti-HCV signal >11 from new anti-HCV-positive testers, or those who had previously tested anti-HCV positive but never had an HCV RNA test conducted, where EDTA plasma is not available. Among 4,718 anti-HCV–positive serum specimens, 1,173 were eligible for reflex testing and had the HCV RNA NAT performed.

CONCLUSION: Reflex HCV RNA serum testing is suitable for samples with high anti-HCV index values. Further evaluation is planned to determine the impact of HCV RNA reflex testing on time to RNA testing and treatment uptake.

P60

Validation of free-living amoebae multiplex real-time PCR assay with endogenous control

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OBJECTIVES: Free-living amoebae (FLA) cause rare but severe clinical disease, including ocular and central nervous system complications. Diagnosis is frequently delayed because of low sensitivity of microscopy and prolonged turnaround time of culture. This study aimed to validate an existing qualitative polymerase chain reaction (PCR) assay, modified by adding the internal control human beta globin (HBG) to assess sample adequacy, for simultaneous detection of the three most common FLA, *Acanthamoeba* spp, *Balamuthia mandrillaris,* and *Naegleria fowleri*.

METHOD: *In silico* and Biotechnology Information Basic Local Alignment Search Tool analysis and optimization of PCR conditions and reagents were completed. Analytical validation was performed using in-house and commercial reference materials, including analytical sensitivity, specificity, and precision. Prospective clinical validation using corneal scrapings and cerebrospinal fluid (CSF) samples was initiated to evaluate clinical sensitivity and specificity against microscopy and culture.

RESULTS: Using genomic DNA from a reference laboratory, the limit of detection (LOD) was 100 copies/reaction for all

three FLA targets. Using serially diluted cultured *Acanthamoeba*, the tissue extraction kit performed optimally with a LOD of 10 cells/mL. The multiplex assay reaction efficiency was >90%. Testing with extracts of other microbial agents of keratitis (*Fusarium, Candida, Staphylococcus aureus, Streptococcus pneumoniae,* herpes simplex virus, varicella zoster virus, and adenovirus) demonstrated no off-target amplification. The coefficient of variation for inter- and intra-assay precision was <3%. A total of 12 samples (including 1 CSF) have been tested for the clinical validation so far. PCR detected *Acanthamoeba* spp in a corneal scraping and swab from one patient that was confirmed by culture. The remaining samples were negative by all tested methods, of which three were HBG positive.

CONCLUSION: The modified FLA multiplex PCR test showed acceptable performance in line with the original assay, with the added benefit of assessment of sample adequacy. Use of this assay will provide improved sensitivity and turnaround time compared with current methods, facilitating earlier diagnosis. Continued clinical validation is required before implementation.

P61

Comparing concentrations of SARS-CoV-2 anti-spike antibodies in multiple dilutions of plasma specimens

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OBJECTIVES: With vaccination, total anti–severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike antibody concentrations total anti-S in blood donor plasma saturates at 250 U/mL tested neat and at 2,500 U/mL when diluted 1:10. We compared total anti-S for samples of <250 U/mL, 250–2,500 U/mL, and >2,500 U/mL using neat, 1:10, 1:100, and 1:400 dilutions.

METHOD: The Roche Elecsys® SARS-CoV-2 total anti-S assay (Roche Diagnostics, Indianapolis, Indiana) is a semi-quantitative assay. Since January 2021, we have used the Roche system to measure total anti-S in blood donor plasma (N > 130,000). A total of 9,306 positive samples <250 U/mL and 5,910 samples ≥250 U/mL were diluted 1:10 and re-tested. Samples originally 250–2,500 U/mL (n = 20) and >2,500 U/mL (n = 20) using a 1:10 dilution were diluted 1:100 and 1:400 and re-tested. Total anti-S were compared using Pearson correlation coefficient, median, and interquartile range (IQR).

RESULTS: Total anti-S for samples <250 U/mL correlated at neat and 1:10 dilutions (r = 0.93, p < 0.0001). Of samples that saturated at 250 U/mL (n = 5,910) when tested neat, total anti-S distributions using a 1:10 dilution were as follows: <250 U/mL (n = 497; 8.4%; median 203 U/mL, IQR 175–227), 250 U/mL (n = 5; 0.1%), and >250 U/mL (n = 5,408; 91.5%). On samples with a total anti-S of 250–2500 U/mL at a 1:10 dilution (n = 20), median total anti-S was as follows: at 1:10, 1,422 U/mL (IQR 948–1,812); 1:100, 1,568 (IQR 1,145–2,085); and 1:400, 1,732 (IQR 1,287–2,289). On samples with a total anti-S of >2,500 U/mL at a 1:10 dilution (n = 20), median total anti-S was as follows: at 1:100, 6,577 (IQR 4,214–13,436) and 1:400, 7,372 (IQR 4,615–14,748). Total anti-S strongly correlated at multiple dilutions: at 1:10 versus 1:100, r = 0.99; 1:10 versus 1:400, 0.99; and 100 versus 1:400, 0.94 (p < 0.001).

CONCLUSION: There is some variation in total anti-S among 1:10, 1:100 and 1:400 dilutions. The 1:400 dilution permits quantitation up to 100,000 U/mL.

P62

Detecting COVID-19 biological markers using a canine scent detection team

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OBJECTIVES: Growing evidence shows that canines can detect microorganisms (including viral infections) and that their accuracy is on par with laboratory. We evaluated whether canines can safely imprint on the scent of coronavirus disease 2019 (COVID-19) gargle, sweat, and breath samples with scientifically rigorous specificity, sensitivity, and inter-reliability to determine whether canine scent detection is a suitable alternative to rapidly detect infected patients. The goal is to protect health while safely re-starting the Canadian economy through an innovative solution to COVID-19 screening.

METHOD: Once trained on the scent of COVID-19, three canines were formally evaluated through an odour recognition test. Gargle, sweat, and breath odours were collected from both inpatients and outpatients. Gargle and sweat odours were transposed to Getxent™ tubes (Getxent,

Neuchâtel, Switzerland), and breath samples were captured on surgical masks. All odours used for the validation were new odours not previously used for training. The dog was required to correctly identify positive COVID-19 samples and discriminate them from negative samples and associated odours. Evaluation occurred in a controlled environment by an external validator. The handler was blinded to where the positive scents were positioned. They announced the dog's alert aloud and dispensed a reward to the dog when the validator acknowledged that it was a true-positive alert.

RESULTS: The dogs detected COVID-19 gargle, sweat, and breath samples with 100% sensitivity and 94% specificity:

- Dog 1: sensitivity 100%, specificity 92.7%, positive predictive value (PPV) 60.38%, negative predictive value (NPV) 100%
- Dog 2: sensitivity 100%, specificity 93.75%, PPV 64%, NPV 100%
- Dog 3: sensitivity 100%, specificity 95.24%, PPV 70.0%, NPV 100%.

CONCLUSION: The results confirmed that three dogs are certified to detect COVID-19 and that using a safe training aid (non-pseudoscent alternative) for training canines is effective. This shows that canines have the ability to act as a fast and reliable assessment tool to enhance screening strategies for COVID-19

P63

Replicative fitness of SARS-CoV-2 variants

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OBJECTIVES: Multiple lineages of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have arisen since the initial spread of the virus in early 2020. The original wild-type strain (Wuhan) has been replaced by successive variants. One hypothesis for the rapid spread of variants is that they have better replicative fitness, allowing faster growth to higher titres in the infected tissues than the wild-type virus. Growth curve experiments were performed on variant isolates recovered in British Columbia.

METHOD: Growth curves were determined using SARS -CoV-2 wild-type virus and isolates of the Alpha, Beta, Gamma, Delta, and Omicron variants, in addition to isolates of interest from clusters in British Columbia. Monolayers of Vero E6 or Vero E6 TMPRSS2 cells in 12 well plates inoculated with virus were incubated and harvested at various time intervals. Supernatant growth medium was removed and stored at –80°C. Cells were trypsinised and frozen. Viral titres were quantified by median tissue culture infectious dose ($TCID_{50}$) and cycle threshold (Ct) values were determined by polymerase chain reaction (PCR).

RESULTS: After inoculation, titres of the wild-type virus in cells remained stable at approximately 10^4 $TCID_{50}$/mL for 4 hours, after which a rapid increase to approximately 10^8 $TCID_{50}$/mL was detected. PCR Ct values decreased, reflecting the increase in cell-associated virus. Viral titres in the supernatant reached a slightly lower maximum titre than virus in cells. Each of the variants reached titres similar to wild-type virus.

CONCLUSION: Our data suggest that SARS-CoV-2 variants do not show substantial differences in their growth in cell culture compared with the wild-type virus. However, our data are based on single isolates. In addition, isolates were passaged a limited number of times compared with the wild-type strain, which was isolated in April 2020. It is possible that further passages would show better adaptation to growth in vitro.

P64

Surface and air contamination with SARS-CoV-2 from hospitalized COVID-19 patients with Delta variant infection in Toronto, Ontario, Canada

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OBJECTIVES: We aimed to determine the burden of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) on surfaces and in air from hospital rooms of inpatients acutely ill with coronavirus disease 2019 (COVID-19) during the 2021 Delta variant outbreak in Toronto, Ontario.

METHOD: Nasopharyngeal (NP) swabs, saliva, high-touch and non-touch surfaces, and air samples were collected from rooms of 52 inpatients with COVID-19 at eight acute-care hospitals in Toronto from July to September 2021. Samples underwent reverse transcription polymerase chain reaction (RT-PCR) for SARS-CoV-2 RNA, and surface samples with a cycle threshold value <34 were cultured to determine potential infectivity. Whole viral genomes were generated.

RESULTS: All patients were diagnosed with clinical NP specimens before or at admission. Of the study samples collected, 67 (85%) NP swabs from 33 (94%) patients and 75 (77%) saliva samples from 43 (93%) patients were positive for SARS-CoV-2 by PCR. SARS-CoV-2 RNA was detected from surfaces (57/300 samples; 27/52 patients) but not air (0/6 samples; 0/6 patients); 5% (1/18) of surface samples yielded viable virus. SARS-CoV-2 RNA was detected in 22% (54/250) of the high-touch surface samples compared with 6% (3/50) of the non-touch surface samples. Whole viral sequences indicated that all surface samples clustered with the corresponding NP swabs from patients occupying the same room.

CONCLUSION: Although SARS-CoV-2 RNA is detectable on surfaces in the rooms of inpatients acutely ill with COVID-19, viral RNA was infrequently detected on non-touch surfaces and was not detected in the limited number of air samples investigated. In addition, recovery of infectious SARS-CoV-2 from surfaces was uncommon. Our findings from this Delta variant cohort are comparable to those of our previous study that investigated environmental contamination in COVID-19 patients with wild-type SARS-CoV-2 infection. Collectively, these data suggest that near-patient surfaces in the acute-care setting likely pose limited risk for health care workers.

P65

Automated assignment of SARS-CoV-2 re-infections from provincial whole-genome sequencing data in British Columbia, Canada

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OBJECTIVES: British Columbia has a comprehensive whole-genome sequencing (WGS) strategy that enables the near real-time monitoring of existing and emerging lineages in addition to identifying re-infections. We developed a methodology that leverages province-wide diagnostic and WGS databases to identify re-infection cases dating back to the start of the pandemic.

METHOD: A bioinformatic pipeline was developed to scan provincial severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) laboratory diagnostic testing database for potential instances of re-infection. Cases were considered re-infections when the following conditions were met:

1. Subsequent infection(s) after an initial confirmed case was resolved
2. WGS indicated distinct lineages or one infection was confirmed via sequencing to be a variant that was not circulating in Canada when the prior infection occurred
3. The difference between observed and expected number of unique single nucleotide polymorphisms (SNPs) in an infection pair exceeded the threshold on the basis of length of time between sampling events. The expected number of mutations was a multiple of global average SARS-CoV-2 mutation rate of one substitution per site per fortnight. The BCFtools (v1.13) "isec" command determined observed mutations.

RESULTS: There were 215 (0.08%) re-infections out of 266,980 total cases examined between July 8, 2020, and December 26, 2021. Time to re-infection varied between 35 and 641 days, with a median of 286 days. The median age of re-infected individuals was 29 years (mean 33 y, range 6–99 y). The most commonly observed lineage in re-infection cases was Omicron (115 cases), followed by Delta (78 cases). The majority of re-infection cases (n = 124) occurred in vaccinated individuals.

CONCLUSION: Re-infection cases of SARS-CoV-2 in British Columbia are rare and occur in a relatively young population. SNP comparison provides an automatable method to monitor for re-infections, with important insights into immune waning and implications for pandemic duration.

P66

Improved identification of yeast and mould isolates with MALDI-TOF VITEK MS (version 3.2)

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Table P66-1: Mould identification

Category	VITEK MS PRIME (%)	VITEK MS (%)
No identification	17/70 (24.3)	18/60 (30)
Correct to species or species complex	53/53 (100)	41/42* (97.6)

*1 discordant result for the MS: *R. microspores* (ref lab *R. oryzae*). PRIME provided a species identification compared with genus level by microscopic morphology in 8 isolates (*Candida sphaerospermum, Fusarium oxysporum, F. solani complex, Purpureocillium lilacinum, P. chrysogenum, Alternaria alternata, Mucor circinelloi*des [*n* = 2])

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OBJECTIVES: Identification of fungi by phenotypic methods on the basis of morphologic features is routinely used in clinical laboratories and is labour intensive, and requires specialized expertise; turn-around time is prolonged and identification (ID) of the species is difficult. The accuracy of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF; VITEK MS and MS PRIME, bioMérieux, Marcy-l'Étoile, France) for the ID of fungi was evaluated.

METHOD: Isolates evaluated were 33 reference yeast strains, which included 13 *Cryptococcus neoformans* and *Cryptococcus gattii* species complexes and 36 reference strains of moulds, which included 23 *Aspergillus fumigatus* from an international collection and 34 clinical isolates. Moulds underwent an inactivation and extraction step with drying of the spot using a halogen light. Discordant results were resolved by a reference laboratory.

RESULTS: Yeast ID was 100% accurate, including *C. gattii* species complex lineages VGI, II, III, and IV (*n* = 8) and *C. neoformans* species complex (*n* = 3). Two genetic hybrids of *C. gattii* and *C. neoformans* were identified as *C. neoformans/gattii* and *C. neoformans*. Candida species were correctly identified, including *Candida auris* (*n* = 2), *C. duobushaemulonii* (*n* = 2) and *C. haemulonii* (*n* = 1).

CONCLUSION: MALDI-TOF MS PRIME accurately identified yeast isolates, including species complex level ID of *C. neoformans* and *C. gattii*. Mould ID was accurate to the genus and species. Species ID was improved compared with morphologic features. Non-ID with the PRIME was lower than with the MS. Further research to reduce the frequency of non-ID and to evaluate detection of azole resistance in *Aspergillus fumigatus* is ongoing.

P67

Evaluation of *Strongyloides* awareness and knowledge among Canadian physicians caring for patients at risk for severe strongyloidiasis: A national cross-sectional survey

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OBJECTIVES: In Canada, a substantial proportion of migrants come from strongyloidiasis-endemic regions, but screening for *Strongyloides* is still not systematically performed for immunocompromised patients. We aim to (1) assess the level of awareness and knowledge of *Strongyloides* among Canadian physicians caring for immunocompromised patients and (2) identify the determinants currently associated with screening for *Strongyloides*.

METHOD: Using an online survey distributed through Canadian medical associations, we collected physicians' demographic information, practice setting details, overall awareness and knowledge of *Strongyloides*, and current practices. Descriptive analysis and logistic regression models were performed to identify the determinants associated with screening for *Strongyloides*.

RESULTS: Thirteen national-level medical associations agreed to participate in our study. Either direct email or e-newsletters were the means of disseminating our survey to the respondents. From November 2020 to August 2021, 368 of 5,194 (7.09%) physicians who were contacted responded to our survey, with an overall 92.66% completion rate. Quebec (46.47%), Ontario (24.18%), and the Prairies (16.58%) were the most represented. Most respondents practiced medicine in academic settings (69.77%). The highest response rates came from infectious disease (ID) specialists or medical microbiologists (38.14%), followed by nephrologists (33.62%). Most respondents (95.60%) had heard about *Strongyloides*. However, more than a third (36.32%) of non-ID specialists considered themselves unfamiliar with *Strongyloides*. Of respondents, 40.47% do not or rarely perform screening tests for strongyloidiasis in high-risk populations. *Strongyloides* screening was associated with younger-aged physicians (25–35 y;

odds ratio [OR] 2.35; 95% CI 1.07 to 5.18); physicians who frequently serve migrants (OR 3.33; 95% CI 1.44 to 7.66); have training in global health (OR 3.71; 95% CI 1.21 to 11.34) and ID or medical microbiology (OR 46.42; 95% CI 15.89 to 135.59).

CONCLUSION: Our survey suggests a general lack of knowledge of *Strongyloides* among Canadian physicians, which ultimately results in a lack of screening in high-risk populations. Further qualitative studies assessing barriers to screening are being conducted.

P68

Validation of an in-house real-time PCR assay for the simultaneous detection of SARS-CoV-2, influenza A, influenza B, and respiratory syncytial virus

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OBJECTIVES: Throughout the first year of the coronavirus disease 2019 (COVID-19) pandemic, the rate of other respiratory viruses circulating plummeted. The recent increase of respiratory syncytial virus (RSV) and influenza A/B cases added pressure on laboratories to rapidly and accurately identify these viruses for infection control purposes. Two existing lab-developed tests (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2] and influenza/RSV) were combined into one reverse transcription polymerase chain reaction (RT-PCR) assay that was validated for the simultaneous detection of all four viruses from respiratory specimens.

METHOD: The combined SARS-CoV-2/Inf/RSV (FLUVID) RT-PCR assay was optimized for the use on the ABI 7500 Fast thermocycler (ThermoFisher Scientific, Waltham, Massachusetts). The following parameters were assessed as part of the assay validation: assay optimization, PCR efficiency, analytical sensitivity and specificity, accuracy, and reproducibility. The FLUVID assay was compared with the separate SARS-CoV-2 and influenza/RSV assays as the reference standards.

RESULTS: The two gene targets for SARS-CoV-2 (envelope-gene and RNA-dependent RNA polymerase) were combined into one filter, as were influenza A and influenza B. RSV and the internal control (human *RNAseP* gene) were optimized for the remaining two filters. The analytical sensitivity of the FLUVID assay for all four targets was comparable with the respective reference assay, and no cross-reactivity with other respiratory pathogens was observed. Accuracy was tested using a total of 226 archived (n = 139) and prospective (n = 87) specimens. In samples positive for a single target, the positive percentage agreement with the respective reference assay was greater than 96% and the negative percentage agreement was greater than 98% for all targets. All discordant results occurred in samples with very low analyte concentrations.

CONCLUSION: Combining the targets for SARS-CoV-2 and the two influenza types into their respective channel allowed for rapid and clinically actionable results. From a surveillance perspective, influenza typing continues to be routinely available at the provincial public health laboratory.

P69

Performance of the 3M Quick Swab method for environmental surface monitoring

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OBJECTIVES: Time kill studies on self-disinfecting surfaces are laborious and time consuming. We describe a partially automated protocol that allows faster results and objective measurement of bactericidal effect.

METHOD: Stainless steel (SS), elemental copper (Cu), and three Cu nanoparticle (NP) coupons were inoculated with *Staphylococcus aureus* or *Pseudomonas aeruginosa.* The 3M Quick Swab (3M, St. Paul, Minnesota) was used to recover bacteria at 30, 60, and 120 minutes post-inoculation. Recovery broth was plated onto 3M Aerobic Petrifilm plates using neat, 1:100, and 1:1,000 dilutions and incubated for 2 days, after which colony forming units (CFUs) were enumerated using their automated plate reader. The broth was also sub-cultured to 5% sheep blood agar plates to assess contamination. Swabbed coupons were sonicated in Letheen broth, sub-cultured, and incubated for 2 days to assess the efficacy of the Quick Swabs at bacterial retrieval and to assess contamination. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry was used to identify aberrant colonies.

RESULTS: Five different surfaces were tested in triplicate at three time points within 3 hours. It allowed the recovery of organisms at 30 minutes, the average time for coupons to dry. CFUs remaining on coupon surfaces after using the Quick

Table P69-1: Colony forming units (CFU/mL) comparing residual bacteria left on metal coupons after use of the 3M™ Quick Swab at 30, 60, and 120 minutes post inoculation. Coupons were sonicated for 5 minutes in Letheen broth to recover residual bacteria

Pseudomonas aeruginosa	**30 min**	**60 min**	**120 min**
Stainless steel (1 mL)	196	204	107
Stainless steel (100 µL)	7	38	20
Copper	10	0	0
NP1	0	0	0
NP2	0	0	0
NP3	0	0	0
Staphylococcus aureus			
Stainless steel (1 ml)	TNTC* (~816)	TNTC* (~1256)	TNTC (~880)
Copper	12	49	16
NP1	1	15	7
NP2	36	1	1
NP3	54	0	2

NP = Nanoparticle

Swabs was insignificant. An inoculum effect was observed on SS. One colony contamination was observed in the two experiments for the Cu coupon at 30 min.

CONCLUSION: The Quick Swab method is rapid, and although more expensive, it is labour and cost efficient.

P70

Can we do SARS-CoV-2 cumulative seroprevalence study in a vaccinated population? Anti-N seroprevalence study among blood donors in Quebec

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OBJECTIVES: Although severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccination was rapidly deployed in Quebec in spring 2021, a new SARS-CoV-2 seroprevalence phase was assessed after the third pandemic wave using anti-RBD and anti-N antibodies among blood donors.

METHOD: Plasma samples from regular donors were collected between June and July 2021and analysed using two enzyme-linked immunosorbent assays capturing SARS-CoV-2 antibodies directed against the receptor binding domain of the spike protein (anti-RBD) and the nucleocapsid protein (anti-N). Data were compared with the National Register for vaccination and infection. Seroprevalence estimates were adjusted for regional distribution, age, and sex.

RESULTS: A total of 2,554 donors were included in the study. One-dose and two-dose vaccination rates were 93.54% and 92.36%, respectively. The anti-RBD seroprevalence rate was 89.61% (95% CI 88.48% to 90.75%), and the anti-N seroprevalence was 6.43% (95% CI 5.52% to 7.34%). Among the 127 unvaccinated donors, 24 (20.17%) had anti-RBD, and 12 (8.01%) had anti-N. Among 73 participants previously infected, 46 (63.01%) were seropositive for anti-N, suggesting a rate of seroreversion of about 36.09%. The median time from diagnosis of coronavirus disease 2019 to sampling collection was longer among anti-N–negative participants than among anti-N–positive participants (240 versus 182 d), and 23/46 (52.17%) of participants with infection ≥6 months before study participation were anti-N negative.

CONCLUSION: The study reveals a lower sensitivity of the determination of past infections by measuring anti-N, probably linked to the earlier seroreversion of the anti-N humoral response than the anti-RBD. This new information illustrates the complexity of monitoring cumulative prevalence in an increasingly vaccinated population during a long-standing pandemic.

P71

Personal protective equipment laboratory testing: N95 particulate filtration efficiency testing prevents more than 2.4 million substandard respirators from entering Canadian PPE supply chain

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OBJECTIVES: To evaluate the proportion of N95 and N95-equivalent respirators from non-traditional suppliers (eg, international or nascent companies) that meet National Institute for Occupational Safety and Health (NIOSH) standards as

fit for health care use and, ultimately, to prevent substandard or counterfeit personal protective equipment (PPE) from entering the Canadian PPE supply chain.

METHOD: With provincial and health authority support, a purpose-built, International Organization for Standardization (ISO)–accredited PPE testing facility was created in a tertiary-care, academic hospital in a major Canadian urban centre. Between September 2020 and March 2021, 13 models of N95 and N95-equivalent respirators were tested. PPE testing is a destructive procedure so a *proportion* of N95 lots are tested to represent the whole lot. A total of 1,750 respirators were selected according to American National Standards Institute (ANSI)/American Society for Quality CZ1.4-1993, representing 4.3 million total respirators. Particulate filtration efficiency (PFE) was evaluated on an industry-standard Automated Filter Tester 8130A (TSI, Shoreview, Minnesota) in accordance with NIOSH Procedure TEB-APR-STP-0059. Respirators were conditioned at 85% ± 5% relative humidity and 38°C ±2°C for 25±1 hours before testing, then challenged with NaCl aerosol neutralized to a Boltzmann equilibrium state at 25°C ±5°C and a relative humidity of 30% ±10%. Particle size distribution was verified to be a count median diameter of 0.075±0.020 microns, with a geometric standard deviation not exceeding 1.86. Descriptive statistics were applied using Excel version 16.48 (Microsoft, Redmond, Washington).

RESULTS: According to ANSI selection criteria and NIOSH testing standards, a total of 1.9 million respirators met 95% filtration efficiency, whereas 2.4 million failed. Although 8/13 (62%) of models tested met NIOSH standards, the 5/13 (38%) of models that failed represented a larger proportion of overall respirators. Results are summarized in Table 1.

Table P71-1: Particulate filtration efficiency results for 13 models of N95 respirators

N95/N95- equivalent Model	Number of respirators tested (Lot size)	Result
A	50 (1000000)	Fail
B	32 (410000)	Pass
C	70 (78450)	Fail
D	50 (1070050)	Fail
E	47 (87550)	Fail
F	32 (38850)	Pass
G	32 (137600)	Pass
H	65 (234400)	Pass
I	70 (616050)	Pass
J	102 (335850)	Pass
K	50 (30000)	Pass
L	50 (100000)	Pass
M	1100 (150000)	Fail
Total Pass	433 (1,902,750)	
Total Fail	1367 (2,486,050)	

CONCLUSION: In conclusion, N95 PFE testing is an effective tool to identify respirators that meet or fail industry standards. In our experience, substandard N95 are not uncommon, and we prevented more than 2.4 million unfit respirators from entering the Canadian PPE supply chain.

P72

Antimicrobial dispensations for uncomplicated urinary tract infections among women residing in long-term-care homes: A retrospective cohort study

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OBJECTIVES: Fluoroquinolone antibiotics are used for treating uncomplicated urinary tract infection (uUTI) despite recommendations to reserve these antibiotics as alternative options. Adverse effects of fluoroquinolones can be problematic for older women. Women residing in long-term care (LTC) are also more likely to live with polypharmacy, which increases their risk of significant cardiac drug interactions associated with fluoroquinolone use. The objective was to describe antibiotic use for uUTI among women residing in LTC.

METHOD: A retrospective cohort study was conducted using administrative data (January 2005–March 2020). Subjects were women aged ≥65 years who resided in a LTC home and were dispensed an antibiotic for a uUTI. Antibiotic dispensations were reported as generic drug names (Anatomical Therapeutic Chemical code). Multiple logistic regression was used to compare outcomes of additional antibiotic dispensation or follow-up care required 7 days after initial antibiotic dispensation of a fluoroquinolone compared with other antibiotics, adjusted using high dimensional propensity scores and inverse probability treatment weighting.

RESULTS: A total of 15,276 uUTI events were reported among 7,078 women. Total yearly antibiotic dispensations for uUTI events declined significantly during the study period, from 1,387 in 2005 to 402 in 2019 ($p < 0.001$). The most dispensed antibiotics were trimethoprim–sulfamethoxazole (25.8%), nitrofurantoin (25.5%), and ciprofloxacin (18.6%). Compared with other antibiotics, fluoroquinolone dispensation resulted in fewer women receiving a subsequent antibiotic (adjusted odds ratio [OR] 0.81, 95% CI 0.74 to 0.88) or a follow-up visit for a uUTI event (adjusted OR 0.88, 95% CI 0.80 to 0.97). No increase in hospitalizations for uUTI events was observed (adjusted OR

0.78, 95% CI 0.53 to 1.16) between individuals dispensed a fluoroquinolone and those dispensed other antibiotics.

CONCLUSION: Antibiotic dispensations to female LTC home residents for uUTI decreased from 2005 to 2019. Fluoroquinolones are associated with a decrease in subsequent antibiotic dispensation and follow-up care for uUTI, although their risk in this patient population may outweigh any potential benefit.

P73

Experience and interest in bacteriophage therapy in Canada: An AMMI Canada survey

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OBJECTIVES: Antibiotic resistance is a clear global threat to human health. The use of bacteriophages ("phages") to treat bacterial infections predates antibiotics and is gaining traction to treat extensively drug-resistant infections internationally. AMMI Canada members were surveyed to determine their interest and experience with phage therapy in Canada.

METHOD: After a brief pilot test, a 12-question survey was sent to 624 AMMI Canada members who are mostly Infectious Disease (ID) physicians and Medical Microbiologists. The initial notice was sent on August 27, 2021, and two reminders were provided. Results were collated and were anonymized.

RESULTS: The response rate was 42 of 624 members (6.7%). Forty-five percent of respondents indicated they were Infectious diseases physicians, 28% identified as both infectious disease physicians and medical microbiologists, while 21% identified as medical microbiologists alone. Zero respondents had provided phage therapy, but 4 (9.5%) had worked with a team that had provided phage therapy, while up to 69% were interested in exploring phage therapy. Respondents reported partnering with various phage therapy centres, including: San Diego (7), Pittsburgh, (6), Israel (2), Houston (1), France (1), Republic of Georgia (1). Development of a patient registry was requested by 76% of respondents. Only 7 respondents would add their name to a phage therapy directory to provide services. Thirty-three respondents were interested or highly interested in participating in a phage therapy working group.

CONCLUSION: This is the first survey, administered to an ID society on phage therapy. Members showed there is still limited experience with phage therapy, but a majority were interested in developing a patient registry. Although the response rate was low, the survey was helpful for establishing a Canadian Phage Therapy Working Group and Steering Committee. Further research on and improved access to Phage therapy is urgently needed for Canadian ID clinicians.

P74

Cohort profile: A plasma donor biobank to study immunity to COVID-19 (PlasCov)

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OBJECTIVES: Despite progress, understanding of the long-term, humoral immunity to coronavirus disease 2019 (COVID-19) is incomplete because of a number of challenges, including the continuous emergence of new variants. To overcome these barriers, our blood service established a biobank dedicated to COVID-19 research, which we describe here.

METHOD: The biobank, launched in March 2021, consists of plasma samples collected through regular plasma donations made at Héma-Québec, the Quebec provincial blood service. At that time, the majority of the Quebec general population was unvaccinated, which enabled us to collect samples from thousands of participating donors both pre- and post-vaccination. Ten fixed plasma centers were designated to collect biobank-dedicated samples.

RESULTS: The biobank includes samples from a population-based cohort of donors of apheresis plasma. As of December 20, 2021, 14,925 of 16,351 (91.3%) donors consented that a small aliquot of their donations be used for biobanking and provided 77,337 samples. Mean number of donations per participant was 5.2, with 63.7% giving 2–38 samples. Approximately one-third (31.3%) of participants donated only a sample before vaccination, another third (32.0%) donated only post-vaccination, and the remaining third donated pre- and post-vaccination (36.7%). Demographic and clinical characteristics are collected as part of routine donor screening. Vaccination and infection are obtained from a government registry of COVID-19–related information.

CONCLUSION: This biobank collects longitudinal plasma samples from thousands of donors. To the best of our knowledge, this is the largest biobank dedicated to COVID-19

research. All researchers in Canada or elsewhere may apply to access the biobank.

P75

Leveraging pandemic-associated teaching challenges to create open educational resources: One instructor's experience teaching microbiology in a professional program

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OBJECTIVES: To describe the experience of one instructor who created and used open educational resources (OER) to teach microbiology in a professional health science program throughout the coronavirus disease 2019 pandemic.

METHOD: Two different forms of instructor-prepared OERs were used. High-resolution photos (plates, Gram stains, and biochemical tests) were posted to Flickr, and laboratory demonstration videos (plate streaking, Gram staining, and susceptibility testing) were posted to YouTube, all under a creative commons license. Students also developed OER through a Wikipedia writing assignment in which articles related to course content were improved.

RESULTS: The use of YouTube videos greatly improved the accessibility of laboratory content for students. Through YouTube analytics, an increase in views was seen preceding the final exam, indicating that students re-watched the content as a study aid. These statistics also revealed that >95% of the 11,000 views were from outside the university and that the learning management systems of other institutions were a substantial source of traffic. Similarly, the Flickr images cumulatively received >55,000 views. Posting these materials with a creative commons license improved access for individuals at institutions in developing countries, whose access to high-quality content may be limited by paywalls. The students' experiences of the Wikipedia assignment were mixed; although many felt it was too much work, the quality of their articles led to all 19 being published by Wikipedia.

CONCLUSION: Although the production of OERs was time consuming and required the development of new skills, it was creatively stimulating for me as an instructor. Beyond allowing the delivery of my course, the analytics features of Flickr and YouTube allowed me to enumerate the impact of each learning item (view count and traffic source), demonstrating the value of my efforts in publishing these resources. I would encourage other instructors to consider open options when creating new teaching materials.

P76

Whole-genome sequencing enhances institutional responses to SARS-CoV-2 outbreaks

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OBJECTIVES: Outbreaks in institutional settings are particularly challenging because infection prevention and control (IPAC), occupational health and safety (OHS), and Public Health must quickly investigate, assess, and isolate infected cases and trace potential exposures to mitigate further spread of the pathogen. Time-resolved severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) whole-genome sequencing (WGS) can help trace origins and explain localized spread of SARS-CoV-2 to aid IPAC, OHS, and Public Health teams control and understand the outbreak dynamics.

METHOD: Samples collected at hospitals, correctional facilities, and testing centers were received and tested for SARS-CoV-2 using quantitative polymerase chain reaction. Positive specimens with an E-gene cycle threshold <30 were sent for WGS using the Illumina COVIDSeq Assay (Illumina, San Diego, California). Bioinformatics analysis generated a viral consensus genome and variant summary for each sample, which were used to cluster similar viral genomes and suggest potential connections between their hosts.

RESULTS: Our lab has sequenced >7,500 SARS-CoV-2 genomes over the past 12 months. Here we report our analysis of six institutional outbreaks—four hospitals and two correctional facilities—ranging from small (n = 4) to large (n = 83) numbers of cases. WGS demonstrated that many individuals involved in the outbreaks share similar or identical genomes and are likely associated by direct or indirect transmission events. However, WGS also identified cases with distinct viral genomes, indicating that they were not actually part of the institutional outbreak.

CONCLUSION: WGS was essential to ensure cases were correctly attributed to the outbreak. Coupling WGS with IPAC, OHS, and Public Health contact tracing enhances the institution's ability to understate the dynamics of transmission and respond appropriately to mitigate the spread or inform policy for reducing future spread. If conducted in a rapid manner, WGS may help facilities with an outbreak to quickly focus on the strains and

transmission pathways that circulate and cause disease among the affected patient population.

P77

Seroprevalence of SARS-CoV-2 antibodies among blood donors in Quebec: Results of phases 1 and 2 of a serial cross-sectional study

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OBJECTIVES: The number of confirmed coronavirus disease 2019 (COVID-19) cases identified by health care systems is one indicator of the progression of the pandemic; however, the true burden of infection can be more precisely estimated by the seroprevalence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) antibodies in a sample broadly representative of the general population. We estimated the seroprevalence of SARS-CoV-2 antibodies among blood donors in Quebec (Canada) in two separate phases of a serial cross-sectional study.

METHOD: Blood samples from regular donors were collected from May to July 2020 (phase 1; first pandemic wave) and from January to March 2021 (phase 2; second pandemic wave). Anti–SARS-CoV-2 seropositivity was assessed with an enzyme-linked immunosorbent assay that captures antibodies directed against the receptor binding domain of the SARS-CoV-2 spike. Seroprevalence estimates were adjusted for regional distribution, age, and sex.

RESULTS: In phase 1, 7,691 blood samples were analyzed, all from unvaccinated donors. The adjusted seroprevalence was 2.2% (95% CI 1.9% to 2.6%), and the proportion of seropositive donors who reported one or more symptoms was 52.2% (95% CI 44.2% to 60.1%). In phase 2, 7,924 blood samples were analyzed, including 620 (7.8%) from vaccinated donors and 7,046 (88.9%) from unvaccinated donors (vaccination status unknown for 3.3%). The adjusted seroprevalence was 10.5% (95% CI 9.7% to 11.3%) in the unvaccinated population and 14.7% (95% CI 13.8% to 15.6%) in the overall population.

CONCLUSION: The seroprevalence of SARS-CoV-2 antibodies has significantly increased in Quebec since spring 2020. Moreover, when compared with the cumulative incidence rate reported by public health authorities (ie, end of phase 1, 0.55%, and end of phase 2, 3.3%), these results suggest that a substantial proportion of infections remain unreported despite improvements in access to COVID-19 testing.

P78

Validation of the BioFire® FilmArray® Gastrointestinal Panel for the identification of enteric pathogens

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OBJECTIVES: The BioFire® FilmArray® Gastrointestinal Panel (FAGI; BioFire Diagnostics, Salt Lake City, Utah) is a multiplex nucleic acid test for the simultaneous detection of 22 bacterial, viral, and parasitic enteric pathogens. The performance of the panel was verified using retrospective specimens.

METHOD: A panel of archived stool specimens were transferred into Carry Blair medium and tested by FAGI. Results were compared with routine laboratory methods as the reference (bacterial targets: culture, *Clostridium difficile*, and Shiga toxin–producing *Escherichia coli* (STEC), including *E. coli* O157; viral targets: real-time polymerase chain reaction; parasitic targets: microscopy). For some of the pathogenic *E. coli,* no reference test was available. Viral pathogen testing is still ongoing, as is *discordant analysis, which will be performed using an alternative molecular assay.*

RESULTS: To date, a total of 81 stool specimens positive for one or more pathogen and five negative specimens have been tested on the FAGI panel. Specimens were positive for one or more bacterial targets (n = 46), pathogenic *E. coli* (n = 19), viral targets (n = 7), and parasitic targets (n = 10). For bacterial pathogens, the FAGI demonstrated sensitivities between 80% (*Salmonella* species) and 100% (*Vibrio* and *Yersinia* species) and specificities of 95.9%–100%. Discordant results observed (false positive, n = 4; false negative, n = 7) are currently being resolved. Pathogenic *E. coli,* viral and parasitic targets included, resulted in sensitivities of 100% (except for norovirus, which had a sensitivity of 80%) and specificities of 100%. The overall agreement of the FAGI with the reference results is 98.4%.

CONCLUSION: These preliminary results demonstrated good performance of the FAGI panel for most targets. Discordant result analysis may improve the final sensitivities and specificities for some targets. The test offers convenient and fast testing of stool samples for enteric pathogens.

P79

In-house PCR assay for the diagnosis of *Mycobacterium tuberculosis* on formalin-fixed paraffin-embedded tissue

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OBJECTIVES: We aimed to optimize and evaluate the performance of a lab developed real-time polymerase chain reaction (LDT PCR) assay for the diagnosis of *Mycobacterium tuberculosis* (MTB) from formalin-fixed paraffin-embedded (FFPE) tissues.

METHOD: FFPE tissues underwent deparaffinisation, tissue lysis, and genomic DNA extraction. Extracts were tested by the LDT PCR targeting the insertion sequence 6110 of *M. tuberculosis* complex. PCR results were compared with the reference standard. MTB PCR results were considered concordant positive if at least one of the following three methods was positive: Ziehl Neelsen (ZN) stain of the tissue, MTB culture from the same tissue, or MTB culture from a different tissue. MTB PCR results were regarded as concordant negative if the MTB culture from the same tissue was negative.

RESULTS: The limit of detection was 5 fg of MTB genomic DNA (~1 genome)/reaction. Using a panel of 18 non-tuberculous mycobacteria strains, the analytical specificity was 100%. A total of 118 FFPE tissues (pulmonary tissue, n = 39; lymph nodes, n = 33; other extra-pulmonary tissues, n = 46) with the following histologic findings were tested to assess the accuracy of the PCR: necrotizing granulomas (n = 72); non-necrotizing granulomas (n = 15); granulomas without further specification (n = 22), or unknown presence of granulomas (n = 8). The PCR concordantly detected MTB in 45 of 50 positive FFPE tissue samples (positive MTB culture, n = 39; ZN stain positive, n = 6) for a sensitivity of 90%. For 68 tissues with a negative reference result, the LDT was concordantly negative for 57, resulting in a specificity of 83.8%. The 16 discordant results (false negative, n = 5; false positive, n = 11) were most likely due to sampling issues or very few organisms present in the tissue.

CONCLUSION: The MTB PCR assay is a valuable tool for the detection of MTB in FFPE tissues that can provide rapid results especially in cases in which MTB culture was not done.

P80

Screening and diagnosis of HIV, hepatitis C virus, and syphilis in a regional community using dried blood spot specimens

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OBJECTIVES: Dried blood spot (DBS) samples can be obtained through finger-stick rather than venipuncture, are able to be stored at room temperature, and do not require special handling for transportation. Therefore, DBS can potentially overcome barriers to sexually transmitted and blood-borne infection (STBBI) testing experienced across Canada. We describe here the prevalence of HIV, hepatitis C virus (HCV), and syphilis among people tested by DBS in a pilot based in a regional community in Canada.

METHOD: DBS samples collected in the community are submitted to a provincial Public Health Laboratory (PPHL). STBBI tests requested are accessioned in the PPHL Laboratory Information System (LIS), then forwarded to Reference Laboratory (RL) for testing. The RL performs the testing requested and then sends the results back to PPHL, which are entered in PPHL LIS and reported to the ordering provider. All STBBI test results from DBS are then available in provincial databases and are reported to public health through standard procedures as required.

RESULTS: DBS samples were collected by community health nurses from 19 clients across this regional community between December 2020 and December 2021. Of those, 14 requested HIV screening, 19 requested HCV screening, and 8 requested syphilis screening. No DBS specimens were reactive for HIV or syphilis antibodies. HCV antibodies were detected in 68% (13/19) of DBS specimens. Of those anti-HCV-reactive specimens, 2 had insufficient sample for confirmatory molecular testing. Among those that received nucleic acid testing, 36% (4/11) had HCV RNA detected.

CONCLUSION: This pilot of DBS for STBBI screening and diagnosis has shown that people with high risk for HCV infection in regional communities are able to be reached with this modality. Partnerships between provincial and reference laboratories can successfully enhance access to testing. Further expansion of DBS is warranted to ensure that STBBI testing is equitably accessible across Canada, particularly in regional areas.

P81

Number of new COVID-19 cases required in a population to detect SARS-CoV-2 RNA in wastewater: Sensitivity assessment

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OBJECTIVES: Wastewater-based surveillance (WBS) of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been considered as a valuable complementary tool for monitoring the prevalence of coronavirus disease 2019 (COVID-19) in a community. However, the number of COVID-19 cases required in a community to produce a detectable viral RNA signal in wastewater (WW) is largely unknown. This study evaluates the sensitivity of quantitative reverse transcription polymerase chain reaction (RT-qPCR) detection of SARS-CoV-2 in WW shedding from clinical COVID-19 cases in the respective communities on the basis of testing results of 1,842 WW samples collected from 12 wastewater treatment plants (WWTPs) in Alberta for 14 months.

METHOD: Probit analysis was used to analyze the probability of SARS-CoV-2 RNA detection in WW in relation to the new COVID-19 cases reported. Probabilities of 50%, 80%, and 99% were estimated using the fitted Probit regression relationships for new COVID-19 cases rates per 100,000 population served by each WWTP.

RESULTS: The analyses determined that RT-qPCR-based SARS-CoV-2 detection threshold at 50%, 80%, and 99% required, respectively, medians of 8 (range 4–19), 18 (9–43), and 38 (17–97) of new COVID-19 cases per 100,000. Namely, the positive detection rate at 50%, 80%, and 99% probability were 0.01%, 0.02%, and 0.04%, respectively, for new cases in the community. The detection sensitivity was higher in large communities than in small ones, but the imputed number of new cases required for a small community was lower.

CONCLUSION: Detecting sensitivity of SARS-CoV-2 RNA in WW at 50%, 80%, and 99% probability required, respectively, medians of 8, 18, and 38 of new COVID-19 cases per 100,000 population in a community. Estimated COVID-19 burden at a community level that would result in a positive detection of SARS-CoV-2 in WW is critical to support WBS application as a warning or monitoring system for COVID-19 prevention and control.

P82

Evaluation of the VITEK MS Prime in microbial identification

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OBJECTIVES: Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry has transformed the microbial identification (ID) process. Rapid ID provides critical information to clinicians to guide timely and appropriate therapy, which reduces mortality and supports antimicrobial stewardship and the ongoing fight against antibiotic resistance. This controlled launch study evaluates the performance and enhancements of the new VITEK MS PRIME (bioMérieux, Marcy-l'Étoile, France).

METHOD: Fifty-three reference strains and 523 patient strains were processed in VITEK MS (MS) and VITEK MS PRIME (PRIME). Organisms tested included a wide variety of aerobic and anaerobic gram-positive and gram-negative bacteria. No more than 10 strains per species were tested to ensure diversity of organisms tested. Isolates with no ID or discordant results underwent further phenotypic testing or were sent to a reference laboratory. New operational features, efficiency, and laboratory workflow were evaluated.

RESULTS: Of the 53 reference strains, all were identified on the PRIME, and 51 were identified on the MS. For the 523 patient strains, no ID occurred for 13 for MS and 26 for PRIME. Of these, 21/22 isolates sent for repeat MS and PRIME testing (bioMérieux, Marcy-l'Étoile, France) were identified, and 8 were identified by phenotypic methods or a reference laboratory. Gram-positive bacilli accounted for the majority of non-ID. Eleven results were discordant as a result of *Enterobacter* (n = 10) or *Citrobacter* (n = 1) species-level ID. Operational evaluation of the PRIME showed workflow improvements as a result of easy slide loading of up to 16 slides, 10-fold faster processing times, and a slide prioritization feature.

CONCLUSION: Performance was similar ,with a non-ID of 5.0% with VITEK MS Prime compared with 2.7% with the VITEK MS, likely resulting from technical spotting technique. Enhanced performance of the PRIME results in a much faster

time to ID. Bench-top design and enhanced features facilitate a much-improved laboratory workflow with ease of loading and increased slide capacity.

P83

Identifying SARS-CoV-2 spike mutation profiles associated with breakthrough infections

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OBJECTIVES: Coronavirus disease 2019 (COVID-19) vaccination is a key tool in the pandemic response. However, mutations in the spike protein have been shown to lower vaccine effectiveness and continue to emerge with new severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) lineages, including the Delta variant. Previous studies characterized mutations associated with breakthrough infections (BTIs), but limited information exists at the population level. Therefore, we aim to identify spike mutations associated with BTI in a community-dwelling population during the emergence and saturation of the Delta variant.

METHOD: We leveraged both genomic and epidemiological date from an ongoing COVID-19 genomic surveillance program. We restricted our analyses to primary COVID-19 cases from individuals aged ≥12 years who were either unvaccinated (controls) or infected ≥14 days after their second vaccination dose (breakthroughs) in a community setting. The unique combination of miss-sense spike mutations were used to assign a spike mutation profile (SMP) to each sample. Elastic net penalized logistic regression was used to identify mutations and SMPs associated with BTI, adjusting for age, sex, geographic location, and population structure in Delta-emerging and Delta-saturated time periods.

RESULTS: The Delta-emerging period had 20,542 observations (1,849 breakthroughs, 18,693 controls), and the Delta-saturated period had 18,391 observations (6,706 breakthroughs; 11,685 controls). Preliminary results show individual spike mutations T19R, G142D, E156G/Δ 157-158, L452R, T478K, P681R, and D950. Spike mutations were associated with BTI in the Delta-emerging period but diversified in the Delta-saturated time period. However, no isolate harboured all identified mutations. Penalized regression identified several naturally occurring SMPs harbouring the most identified mutations associated with BTI.

CONCLUSION: We report a method of profiling spike mutations naturally occurring in the community and identify Delta variant profiles to be strongly associated with BTI. We are currently validating the breakthrough potential of the identified SMPs using neutralization assays and plan to apply this profiling strategy to characterize the Omicron variant.

P84

Validation of saline gargle samples for the detection of anti-SARS-CoV-2 antibodies using an electrochemiluminescence multiplex immunoassay

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OBJECTIVES: Mucosal immunity theoretically plays an important role in coronavirus disease 2019 (COVID-19) prevention. To help identify correlates of protection against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, we validated the detection of anti–SARS-CoV-2 immunoglobulin G (IgG) antibodies in saline gargle mouth rinse for downstream application to cohort studies.

METHOD: We used residual saline gargles previously submitted for COVID-19 clinical diagnosis that had tested negative. Samples from three population groups were included (a) individuals who previously tested positive for COVID-19 by polymerase chain reaction within the past 3 months, (b) fully vaccinated individuals who received their second dose at least 2 weeks earlier and within the past 6 months, and (c) individuals with no known previous SARS-CoV-2 infection or COVID-19 vaccination. Samples were tested on an electrochemiluminescence assay (Meso Scale Discovery, Meso Scale Diagnostics, Rockville, Maryland) for SARS-CoV-2 anti-spike (S), nucleocapsid (N), and receptor binding domain (RBD) IgG.

RESULTS: Reactivity cut-offs were determined for SARS-CoV-2 S (2.4 AU/mL), N (3.1 AU/mL), and RBD (1.4 AU/mL) by using three standard deviations from the geometric mean of negative controls (group c). One hundred thirty-eight samples have been tested for a preliminary sensitivity of 95% for S (95% CI 82% to 99%), 92% for RBD (95% CI 79% to 98%), and 32% for N (95% CI 17.5% to 49%); specificity for S was 96% (95% CI 90% to 99%), 97% for RBD (95% CI 91% to 99%), and 95% for N (95% CI 89% to 98%). An overall positive/negative interpretation was made on the basis

of the reactivity of each sample to at least two out of three antigens with a sensitivity of 95% (95% CI 82% to 99%) and a specificity of 96% (95% CI 90% to 99%).

CONCLUSION: Saline gargle samples can be used to accurately detect the presence of IgG antibodies against SARS-CoV-2. Validation results will be used for future studies that aim to understand the strength, scope, and longevity of the antibody response to SARS-CoV-2 and to identify correlates of protection.

P85

Evaluation of quantitative assays for immunoglobulin G antibodies against SARS-CoV-2

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OBJECTIVES: Detection of antibodies against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has limited indications. In specific clinical settings, quantitative detection of immunoglobulin G (IgG) antibodies directed against the spike protein may be of value. We evaluated three such assays.

METHOD: Quantitative assays for anti-spike IgG antibodies against SARS-CoV-2 were evaluated using serum samples that previously tested positive using a total antibody assay. The samples tested included 318 samples from patients with previous coronavirus disease 2019 (COVID-19) infection, who were positive in anti–SARS-CoV-2 total antibody assays and either positive or negative for antibodies against the N antigen. A second group of 81 antenatal samples, collected before the introduction of vaccines, were positive in an anti–SARS-CoV-2 total antibody assay. The assays were run on Architect i2000SR (Abbott, Chicago, Illinois), Liaison XL (DiaSorin, Saluggia, Italy), and ADVIA Centaur XP (Siemens, Munich, Germany) analyzers, respectively. Assays from Abbott and Siemens used the S1 receptor binding domain antigen, whereas the DiaSorin assay used a trimeric spike glycoprotein antigen.

RESULTS: Using the manufacturers' cut-offs, sensitivity of the three IgG assays in patients with previous COVID-19 infection ranged from 76% to 99%. Sensitivity was greater in samples that were also positive for IgG antibodies against the N antigen. Similar differences in sensitivity were observed in antenatal samples. Linearity between the assays was good despite the differences in sensitivity between the three IgG assays.

CONCLUSION: Quantitative or semi-quantitative anti-spike IgG assays may be useful in identifying candidate patients for monoclonal antibody administration. However, commercial assays demonstrated a range of sensitivities when tested on patients with previously diagnosed COVID-19 infection. More extensive evaluations should be performed to confirm the differences in performance before they are widely used.

P86

Vaccinated and unvaccinated SARS-CoV-2 Delta variant cases display similar baseline viral loads after culture in respiratory samples

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OBJECTIVES: Current coronavirus disease 2019 (COVID-19) vaccines are effective at preventing serious illness, but breakthrough infections are expected. Reverse transcription polymerase chain reaction (RT-PCR) assays are used to detect severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA; however, measurable RNA can reflect viable and non-viable virus. Previous studies on the association between vaccination status and infectivity used viral culture but did not adjust for important covariates of patient demographics, sampling and testing methods, and viral lineage. We used a restricted and matched case–control design to better understand the impact of vaccination on infectivity.

METHOD: A sample size of 17 pairs (unvaccinated and vaccinated COVID-19 cases) was estimated to be required. We restricted cases to those aged ≥12 years with primary Delta variant infections sampled within 5 days of symptom onset using nasopharyngeal (NP) swabs. Pairs were matched on patient age, sex, region of residence, in-house RT-PCR E gene cycle threshold (Ct.e) value (within 1), and viral whole genome (within 2 amino acid mutations). Vero-TMPSSR2 cells were inoculated with samples and incubated for up to 6 days. Cultures from pairs (1/4 dilution) were tested by RT-PCR when cytopathic effect (CPE) was observed in at least one sample.

RESULTS: CPE was observed between 2 and 6 days with no difference between pairs. Preliminary results on nine pairs revealed that samples from both unvaccinated and vaccinated Delta variant cases generally produced CPE below a Ct.e of

22.5, with an average viable virus Ct.e after growth of 19.05 and 17.8, respectively. CPE was not observed above a sample Ct.e of 22.8; for these, detectable Ct.e after culture inoculation (>32) reflects residual sample RNA or very minimal growth.

CONCLUSION: COVID-19 vaccination does not reduce viral growth from NP samples in culture. Our highly restricted and matched case–control study enables a more reliable assessment of how vaccination status can impact SARS-CoV-2 infectivity. We are now collecting data for the Omicron variant.

P87

Evaluation of an extraction method developed for viral RNA extraction for detection of SARS-CoV-2 from nasopharyngeal swabs and gargle specimens

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OBJECTIVES: Inconsistent supplies of critical reagents required during the coronavirus disease 2019 pandemic affected the ability to run molecular diagnostic tests. In light of these shortages, we evaluated a viral RNA extraction method using new commercial reagents for extraction and subsequent polymerase chain reaction (PCR) detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA from nasopharyngeal swab (NPS) and gargle specimens.

METHOD: New molecular biology reagents and EasySep™ magnetic particles (prototype from STEMCELL Technologies, Vancouver, British Columbia) were used to extract viral RNA from SARS-CoV-2 clinical specimens. Results were compared with routinely used reference methods: MagMAX Viral/Pathogen Nucleic Acid Isolation Kit (ThermoFisher Scientific, Waltham, Massachusetts), MagNA Pure Compact Nucleic Acid Isolation Kit I (Roche), and MagNA Pure 24 Total NA Isolation Kit (Roche). Extracts were subsequently tested by means of in-house real-time PCR for detection of SARS-CoV-2 targeting RdRP and E gene.

RESULTS: A total of 100 specimens (NPS positive, n = 24; NPS negative, n = 24; NPS indeterminate [ie, CT > 38], n = 2; gargle positive, n = 25; gargle negative, n = 25) were included in this evaluation. For all clinical samples extracted using reagents and EasySep particles (STEMCELL), PCR results were in 100% concordance with the reference result for both positive and negative samples. One sample with an indeterminate reference result also gave an indeterminate result for the extract. The second indeterminate result tested positive when extracted with STEMCELL reagents. Variability for samples with low viral loads is expected, and this result was not regarded as discordant. Overall, the majority of SARS-CoV-2 cycle threshold (Ct) values for extracts using EasySep reagents were comparable with Ct values of reference results.

CONCLUSION: The newly developed reagents (STEMCELL) provided reliable extraction of SARS-CoV-2 viral RNA from NPS and gargles for the subsequent detection by real-time PCR. Identification of an alternate local supplier for extraction reagents could mitigate critical supply chain issues moving forward.

P88

Monitoring cycle threshold values of variants of concern in British Columbia, May 2021–December 2021

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OBJECTIVES: Monitoring cycle threshold (Ct) values as proxy for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral load and infectiousness may help predict transmission dynamics and guide public health decision making. This is particularly important in the context of the recent emergence of the Omicron variant. The first objective of this study was to investigate Ct value distribution of unvaccinated and vaccinated adults in British Columbia from positive clinical nasopharyngeal (NP) swabs from May 2021 to December 2021. The second objective was to adapt an existing methodology for epidemic prediction based on population-level Ct values.

METHOD: We collected and linked data from provincial laboratory and vaccination datasets. Ct values from the enveloI(E) gene polymerase chain reaction (PCR) target were assessed across several laboratory-developed and commercial assays and stratified on the basis of vaccination status. Markov chain Monte Carlo (MCMC) modelling was used to predict epidemic trends in two community outbreak settings in British Columbia.

RESULTS: A total of 18,895 NP swabs positive for SARS-CoV-2 were included. The Delta variant demonstrated the highest viral burden among the lineages and was highest in unvaccinated individuals (median Ct 19.7, IQR 7.2) compared with vaccinated individuals (median Ct 20.0, IQR 6.6). The Omicron variant showed slightly reduced viral burden compared with Delta in unvaccinated individuals (median Ct 20.7, IQR 5.9), but not in vaccinated individuals (median Ct 20.4, IQR 5.7). MCMC modelling results from the outbreaks demonstrated that analysis of aggregated Ct values could provide reasonable fit of epidemic trend projection.

CONCLUSION: These findings suggest the potential of coronavirus disease 2019 vaccination to reduce onward transmission by slightly lowering viral burden for certain variants. Modelling based on aggregated Ct values to predict epidemic trends may be a useful tool in outbreak settings. Further work will incorporate Ct distribution adjustment for covariates including age and assay used and will extend the modelling approach to provincewide data to assess public health utility.

P89

Sustained 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 as a result of coronavirus disease 2019 (COVID-19). CPE numbers were noted to correspondingly decrease in 2020 in a large tertiary-care clinical microbiology laboratory service in an urban metropolitan region. The goal of this study was to review whether the drop in the frequency of CPE was sustained in 2021.

METHOD: The total number of CPE per year (all CPE/year excluding duplicates) and the total number of individual carbapenemases per year (all carbapenemase/year excluding duplicates) were graphed from 2009 through 2021. The trend from 2009 through 2019 was compared with that from 2019 through 2021, when international travel was reduced. Trend lines and χ^2 test for trend were completed using Excel (Microsoft, Redmond, Washington) and GraphPad Instat (GraphPad, San Diego, California), respectively.

RESULTS:

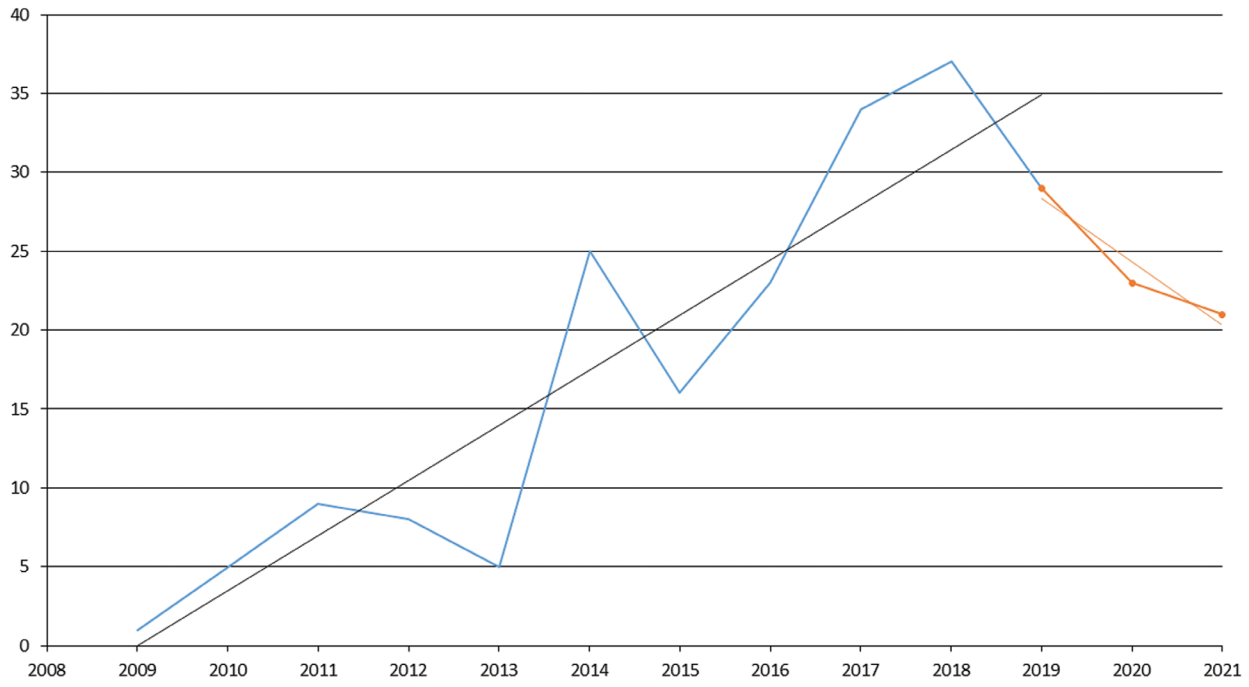

Figure P89-1: Total number of CPE (all CPE/year excluding duplicates)
CPE = Carbapenemase-producing Enterobacterales

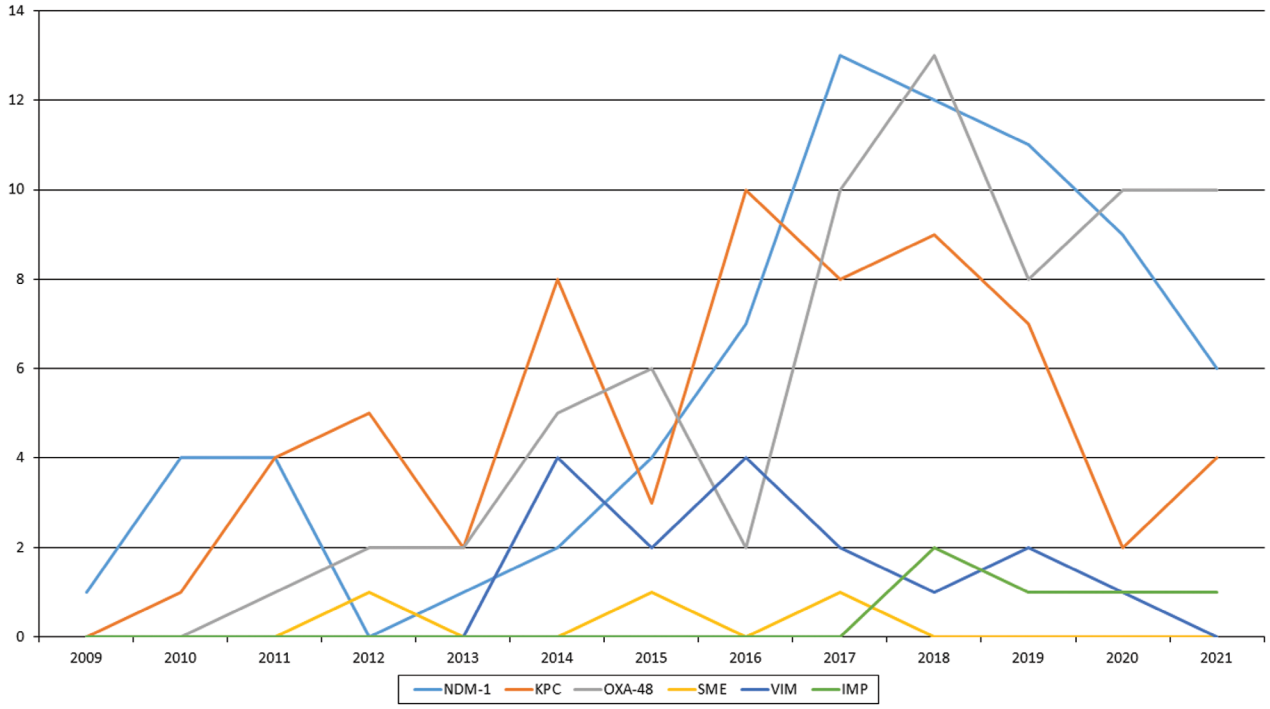

Figure P89-2: Total number of CPE (all CPE/year excluding duplicates)
CPE = Carbapenemase-producing Enterobacterales

CONCLUSION: A continued drop in the frequency of CPE was noted in 2021, correlating with a drop in all carbapenemases with the exception of OXA-48/OXA-48-like and IMP enzymes. A silver lining of the disruption COVID-19 has caused the world may be a decrease in the rise of CPE related to a reduction in international travel.

P90

Performance of the new Xpert MTB/RIF Ultra assay for the detection of *Mycobacterium tuberculosis* complex

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OBJECTIVES: The new generation Xpert® MTB/RIF Ultra (Ultra; Cepheid, Sunnyvale, California) is a rapid molecular assay for the detection of *Mycobacterium tuberculosis* (MTB) complex and rifampin (RIF) resistance. The assay has decreased limit of detection for MTB and improved detection of RIF resistance in comparison with the previous generation assay. The performance of Ultra for the detection of MTB was evaluated in retrospective frozen sputum sediments compared with culture and smear.

METHOD: Sputa, collected between May 2017 and November 2019, were concentrated before acid-fast bacillus smear and culture (BACTEC™ MGIT 960, BD, Franklin Lakes, New Jersey; Lowenstein-Jensen). Identification and susceptibility were performed at the provincial reference laboratory. Sediments were frozen at –20°C, and a panel of MTB positive (n = 67), non-tuberculous mycobacteria (NTM; n = 19) and culture-negative specimens (n = 31) were selected for subsequent testing by Ultra.

RESULTS: Of the 21 smear-positive, MTB culture-positive sputum sediments, 20 tested concordantly positive by Ultra, resulting in a positive percentage agreement (PPA) of 95.2%. The average volume of these samples was 0.4 mL, below the manufacturer's recommended volume (0.5 mL). For the 46 smear-negative, MTB culture-positive sputum sediments, 28 tested positive for MTB by Ultra, resulting in a PPA of 60.9%. Excluding the samples with suboptimal volume (<0.5 mL), the PPA increased to 73.9%. All of the 50

MTB negative sputum sediments (including NTM positive) tested concordantly negative by Ultra, resulting in a negative percentage agreement of 100%. One false-positive result for RIF resistance by the TB Ultra was observed. A validation of bronchial specimens is currently underway.

CONCLUSION: The Ultra performed as expected for smear-positive samples. In contrast, some variability was observed with smear-negative specimens that could potentially be explained by several factors: study sample size, sample volume available, concentration method, freeze–thaw cycle, storage time, and the like. A prospective study will be needed to confirm these results.

P91

Performance verification of the fully automated Aptima BV and CV/TV assays

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OBJECTIVES: The fully automated Panther platform on the Aptima side can detect the three most common causes of infectious vaginitis: bacterial vaginosis (BV), candida vaginitis (CV) and *Trichomonas vaginalis* (TV). The performance of the two new assays (Aptima BV and Aptima CV/TV, Aptima, Arlington, Virginia) was verified in this study.

METHOD: Retrospective specimens from patients who had two vaginal swabs collected simultaneously were stored at –80°C for this verification. In general, an ESwab™ collection device (COPAN, Murrieta, California), for routine Gram stain examination for BV and CV, and an Aptima Multitest collection tube, submitted for CT/GC testing, are submitted concomitantly as local current practice. Residual Aptima swabs were tested by the Aptima BV or CV/TV panel, and the results were compared with routine test results.

RESULTS: To date, 94 specimens have been tested with the BV assay (Gram stain positive, $n = 46$; Gram stain negative, $n = 48$); 43 tested concordantly positive, and 45 tested concordantly negative for a sensitivity of 93% and a specificity of 94%. Six discordant results (false positive, $n = 3$; false negative, $n = 3$) were observed. A total of 68 specimens were tested with the CV/TV assay (gram stain positive for yeast, n = 18; Gram stain negative for yeast, n = 50; TV not tested). Fifteen were concordantly positive for CV (sensitivity = 83%), and 43 were concordantly negative (specificity = 86%). A total of 10 discordant results (false positive, $n = 7$; false negative, $n = 3$) occurred. All 67 valid results were negative for TV by the CV/TV assay. One sample gave an invalid result for each assay.

CONCLUSION: The Aptima BV and CV/TV assays performed well for the detection of bacterial and candida vaginosis when compared with modified Nugent score. Automation of microscopy examination will free technologists in the context of the national shortage of qualified staff.

P92

Evolving detection strategies for an evolving virus: Development of real-time PCR assays for all SARS-CoV-2 variants of concern

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OBJECTIVES: As severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) continues to circulate in the population, variants with potentially higher rates of transmissibility and disease severity, escape from natural and vaccine-induced immunity, and reduction in susceptibility to monoclonal antibodies have emerged. Rapid detection of these variants of concern (VOCs) with the implementation of public health measures are imperative to control the spread of these variants.

METHOD: To detect the SARS-CoV-2 VOCs reported to date, five real-time reverse transcriptase polymerase chain reaction (RT-PCR) assays were designed to target the critical discriminatory mutations responsible for the following amino acid changes in the spike protein: a combination of 69/70

deletion/N501Y for B.1.1.7 (Alpha), N501Y/K417N/242-244 region/E484K for B.1.351 (Beta), N501Y/K417T/E484K for P.1 (Gamma). and L452R/P681/E484Q for B.1.617.2 (Delta). The assay targeting the 69/70 deletion and N501Y was modified to include the detection of B.1.1.529 (Omicron).

RESULTS: The sensitivity of the assays ranged from 94.4% to 100% for the detection of known positives, the specificity ranged from 98.6% to 100%, and the limits of detection varied from 2 copies/reaction to 25 copies/reaction. The intra- and inter-assay variability for all the assays were less than 5%, and no cross-reactivity with common respiratory pathogens was observed with any assay. Lineage designation based on full genome sequencing is considered the gold standard, and a comparison of the lineage designation by the VOC RT-PCR assays and full genome sequencing showed clinical sensitivities of 99.9%–100%, clinical specificities of 99.6%–100%, positive predictive values of 99.8%–100%, and negative predictive values of 99.9%–100%.

CONCLUSION: The implementation of high throughput variant screening assays promptly after the identification of VOCs worldwide has helped in the identification of circulating genotypes and emerging trends to guide public health policies.

P93

Building consensus on antimicrobial stewardship nudges

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OBJECTIVES: To use antimicrobial sensitivity testing reports to nudge antimicrobial stewardship–focused prescribing, consensus on the optimal antimicrobial for a specific clinical situation is required, yet difficult to find. We aimed to develop a consensus approach to optimal antimicrobial prescribing on the basis of specific clinical vignettes, to validate this approach with experts, and to use these vignettes to test various nudging strategies for antimicrobial susceptibility reporting.

METHOD: Our group initially developed an approach to define the actions that may occur in response to an antimicrobial susceptibility report. These actions were initiation, escalation, de-escalation, or discontinuation of antimicrobials. On the basis of these actions, we developed realistic clinical vignettes with several antimicrobial susceptibility reporting strategies. The baseline strategy used antimicrobials that would typically be tested for the clinical isolate in the vignette. The intervention strategies were a selective reporting, framing, and eye-level reporting strategy. To define which antimicrobials were included in each intervention strategy, a modified Delphi panel process was used to define optimal management of each clinical vignette, given the information available. With each vignette presented, the team discussed preferences and values leading to the optimal antimicrobial approach to the vignette. Consensus was achieved by discussion, and antimicrobials were included on the basis of unanimous decision. To validate this process, a panel of nine infectious disease physician reviewers evaluated all vignettes and antimicrobial choices and provided feedback.

RESULTS: Sixteen vignettes were constructed, four from each action step. Clinical scenarios were routine infections common in hospitalized patients and included bloodstream infections, urinary tract infections, pneumonia caused by bacteria, and yeasts. One to two antimicrobials were deemed optimal for each vignette. Expert reviewer agreement with the optimal therapy was high (83%).

CONCLUSION: Achieving consensus on preferred antimicrobial therapy for common infections is challenging but possible and builds toward a more optimized approach to reporting antimicrobial susceptibility testing that supports antimicrobial stewardship.

P94

Development and validation of a multiplex assay for the simultaneous detection of *Echinococcus multilocularis* and *Echinococcus granulosus*

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OBJECTIVES: Alveolar echinococcosis (AE) is a life-threatening parasitic infection of the liver with local and metastatic spread to distant organs, caused by larval multiplication of canid

tapeworm, *Echinococcus multilocularis*. In 2012, a pathogenic European strain was first detected in wildlife in western Canada, followed by an increasing number of human cases. To study its prevalence and spread in Alberta, a real-time polymerase chain reaction (PCR) assay was designed for the detection and differentiation of *E. multilocularis* and *E. granulosus* in patients presenting with primary hepatic lesions

METHOD: Previously published real-time PCR assays targeting the *nad2* gene of *E. multilocularis* and *cox1* gene of *E. granulosus* were modified and multiplexed. Detection was performed on paraffin embedded, fresh, or formalin-fixed liver tissue samples. The *Beta 2-microglobulin* gene present in all human cells co-extracted with the parasite nucleic acid was used as an internal extraction, amplification, and inhibition control.

RESULTS: The 95% limit of detection using Probit analysis on quantitated synthetic oligonucleotides was 3 copies/reaction for both gene targets. Assay reproducibility for positive samples with a high and low parasitic load tested in triplicate on three independent runs showed that the %CV ranged from 0.91% to 2.97%. Linear amplification of target was noted over seven logs of template concentration. Accuracy comparison was performed using specimens tested at the reference laboratory (University of Bern, Bern, Switzerland), and the following assay parameters were calculated (sensitivity = 100%, specificity = 90.0%, positive predictive value = 93.86%, and negative predictive value = 100%).

CONCLUSION: Assay performance was comparable to that of a reference test. Local testing improves timely diagnosis and surveillance of human AE, particularly in view of the recent rise in AE cases in Canada.

P95

Determination of optimal duration and conditions for long-term storage of fecal filtrate samples used for fecal microbiota transplants and microbiota research

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OBJECTIVES: Fecal microbiota transplants (FMT) using frozen filtrate are used for patients with recurrent *Clostridioides difficile* infection. Stool storage is also key to researching the association between gastrointestinal dysbiosis and disease states. Previously, we examined the stability of frozen filtrate up to 24 months. The objective of this study was to determine the stability after 5 years of storage.

METHOD: Fresh stool from high-diversity (HD) and low-diversity (LD) donors was homogenized with sterile saline with or without 10% glycerol and stored at –20°C and –80°C. Filtrate aliquots were thawed after 5 years, plated onto selective agars, and compared with baseline to determine loss of microbial growth (LMG). gDNA was also isolated, and 16s rRNA gene amplicon sequencing was performed to evaluate microbiota composition compared with baseline.

RESULTS: HD and LD fecal filtrate stored at –20°C without 10% glycerol for 5 years had the highest LMG (54% and 67%, respectively) followed by filtrate stored at –20°C with glycerol (50% and 67%) and filtrate stored at –80°C without glycerol (8% and 20%). Filtrate stored at –80°C with 10% glycerol had the least LMG (9% and 10%). For HD filtrate, 16s rRNA microbiota profiles indicated high preservation of filtrate stored at –80°C with 10% glycerol, followed by –20°C with 10% glycerol and then –80°C and –20°C without 10% glycerol; trends were the same for the LD filtrate but with altered proportions of phyla and genera in the LD filtrate in all storage conditions.

CONCLUSION: Stool filtrate from HD donors such as those used for FMT retains bacterial viability and microbiota preservation when stored at –80°C with 10% glycerol for up to 5 years. For LD stools such as those from patients with disease states, 16s profiles are affected in all storage conditions and durations of storage.

P96

A contingency plan for N95 filtering facepiece respirator (FFR) shortages: Hydrogen peroxide vapor reprocessing of N95 FFRs

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OBJECTIVES: Global N95 filtering facepiece respirator (FFR) shortages during 2020 caused numerous jurisdictions to explore alternative respiratory protection options: extended use of N95 FFRs, elastomeric respirators, and reprocessing (decontaminating) of single-use N95 FFRs. Previous studies have shown hydrogen peroxide vapor (HPV) to be effective at decontaminating N95 FFRs with minimal negative effect on filtration efficiency. However, all studies to date have focused on new, unworn N95 FFRs. A large-scale reprocessing project using HPV was undertaken in a Canadian province, collecting and reprocessing more than 150,000 N95 FFRs from 28 health care facilities. To ensure the performance of N95 FFRs after reprocessing, more than 1,100 respirators were evaluated for filtration efficiency.

METHOD: More than 150,000 N95 FFRs were collected from 28 health care facilities and reprocessed using one of four HPV sterilizers: Sterrad 100NX, Sterrad 100S, Stryker VP4, and Sterris VProMax. Filtration efficiency testing is a destructive process, and so a representative sample of more than 1,100 N95 FFRs were tested in accordance with standard method TEB-APR-STP-0059. As a control, 234 unworn N95 FFRs were also reprocessed and tested for filtration efficiency. Bivariate analysis was performed using R (version 3.5.2; R Foundation for Statistical Computing, Vienna, Austria) to determine whether worn FFRs had a higher likelihood of failing filtration efficiency (<95%) after reprocessing.

RESULTS: A total of 1,138 N95 FFRs were assessed for filtration efficiency, with 106 FFRs (9%) exhibiting filtration efficiency of less than 95%. The various reprocessing machines affected filtration efficiency differently: among FFRs failing to exhibit 95% filtration efficiency, 79% were reprocessed with the 100NX, 18% with 100S, 2% with VP4, and 1% with Steris VProMax (Table P96-1). Worn N95 FFRs had an approximately 83% lower odds of passing (OR 0.17, 95% CI 0.061 to 0.39) compared with unworn N95 FFRs.

Table P96-1: Effect of hydrogen peroxide reprocessing on N95 respirator filtration efficiency

	Filtration Efficiency Final Result*		
	Fail (n=106)	**Pass (n=1032)**	**Overall (n=1138)**
Filter efficiency			
Mean (SD)	89.5 (5.85)	98.9 (1.04)	98.0 (3.39)
Median [Q1 – Q3]		99.1 [98.4-99.6]	
Reprocessor			
100NX	84 (79.2%)	278 (26.9%)	362 (31.8%)
100S	19 (17.9%)	336 (32.6%)	355 (31.2%)
V-Pro MAX	1 (0.9%)	137 (13.3%)	138 (12.1%)
VP4	2 (1.9%)	281 (27.2%)	283 (24.9%)
N95 model			
1860	69 (65.1%)	375 (36.3%)	444 (39.0%)
1860S	33 (31.1%)	318 (30.8%)	351 (30.8%)
1870+	4 (3.8%)	339 (32.8%)	343 (30.1%)
Worn or unworn			
Unworn	5 (4.7%)	229 (22.2%)	234 (20.6%)
Worn	101 (95.3%)	803 (77.8%)	904 (79.4%)

CONCLUSION: Worn N95 FFRs have a significantly higher likelihood of failing filtration efficiency after HPV reprocessing than unworn FFRs, an important safety consideration when exploring alternative respiratory protection options.

P97

Yield of routine SARS-CoV-2 pre-surgical testing, 2020–2021

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OBJECTIVES: Because little is currently known about the yield of routine pre-procedural testing, including which indicators may be used to guide an approach to testing, our objective was to examine the value of pre-procedural testing for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) as it relates to local epidemiology.

METHOD: We prospectively collected data for all consecutive patients undergoing pre-procedural testing for SARS-CoV-2 at one tertiary centre in a major Canadian city between April 19, 2020, and October 31, 2021. All patients underwent symptom screening and pre-procedure testing for coronavirus disease 2019 before the date of the procedure. This included outpatients scheduled for elective procedures (approximately 90% of all procedures) as well as inpatients anticipated to require surgery during admission. As a comparison, we also prospectively documented the positivity rate of SARS-CoV-2 in the emergency department (ED) and the local region during the same period of study.

RESULTS: During the study period, 41,978 pre-operative tests were performed, yielding a total of 131 positive results and a positivity rate of 0.31%. During the same period, 40,057 ED tests were performed, yielding a total of 1,516 positive results and a positivity rate of 3.8%. Examining the trends of positivity among these two areas compared with the regional positivity (Figure P97-1), it appears that, unlike yield from ED testing, pre-operative positivity does not correlate with local prevalence and had a persistently low yield throughout the pandemic.

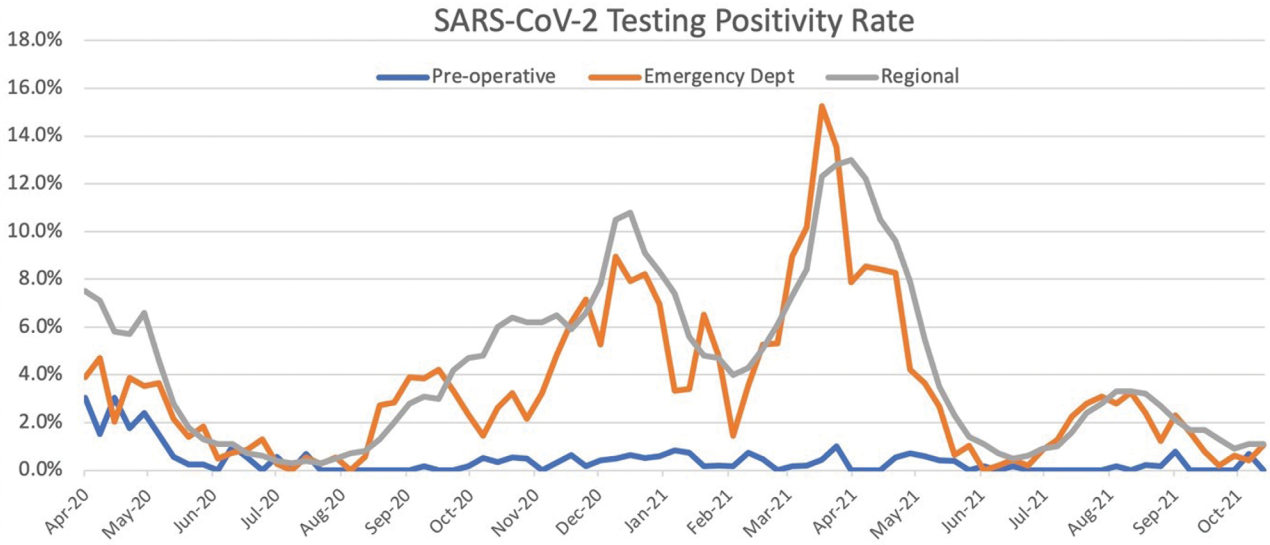

Figure P97-1: Positivity rate for SARS-CoV-2 testing in the pre-operative setting, emergency department, and regional area

CONCLUSION: Here, we demonstrate a low prevalence of SARS-CoV-2 among patients undergoing surgery during the pandemic regardless of local prevalence. This is likely in part because of rigorous symptom screening protocols before surgery in a carefully selected population. Additional study is needed to determine how routine pre-operative testing is affected by the emergence of the Omicron variant when community prevalence exceeds a high threshold.

P98

COVID-19 Sewer Cage passive samplers: A targeted solution for building-scale detection of SARS-CoV-2 in high-risk communities

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OBJECTIVES: Wastewater surveillance has been a critical component of coronavirus disease 2019 (COVID-19) surveillance. A passive sampler (COVID-19 Sewer Cage [COSCa]) was optimized and verified for building-scale detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at university residences. This sampling method can complement current COVID-19 surveillance efforts by providing a more targeted approach to monitoring specific communities.

METHOD: The COSCa passive sampler contains an electronegative filter that captures virions and nucleic acid fragments as wastewater flows through the sampler. Viral particles and nucleic acids were eluted off the filter, run through a viral concentration protocol, and tested for SARS-CoV-2 targets by means of quantitative real-time reverse transcription polymerase chain reaction (RT-qPCR). The suitability of the COSCa passive sampler was tested in triplicate on three separate occasions by spiking gamma-irradiated SARS-CoV-2 into wastewater. Coefficients of variation (CV) were calculated for cycle threshold (Ct) values and percentage recovery between triplicates (intra-CV) and between simulations (inter-CV). After this method was optimized and verified, university residences were monitored using this sampling method two to three times per week over a 4-month period.

RESULTS: The intra-CV of Ct values ranged from 13% to 22% (n = 9) across all three simulations with an inter-CV of 30% (n = 3). An average recovery of 3.5% was observed for gamma-irradiated SARS-CoV-2 (n = 9), with an intra-CV ranging from 31% to 39% (n = 9) and an inter-CV of 12% (n = 3). Over the 4-month surveillance period, consisting of 72

samples, SARS-CoV-2 was detected in 20 samples, with viral concentrations ranging between 1.66×10^3 genomic copies/L wastewater and 5.22×10^5 genomic copies/L wastewater.

CONCLUSION: This study confirms that the COSCa passive sampler can reliably capture SARS-CoV-2 in wastewater. Moreover, the short-term surveillance of university residences demonstrated the utility of the COSCa passive sampler for targeted monitoring of SARS-CoV-2 in high-risk communities.

P99

Verification of a custom lyophilized antimicrobial susceptibility testing panel for multi-drug-resistant gram-negative organisms

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OBJECTIVES: Timely and reliable front-line antimicrobial susceptibility testing (AST) for novel antimicrobial agents is critical, given the rise of multi-drug-resistant gram-negative (MDR-GN) organisms. There is a need for efficient gold standard–verified automated AST methods for MDR-GN organisms. This study verified a custom lyophilized AST panel for MDR-GN antimicrobial agents against a custom gold-standard frozen BMD panel.

METHOD: ThermoFisher's custom frozen and lyophilized Sensititre microdilution panels (ThermoFisher Scientific, Waltham, Massachusetts) were tested against 70 Enterobacterales, 30 *Pseudomonas aeruginosa,* 20 *Acinetobacter* spp, 15 *Stentrophomonas maltophilia,* 14 *Burkholderia cepacia,* 5 non-fermenters, and 5 *Aeromonas* spp. Very major errors (VME), major errors (ME), minor errors (MinE), and categorical/essential agreements (CA/EA) were calculated, and acceptability was determined

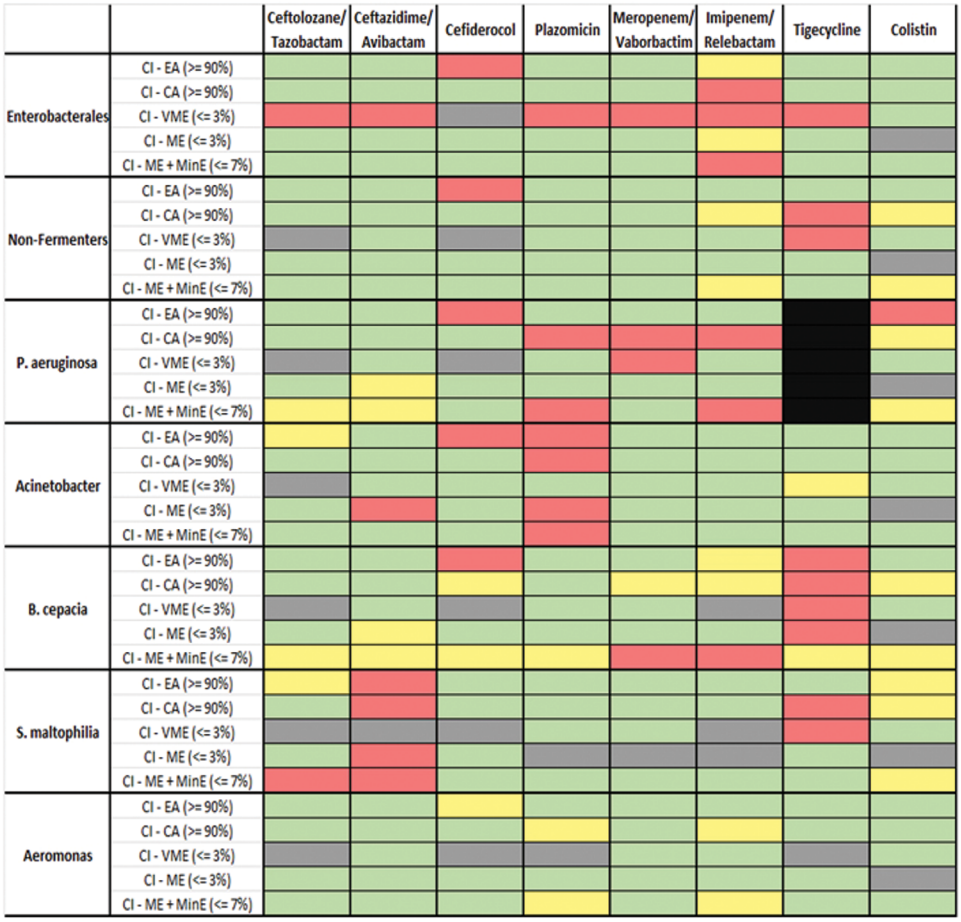

Figure P99-1: Results of Ivophilized vs, frozen panel. Green Point estimate agreement within threshold. Yellow Point estimate disagreement with threshold, agreement within confidence interval (red = disagreement with threshold and confidence intervals; grey = not enough isolates for that category; black = not applicable)

using both Cumitech31A and EUCAST thresholds and 95% CIs.

RESULTS: Preliminary results (43 Enterobacterales, 5 non-fermenters, 26 *P. aeruginosa,* 20 *Acinetobacter* spp, 13 *B. cepacia,* 4 *S. maltophilia,* and 5 *Aeromonas* spp) reveal that ceftolozane–tazobactam had acceptable EA/CA/VME/ME/MinE for all species except Enterobacterales and *S. maltophilia,* whereas ceftazidime–avibactam had acceptable EA/CA/VME/ME/MinE for all except Enterobacterales, *Acinetobacter* spp, and *S. maltophilia.* Cefiderocol had acceptable CA/VME/ME/MinE for all but had acceptable EAs only for *S. maltophilia* and *Aeromonas* spp. Plazomicin had acceptable EA/CA/VME/ME/MinE for all except Enterobacterales, *P. aeruginosa,* and *Acinetobacter* spp. Meropenem–vaborbactim and imipenem–relebactam had acceptable EA/CA/VME/ME/MinE for all except Enterobacterales, *P. aeruginosa,* and *B. cepacia.* Tigecycline only had acceptable EA/CA/VME/ME/MinE for *Acinetobacter* and *Aeromonas* spp, whereas colistin had acceptable EA/CA/VME/ME/MinE for all except *P. aeruginosa.*

CONCLUSION: The lyophilized panel performs reasonably well, but does not yet support the replacement of the gold-standard frozen BMD for all drug-organism combinations. Further testing and reconciliation of errors is needed and still underway.

P100

Evaluation and comparison of optimal laboratory screening methods using a custom dulcitol agar, commercially available chromogenic agars, and polymerase chain reaction in detecting *Candida auris* growth

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OBJECTIVES: *Candida auris* is an emerging threat. The optimal *C. auris* screening method was determined by comparing a custom dulcitol agar (DA), BD BBL CHROMagar Candida (BD, Franklin Lakes, New Jersey), Micronostyx Colorex Candida Plus Agar (M; Micronostyx, Ottawa, Ontario), ThermoFisher Auris Enrichment Broth (AEB; ThermoFisher Scientific, Waltham, Massachusetts), and the BioGx *C. auris* research-use-only polymerase chain reaction (PCR) kit (BioGx, Birmingham, Alabama).

METHOD: Twenty *C. auris* isolates (9 multi-drug resistant, and 11 non-multi-drug resistant) were used to spike nasal–axillary–groin–perineum–rectal swabs. The 20 spiked samples were directly inoculated onto DA and M agars and incubated at 37°C and 42°C and inoculated into AEB and incubated at 250 rpm for 48 hours at 37°C before subculturing onto BD and M plates at 37°C and 42°C. *C. auris* growth as determined by colony morphology and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. DNA was also extracted using EasyMag (bioMérieux, Marcy-l'Étoile, France) from spiked samples and from AEB after 24 hours incubation followed by PCR.

RESULTS: All culture and PCR methods detected *C. auris* from 100% (20/20) of the *C. auris* spiked samples except for direct-to-agar culture on M at 42°C, which only isolated *C. auris* from 95% (19/20). Direct PCR provided results within 24 hours, broth-enriched PCR provided results between 24 and 48 hour, direct-to-agar provided results at 48 hours, and broth-enriched cultures provided results within 72 hours. Of all the agars, M was preferred given the specific *C. auris* chromogen allowing for easy detection. Broth-enriched cultures were also easy to work with given that AEB minimized breakthrough of non-auris *Candida* isolates, but more hands-on time was required and turnaround time (TAT) was longer. PCR allowed for rapid TAT but also had more hands-on-time than direct-to-agar methods given the lack of automation.

CONCLUSION: Direct inoculation onto M agar incubated at 37°C showed the most promise in reliably identifying *C. auris* within the shortest TAT. AEB cultures and PCR are also acceptable alternatives that may have lower limits of detection but require more hands-on-time.

P101

Commercial lateral flow assay evaluation for rapid detection of carbapenemase-producing Enterobacteriaceae

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OBJECTIVES: Carbapenemase producing Enterobacteriaceae (CPE) are emerging around the world, including Canada,

Table P101-1: Carbapenemase types in the test panel

No. of strains	Carbapenemase enzyme type
33	KPC
33	NDM
11	OXA-48/OXA-48 like
10	VIM
5	IMP
8	SME
2	NMC
1	SPM
60	None

and are associated with case fatality rates as high as 50%. Gastrointestinal carriage of CPE may serve as the reservoir for cross-contamination in the health care setting; thus, active surveillance is important for effective containment and outbreak prevention. In this study, we evaluate a commercial lateral flow assay for the detection of CPE using a panel of CPE, non-CPE carbapenem-resistant, and carbapenem-susceptible strains.

METHOD: A panel of strains was assembled, including clinical strains from our laboratory and highly characterized strains selected from the Centers for Disease Control and Prevention–Food and Drug Administration Antibiotic Resistance Isolate Bank, as indicated in Table P101-1. NG-Test Carba5, a commercial lateral assay for detection of CPE, was evaluated, which tests exclusively for KPC, NDM, OXA-48-like, VIM, and IMP types. All other CPE types are not detected, including SPM, SME, and NMC included in the isolate bank, and are marked as true negatives on the assay. Bacterial isolates grown on blood agar plates were inoculated into Carba5 buffer mix and vortexed; 100 µL of sample was absorbed into assay pad that detects CPE target within 15 minutes. Carbapenemase production was confirmed as present or absent from all strains by polymerase chain reaction (PCR).

RESULTS: Sensitivity and specificity were 98.9% and 98.6%, respectively. The only isolate the assay did not identify was IMP-14, which was also difficult to detect using PCR. Isolates with both NDM and OXA-48-like CPE types simultaneously were correctly detected by the assay.

CONCLUSION: NG-Carba 5 lateral flow assay shows both high sensitivity and specificity and should be considered as both an effective and an efficient method for the detection of five CPE enzyme types.

P102

Development and validation of methods for testing SARS-CoV-2 in wastewater as a population-level COVID-19 surveillance tool to complement clinical testing

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OBJECTIVES: The coronavirus disease 2019 (COVID-19) pandemic prompted the need for innovative testing approaches to monitor the presence and dynamics of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in communities worldwide. Methods to detect and quantify SARS-CoV-2 in influent wastewater were developed and validated, as were methods to compare viral concentrations with clinical case counts. Wastewater testing complements COVID-19 surveillance by serving as an early detection system and by monitoring populations not captured by clinical testing as a result of testing accessibility and capacity.

METHOD: Twenty-four-hour composite samples of influent wastewater were collected from five wastewater treatment plants one to three times per week over the course of 12 months. Wastewater samples were concentrated using ultrafiltration and nucleic acids extracted from the resulting viral concentrate. Samples were tested for SARS-CoV-2 targets using quantitative real-time reverse transcription polymerase chain reaction (RT-qPCR). Concentrations of SARS-CoV-2 targets in wastewater were determined using external standard curves. Viral signals were then compared with case counts that were mapped to the sewer catchment for each treatment facility.

RESULTS: Of 428 wastewater samples, 421 tested positive for one or more SARS-CoV-2 targets. Viral concentrations ranged from 8.54 × 102 genomic copies/L wastewater to 1.80 × 105 genomic copies/L wastewater. The viral signal of SARS-CoV-2 trended closely with clinical case numbers overall,

with correlations ranging from 0.456 to 0.883 depending on the wastewater treatment plant.

CONCLUSION: When the incidence of SARS-CoV-2 remains stable and within testing capacities, the concentration of SARS-CoV-2 trends correlates closely with clinical cases. However, as clinical testing becomes saturated during the Omicron wave of the pandemic, we anticipate that the correlation between clinical cases and the concentration of SARS-CoV-2 in wastewater will be affected. Wastewater testing can serve as an unbiased surveillance as testing criteria change over the course of the pandemic.

P103

Analytical validation of saline gargle mouth rinses for detection of influenza A, influenza B, and respiratory syncytial virus by nucleic acid amplification tests

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OBJECTIVES: Saline gargle mouth rinses were validated as a diagnostic sample for coronavirus disease 2019 (COVID-19) in response to swab shortages during the pandemic. To increase clinical laboratory testing efficiencies, we aimed to validate gargle samples for the detection of influenza A, influenza B, and respiratory syncytial virus (RSV) by nucleic acid amplification tests.

METHOD: Influenza A, influenza B, and RSV cultures were standardized for viral load and pooled. The pooled culture was spiked, in triplicates, into Minimum Essential Medium (MEM) and saline for a reverse transcription polymerase chain reaction (RT-PCR) cycle threshold (Ct) target just below the assay limit of detection (~30) and tested for initial evaluation by in-house RT-PCR. Then, saline gargle and YOCON VTM pools were created from previously collected patient samples, spiked with viral cultures to Ct ~30, and tested with three multiplex RT-PCR tests: lab-developed test (LDT; $n = 10$), Xpert ($n = 3$), and Biofire ($n = 3$). Additional aliquots were incubated at 4°C, room temperature, and 30°C for the LDT RT-PCR at days 0, 3, 5, and 7 to mimic possible storage conditions.

RESULTS: Initial comparisons between spiked MEM and saline revealed that the viruses can be reliably suspended and detected in saline. All platforms accurately detected influenza A, influenza B, and RSV at Ct ~30 in spiked saline gargles. Mean Ct values were comparable and stable between saline gargle and YOCON VTM spiked samples for all viruses and at 4°C and room temperature over 7 days. Ct values at 30°C increased notably by day 7 for all viruses.

CONCLUSION: Influenza A, influenza B, and RSV can be reliably detected over several days of storage in culture spiked saline gargle mouth rinses by in-house and commercial multiplex RT-PCR tests. A head-to-head clinical trial comparing gargles and nasopharyngeal swabs is now underway to further validate saline gargles as an acceptable diagnostic sample for detection of influenza A, influenza B, and RSV.

P104

Development of a triplex real-time PCR assay for the detection of *Borrelia* spp and *Borrelia burgdorferi* for tick surveillance in Alberta

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OBJECTIVES: Lyme borreliosis is a serious disease caused by the spirochete *Borrelia burgdorferi sensu stricto* (*ss*) in North America and genospecies *B. afzelii* or *B. garinii* in Europe, carried by *Ixodes* ticks. The incidence of Lyme borreliosis has been increasing in Canada, largely driven by the expansion of tick habitats. Although not yet considered endemic in Alberta, introduction of infected ticks from diverse sources poses a significant risk. We developed a multiplex real-time polymerase chain reaction (PCR) assay, using salmon sperm DNA as an extraction and inhibition control, for the detection of *B. burgdorferi ss* in *Ixodes* ticks collected from companion animals as a passive surveillance measure in Alberta.

METHOD: Two real-time PCR assays utilizing hydrolysis probes targeting the 23S gene of *Borrelia* spp and the *ospA* gene of *B. burgdorferi ss* were multiplexed with an assay

for the detection of salmon sperm DNA to monitor for extraction efficiency and PCR inhibition. Nucleic acid was extracted from ground ticks spiked with salmon sperm DNA using the QiaAMP DNA Mini Kit (Qiagen, Germantown, Maryland) and tested on the ABI 7500 FAST Real-time PCR platform (ThermoFisher Scientific, Waltham, Massachusetts).

RESULTS: The 95% limit of detection for the 23S and *ospA* targets was 8.16 and 18.61 copies/reaction, respectively. No cross-reactivity was observed when the assay was tested on high titres of pathogens with overlapping clinical symptoms. The assay was reproducible at high and low bacterial loads with the % coefficient of variation for intra-assay variability ranging from 0.20% to 1.74% and the inter-assay variability ranging from 0.11% to 1.24% for both gene targets. Six positive and 16 negative ticks were provided by the National Microbiology Laboratory (NML), and all results were concordant with the exception of one tick that tested positive at NML and negative by the triplex assay.

CONCLUSION: Passive surveillance of *Ixodes* ticks collected from companion animals for *B. burgdorferi* will help monitor changes in prevalence of this pathogen.

P105

Tracking of SARS-CoV-2 variants of concern in Alberta, Canada

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OBJECTIVES: All five severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOCs; Alpha, Beta, Gamma, Delta, and Omicron) were reported in Canada soon after they were declared VOCs. Here we describe the trends of VOC circulation in Alberta, Canada.

METHOD: The primary means of identifying VOCs were real-time reverse transcription polymerase chain reaction assays targeting discriminatory mutations characteristic of each VOC. Before implementation of these assays, Sanger sequencing of the spike gene and genome sequencing was used for detection. All SARS-CoV-2–positive samples were subjected to VOC testing except during May 1–31, 2021; September 10–November 24, 2021; and December 24, 2021–January 6, 2022, when a targeted approach was undertaken because of high sample volumes. Cases of VOCs were analyzed based on geography, age, and sex.

RESULTS:

Table P105-1: Circulation of variants of concern in Alberta, Canada

Variant	Date of collection for first positive	Date of peak detection (highest % of tested samples)	Total positives detected by RT-PCR
Alpha	December 13, 2021	May 5, 2021 (83.7)	47,444
Beta	January, 20 2021	July 2, 2021 (13.5)	91
Gamma	March 10, 2021	July 3, 2021 (10.8)	1,462
Delta	April 24, 2021	August 29, 2021 (93.3)	69,122
Omicron	November 23, 2021	December 31, 2021 (90.1)*	10,790

** Ongoing peak*
RT-PCR = Reverse transcription polymerase chain reaction

Alpha became the predominant lineage by the end of March 2021, with the last case detected on November 15, 2021. Neither Beta nor Gamma became predominant lineages, but Delta overtook Alpha as the dominant strain by mid-July 2021. Delta continued to be detected at high levels until late December 2021 when Omicron cases rose rapidly. VOC detection was highest in the two urban centres, reflecting the higher proportion of samples tested from those areas (35.8% of VOC cases detected in Calgary; 28.4% in Edmonton) and in the group aged 20–39 years (37.1%), with an equal distribution between females (49.8%) and males (50.2%).

CONCLUSION: The prompt implementation of high throughput variant screening assays after the identification of VOCs has helped in the identification of circulating genotypes and emerging trends to guide public health policies.

P106

Evaluation of a novel low-concentration chlorine dioxide mist for disinfection of airborne bacteria and viruses, including SARS-CoV-2

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OBJECTIVES: Many human-to-human transmissions of bacteria and viruses including severe acute respiratory syndrome

coronavirus 2 (SARS-CoV) are airborne. Instead of using high-power purifiers, a novel low-concentration chlorine dioxide (ClO_2) mist containing phytoncide (wood essential oil) has been developed. ClO_2 is well known to be safe for drinking water disinfection but not effective in a mist form. The objective of this work is to develop the optimal specification and conditions for dispensing ClO_2 with phytoncide in health facilities and to evaluate its disinfection effectiveness.

METHOD: Three different formulations were prepared for assessing acute bactericidal power, aiming at instant bactericidal or viral inactivation effect in a short period of time such as minutes. The concentration of ClO_2 ranges from 250 ppm to 1,000 ppm. The phytoncide in solution ranges from 0.1 to 5 wt%. Multiple airborne bacterial samplings were collected in a hospital before and after the application of ClO_2 oil mist at different diffusion rates (10–2,000 mL/h) via a ultrasound-based diffuser in standard-sized rooms. SARS-CoV-2 on a film was also exposed to the ClO_2 oil mist.

RESULTS: After the disinfection process, surface bacteria swab and airborne bacteria sampling were conducted at more than 50 hospital locations. The results show that the bactericidal efficacy for all locations exceeds 90% at a diffusion rate of 200 mL/h. The mist also completely inactivates the SARS-CoV-2 virus after 5 minutes of exposure. For the measurement of ClO_2 concentration, the concentrations of ClO_2 for all locations are below 0.1 ppm, which is the permissible exposure limit of inhalation for ClO_2.

CONCLUSION: This novel combination ClO_2 and phytoncide mist delivered at low diffusion rates and low concentrations is shown to be an effective and safe disinfectant for preventing airborne transmissions of harmful organisms, including bacteria and viruses.

P107

Implementation of ID NOW during a community outbreak of COVID-19 in a large ski resort

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OBJECTIVES: The ID NOW™ (Abbott, Chicago, Illinois) coronavirus disease 2019 (COVID-19) test is a point-of-care molecular assay that targets the COVID-19 RdRP gene and provides results with a short turnaround time. The objective was to demonstrate the step toward implementing a high-quality COVID-19 point-of-care testing program and assess its performance compared with routine real-time polymerase chain reaction (PCR) detection.

METHOD: In February 2021, a major COVID-19 outbreak declared itself in a large ski resort, and a new workflow and protocol for onsite testing was established. An outdoor mobile home collection site was transformed into a testing site. Symptomatic patients presenting for testing were offered an additional nasal swab with the possibility of having their results within 30 minutes via text message. Nasal swabs were processed by a trained nurse on the ID NOW, and the results were compared with routine real-time PCR results of the paired nasopharyngeal swabs. Overall feedback from the clinical team and from patients were collected during the project period.

RESULTS: At the time of the implementation, the laboratory positivity rate for this region was approximatively 49%. The testing clinic went live within 24 hours and was fully functional within a week. Training plans and standard operation procedure were made available for future implementation. During the working week of implementation, the sensitivity of the assay was 85.7% and the specificity was 100% compared with routine laboratory testing. The assay missed three patients who were positive on the routine assay with cycle threshold (Ct) values above 34 (*Orf* gene). This intervention allowed for direct impact on behaviour while maintaining laboratory standards

CONCLUSION: ID NOW is a reliable tool in the beginning of an outbreak in the community and demonstrated very good concordance with nasal swabs with Ct values below 34. The rapid turnaround time seems to be favorable in the active population found in that region.

P108

Impact of recent COVID-19 vaccination in health care workers: An observational cohort study in the context of an acute-care outbreak

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OBJECTIVES: In British Columbia, early phases of coronavirus disease 2019 (COVID-19) vaccine rollout coincided with

its second wave, which was characterized with greater-scale outbreaks in acute-care facilities. We aimed to examine the impact of recent COVID-19 vaccination among health care workers (HCWs) in the context of an outbreak occurring in a large tertiary hospital.

METHOD: We retrospectively analyzed a cohort of recently vaccinated and unvaccinated HCWs who were actively screened over a 3-week period in late winter 2021 during a COVID-19 outbreak involving three acute-care medical units. Outbreak and vaccination data were obtained from line lists provided by Public Health as well as British Columbia's Provincial Immunization Registry.

RESULTS: The cohort consisted of 335 HCWs. When the outbreak was declared, 156 (46.6%) HCWs were unimmunized, 155 (46.2%) were partially vaccinated, and a minority (7.1%) were fully vaccinated. A total of 21 confirmed staff cases were documented with whole-genome sequencing analysis, demonstrating tight clustering of cases and a causal variant belonging to lineage B.1.2. Attack rate for unimmunized HCWs was measured at 8.4%, whereas attack rate for partially or fully immunized HCWs was 4.4%. No cases were identified among the fully vaccinated group. During the studied period, an excess COVID-19 risk of 39% was observed among unimmunized HCWs.

CONCLUSION: Recent COVID-19 immunization among health care workers was associated with an inferior attack rate during an acute-care outbreak. Our study provides insights supporting effectiveness of partial immunization in the presence of a high rate of SARS-CoV-2 transmission. Although the effectiveness of the complete vaccination series remains undeniably optimal, our findings potentially suggest that in context of scarce vaccine supply and the predominantly circulating Beta SARS-CoV-2 variant, partial immunization remains beneficial to mitigate transmission. Assessment of vaccine impact will require similar investigations to be carried out in light of new variants of concern.

STUDENT POSTER PRESENTATIONS

SP01

Alterations in the nasopharyngeal microbiome associated with SARS-CoV-2 infection severity

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OBJECTIVES: The nasopharyngeal mucosal microbiome has been hypothesized to influence susceptibility to respiratory viral infection through its immunomodulatory effects on the host. Several studies have attempted to elucidate the relationship between coronavirus disease 2019 (COVID-19) infection and the nasopharyngeal microbiome with varying success, and most did not account for disease severity. This study aims to assess whether there are COVID-19–associated alterations in the nasopharyngeal microbiome in hospitalized and non-hospitalized patients with and without SARS-CoV2 infection.

METHOD: Archived nasopharyngeal swabs collected from four study populations were included, distributed equally between hospitalized and community-dwelling patients infected or not infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Total nucleic acid extraction was performed for all samples, followed by full-length 16S rRNA amplicon sequencing using the Oxford Nanopore MinION sequencing device (Oxford Nanopore Technologies, Oxford Science Park, United Kingdom). Bioinformatics was performed using the EPI2ME and BugSeq 16S pipelines.

RESULTS: We assessed whether there were significant differences in alpha and beta diversity among our study groups. We did not find significant changes in alpha diversity (Kruskal–Wallis test, $p > 0.05$) among our study groups. We found significant differences in beta diversity in the nasopharyngeal microbiota only at the phylum rank (PERMANOVA, $p = 0.008$), but not at the genus, species, or family ranks ($p > 0.05$). Differential taxonomic abundance was also assessed using ALDEx2. We did not observe any significant differences in taxon abundances, although there did appear to be a trend toward a higher abundance of Enterobacteriaceae among hospitalized SARS-CoV-2–positive patients.

CONCLUSION: Significant microbiome beta, but not alpha, diversity differences were observed across our study groups, but few taxon-specific alterations in the nasopharyngeal microbiome were associated with COVID-19 disease severity. A higher abundance of Enterobacteriaceae among hospitalized infected patients may be due to medical interventions such as antibiotic exposure or intubation. Full-length 16S rRNA sequencing may confer greater taxonomic resolution than

short-read amplicon sequencing, providing further validation to our results.

SP02

Development of a public-facing, interactive human provincial antibiogram

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OBJECTIVES: Antibiotic resistance is a global health care concern. Trends in antibiotic resistance can be tracked using local antibiograms that summarize the antimicrobial susceptibility of commonly isolated human bacterial pathogens to first-line antibiotics. The purpose of this work is to create a cumulative, interactive, and publicly accessible antibiogram to capture antimicrobial susceptibility rates across Alberta, Canada. The creation of such a platform will allow for the evaluation of antimicrobial resistance rates among human pathogens of concern over time.

METHOD: Antimicrobial susceptibility data for 2020 were extracted and collated from three laboratory information systems used across the province and processed as per guidelines by the Clinical and Laboratory Standards Institute (M39). Processing steps included the exclusion of duplicate organisms from the same patient, the removal of testing data with less than 70% the maximum number of isolates for a given organism, inclusion of only first-line antibiotics and commonly encountered bacterial pathogens, and the inclusion of testing data with >30 unique isolates. Percentage susceptibilities were calculated for each organism group, and the data were visualized in Tableau (Tableau Software, Seattle, Washington).

RESULTS: A total of 43 pathogens or pathogen groups were included in the final 2020 provincial antibiogram, of which 18 were gram-positive and 25 were gram-negative. Among first-line antibiotics, 19 were included for gram-positive organisms, and 21 were included for gram-negative organisms. Interactive antibiograms, with percentage susceptibility for every included organism–antibiotic combination, were generated for each gram type and are available online at https://public.tableau.com/shared/GC63BT3P5?:display_count=n&:origin=viz_share_link

CONCLUSION: A cumulative provincial antibiogram will be useful for surveillance of antimicrobial resistance rates across the province, capturing trends that may not be apparent at the local level and contributing to Canada-wide resistance surveillance. Continued addition of yearly antimicrobial susceptibility data, as well as the application of data filters (eg, by age, specimen type, location), can help guide researchers to address provincially relevant resistance issues.

SP03

Test performance of GeneXpert® MTB/RIF assay for detection of *Mycobacterium tuberculosis* complex in lymph node specimens

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OBJECTIVES: This study evaluated the performance of GeneXpert® MTB/RIF assay (Cepheid, Sunnyvale, California) for detection of *Mycobacterium tuberculosis* complex (MTBC) in lymph node biopsy specimens.

METHOD: A retrospective review was conducted on lymph node specimens that underwent testing by GeneXpert® MTB/RIF assay at our regional microbiology laboratory from May 1, 2015, to May 1, 2021. The GeneXpert MTB/RIF testing was performed only on selected samples when either pathology showed granulomatous inflammation or *M. tuberculosis* infection was suspected clinically. The results were compared with acid-fast smear and mycobacterial culture performed at the provincial reference laboratory. MTBC-positive and MTBC-negative culture results were deemed to be the gold-standard diagnostic method. *Z*-score was used to determine statistically significant difference between the test performance of acid-fast smear and GeneXpert.

RESULTS: A total of 26 lymph node specimens had GeneXpert MTB/RIF testing performed during the study period.

Table SP03-1: Acid-fast smear and GeneXpert MTB/RIF versus mycobacterium culture results of the 26 lymph node specimens in the current study

Mycobacterium culture	Acid-fast smear positive	Acid-fast smear negative	GeneXpert MTB/RIF positive	GeneXpert MTB/RIF negative
Positive (*n* = 13)	3	10	10	3
Negative (*n* =13)	1	12	3	10

MTBC = Mycobacterium tuberculosis *complex*

GeneXpert was determined to have sensitivity and specificity of 77% and 77%, respectively, whereas acid-fast smear showed sensitivity and specificity of 23% ($p < 0.05$ versus GeneXpert) and 92%, respectively, for detection of MTBC in lymph node specimens. Three of the four acid-fast positive smear specimens also had positive GeneXpert results; 10 of the 22 acid-fast negative specimens also had negative GeneXpert results.

CONCLUSION: The data suggest that the GeneXpert MTB/RIF assay is a useful diagnostic tool to detect MTBC in lymph node specimens where clinical suspicion for tuberculosis infection is high. The GeneXpert assay showed superior sensitivity compared with acid-fast smear. A larger sample size is needed to validate the use of the assay for diagnosing tuberculosis lymphadenitis.

SP04

Point prevalence survey of piperacillin–tazobactam use on general surgery wards followed by pilot prospective audit and feedback recommending the use of intravenous amoxicillin–clavulanate

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OBJECTIVES: Intravenous amoxicillin–clavulanate has recently been made available on the Canadian market and may present a narrower spectrum alternative to piperacillin–tazobactam in select infectious syndromes. This antimicrobial stewardship and quality improvement study took a two-phase approach to evaluate when intravenous amoxicillin–clavulanate may be used as an alternative to intravenous piperacillin–tazobactam for patients admitted to general surgery wards.

METHOD: Phase 1 was a point prevalence survey of piperacillin–tazobactam use on general surgery wards at four acute-care hospitals at four separate time points in 2021 (September 29, October 21, November 19, and December 13). Whether or not the use of piperacillin–tazobactam was discordant with best practices and antimicrobial stewardship guidelines was assessed. During phase 2, a pilot prospective audit and feedback will be completed to assess piperacillin–tazobactam use on the general surgery wards at the four sites, with feedback completed once per week for a time period of 4 months from January to May 2022. Intravenous amoxicillin–clavulanate will be suggested as a first- or second-line alternative by the antimicrobial stewardship team when appropriate, and uptake of the recommendations will be recorded.

RESULTS: During phase 1, 52 general surgery patients were reviewed. Piperacillin–tazobactam use was considered to be discordant with guidelines and antimicrobial stewardship practices in 25 cases (48%). Of these, intravenous amoxicillin–clavulanate would have been the first-line recommended alternative agent in 2 cases (3.8%).

CONCLUSION: Antimicrobial stewardship interventions to optimize piperacillin–tazobactam use on general surgery units are needed, where use is inappropriate almost half of the time. Intravenous amoxicillin–clavulanate may present a narrower-spectrum alternative to piperacillin–tazobactam in certain circumstances. Further results will follow on completion of phase 2.

SP05

Performance of immunoglobulin G serology on finger prick capillary dried blood spot samples to detect a SARS-CoV-2 antibody response

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OBJECTIVES: Measuring humoral immunogenicity of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccines presents an immediate challenge to public health practitioners. We investigate the diagnostic accuracy and predictive value of finger prick capillary dried blood spot (DBS) samples tested by a quantitative multiplex anti-immunoglobulin G (IgG) assay to detect SARS-CoV-2 antibodies after infection or vaccination.

METHOD: This cross-sectional study involved participants ($N = 6,841$) from several serological surveys conducted with non-hospitalized children and adults throughout 2020 and 2021 in British Columbia, Canada. Analysis used paired DBS and serum samples from a subset of participants ($n = 642$) before vaccination to establish signal thresholds and calculate diagnostic accuracy by logistic regression. Discrimination of the logistic regression model was assessed by receiver operating characteristic (ROC) curve analysis in an $n = 2,000$

bootstrap of the paired sample (n = 642). The model was cross-validated in a subset of vaccinated persons (n = 90). Unpaired DBS samples (n = 6,723) were used to evaluate anti-IgG signal distributions.

RESULTS: In comparison with paired serum samples, DBS samples from an unvaccinated population possessed a sensitivity of 79% (95% CI 58% to 91%) and specificity of 97% (95% CI 95% to 98%). ROC curve analysis found that DBS samples accurately classify SARS-CoV-2 seroconversion at an 88% percent rate, area under the ROC curve = 88% (95% CI 80% to 95%). In recipients of one or two coronavirus disease 2019 vaccine doses, the sensitivity of DBS testing increased to 97% (95% CI 83% to 99%) and 100% (95% CI 88% to 100%), respectively. Modelling found that DBS testing possesses a high positive predictive value (98%; 95% CI 97% to 98%) in a population with 75% seroprevalence.

CONCLUSION: DBS testing should be considered as an alternative to venipuncture to reliably detect SARS-CoV-2 antibodies and classify seropositivity from natural infection or vaccination.

SP06

Non-O157 Shiga toxin–producing *Escherichia coli* in Alberta, Canada, 2018–2021

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OBJECTIVES: Shiga toxin-producing *Escherichia coli* (STEC) are a group of foodborne gastrointestinal pathogens responsible for disease manifestations including hemorrhagic colitis and hemolytic uremic syndrome. Recently, it has been recognized that non-O157 serotypes contribute significantly to the burden of disease and have been under-recognized by traditional detection algorithms. We describe the epidemiology of non-O157 STEC in Alberta from 2018 to 2021.

METHOD: All stools submitted for bacterial pathogen detection were tested for STEC in accordance with Canadian guidelines. Positive stool samples and enriched broth cultures were referred to Alberta Precision Laboratories for isolation. Mauve colonies on CHROMagar STEC plates underwent colony quantitative polymerase chain reaction targeting the *stx*1 and *stx*2 genes. Serotyping was referred to the National Microbiology Laboratory. All non-O157 STEC from clinical samples were included in this retrospective analysis.

RESULTS: From January 2018 to September 2021, a total of 705 isolates were identified with increased case numbers over the summer months. Patients aged 18 years and younger made up 43% of cases, with 31% among those aged 0–9 years. There was a slight female predominance (55%). The Calgary zone had the most isolates, followed by Edmonton. There was a total of 52 different serogroups detected; the most common were O26, O103, O111, O121, and O118. The distribution of *stx* gene was as follows: *stx*1, n = 530; *stx*2, n = 105; and *stx*1/*stx*2, n = 49.

CONCLUSION: The epidemiology of non-O157 STEC in Alberta has not previously been described. Hundreds of cases are detected annually, particularly in the pediatric population. Many different serogroups are present; the most prevalent serogroups differ from those previously reported in North America. Our results demonstrate 23% positivity for *stx*2, which has been associated with more severe disease. These results underscore the importance of implementing algorithms capable of detecting non-O157 STEC and highlight the need for further characterization of their virulence factors and clinical impact.

SP07

Characterization of extensively drug-resistant carbapenemase-producing Enterobacterales in Canada, 2019–2020

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OBJECTIVES: Canadian data regarding the epidemiology of extensively drug-resistant (XDR) carbapenemase-producing Enterobacterales (CPE) are scarce. We investigated the characteristics of XDR CPE relative to non-XDR CPE.

METHOD: The Canadian Nosocomial Infection Surveillance Program collected data on adult and pediatric patients colonized or infected with CPE between 2019 and 2020. We defined CPE as XDR when resistant to five or six different antibiotic groups as defined by the new Canadian recommendation. We performed microbroth dilution (Sensititre, panel CAN1MSTF; ThermoFisher Scientific, Waltham, Massachusetts) to determine antibiotic susceptibilities using Clinical and

Laboratory Standards Institute breakpoints and polymerase chain reaction to identify carbapenemase genes.

RESULTS: We identified 482 CPE isolates among 440 patients from 33 of 72 participating hospitals. More than half were colonized or infected with a XDR CPE (259/440; 59%). XDR status was significantly associated with international travel in the year before positive culture (44% versus 26%; $p = 0.002$), travel to South Asia (56% versus 28%; $p = 0.010$), acquisition from health care outside of Canada (27% versus 13%; $p = 0.005$), and presence of NDM carbapenemase gene (46% versus 11%; $p < 0.001$). For novel combination antibiotics, we found eligible XDR isolates exhibited a significantly higher percentage resistance to meropenem–vaborbactam (6% versus 0%; $p = 0.006$) and imipenem–relebactam (14% versus 4%; $p = 0.006$), but not ceftazidime–avibactam (2% versus 1%; $p > 0.9$). Among XDR CPE, percentage resistance to tigecycline and colistin was 0.4% and 2.9%, respectively. Results did not show an association between XDR status and mortality; however, data were limited (10 deaths in 51 infected patients; 20%).

CONCLUSION: To help guide empiric antibiotic therapy, we present factors associated with XDR status. The study was limited in that tested novel combination antibiotics lacked activity against New Delhi metallo-β-lactamase (NDM); thus, treatment options for NDM XDR CPE are limited to tigecycline, colistin, and novel antibiotics not yet tested (eg, cefiderocol). Emerging resistance to novel combination antibiotics among non-NDM CPE isolates demonstrates the importance of continued surveillance of XDR CPE.

SP08

Examining the quality of antibiotic prescribing for community-acquired pneumonia in British Columbia outpatient care

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OBJECTIVES: Canada has yet to disseminate an action plan that focuses on the quality of antibiotic prescribing. Moreover, examining prescribing quality is difficult in the absence of encompassing guidelines, comprehensive clinical data, and the high level of ambiguity in defining inappropriate use. This

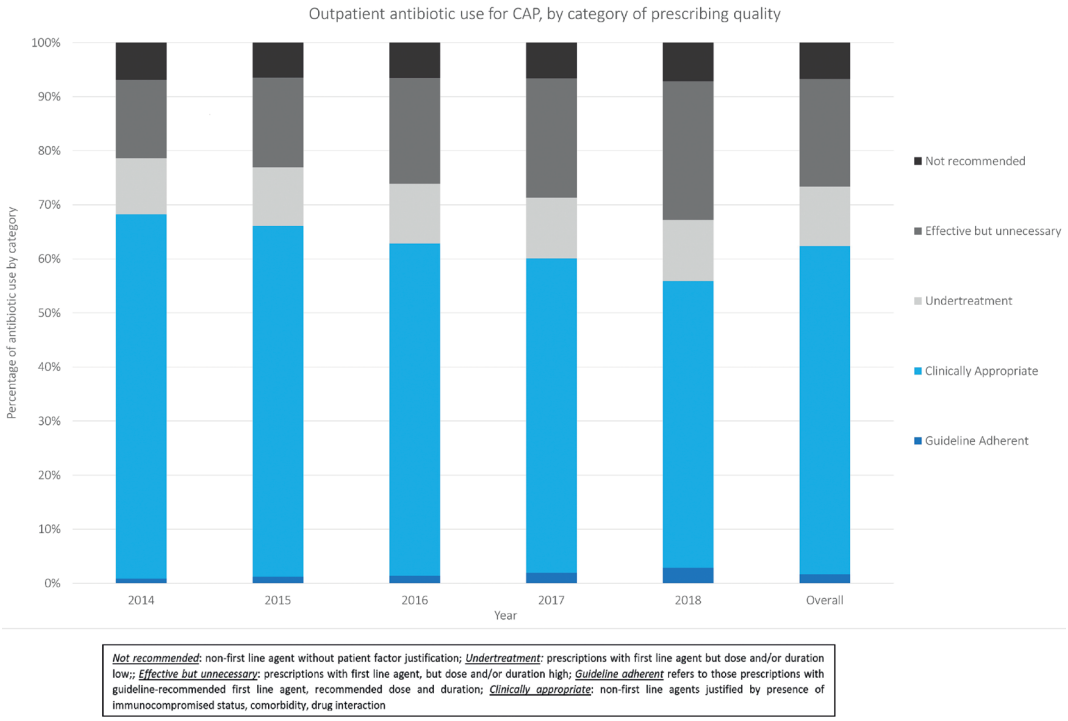

Figure SP08-1: Outpatient antibiotic use for community acquired pneumonia, by category of prescribing quality

retrospective cohort study is the first in British Columbia to quantify appropriate prescribing for older adults diagnosed with community-acquired pneumonia (CAP) in the outpatient setting. Because CAP confers high rates of antibiotic use, delineating appropriate use for this indication is paramount.

METHOD: All visits to a primary care physician for CAP were identified for older adults (aged >65 y) from January 1, 2014, to December 31, 2018. Acute episodes of infection were defined as all CAP-related *International Classification of Diseases, Ninth Revision,* codes within 14 days of a previous visit. If multiple antibiotic prescriptions were present per episode, only the first dispensation was examined. Categories of prescribing quality were as follows: (1) *guideline adherent*, (2) *effective but unnecessary*, (3) *under-treatment,* (4) *clinically appropriate,* and (5) *not recommended.* The first three categories review first-line agent, dose, and duration, and categories 4 and 5 incorporate patient factors to assess prescribing quality of non–first-line agents. Proportions of prescribing were calculated for each category, then subdivided by sex and age.

RESULTS: Our study period included 47,148 patients, with 118,606 episodes of CAP. Overall, 46% of CAP episodes were prescribed, with 34% of antibiotics issued concordant with guideline-recommended first-line agents ($N = 18,483$). Clinically appropriate (59%) and guideline adherent (2%) prescribing accounted for the majority of all antibiotic use, followed by effective but unnecessary (30%), not recommended (7%), and under-treatment (2%).

CONCLUSION: A total of 61% of all antibiotics issued for CAP among British Columbia older adults were appropriate. This is the first study to report trends in prescribing quality—by agent, dose, duration, and various patient factors—for British Columbia outpatient care.

SP09

Comparison of inpatient infectious diseases consultations at tertiary academic hospitals in 2015–2016 and 2020–2021

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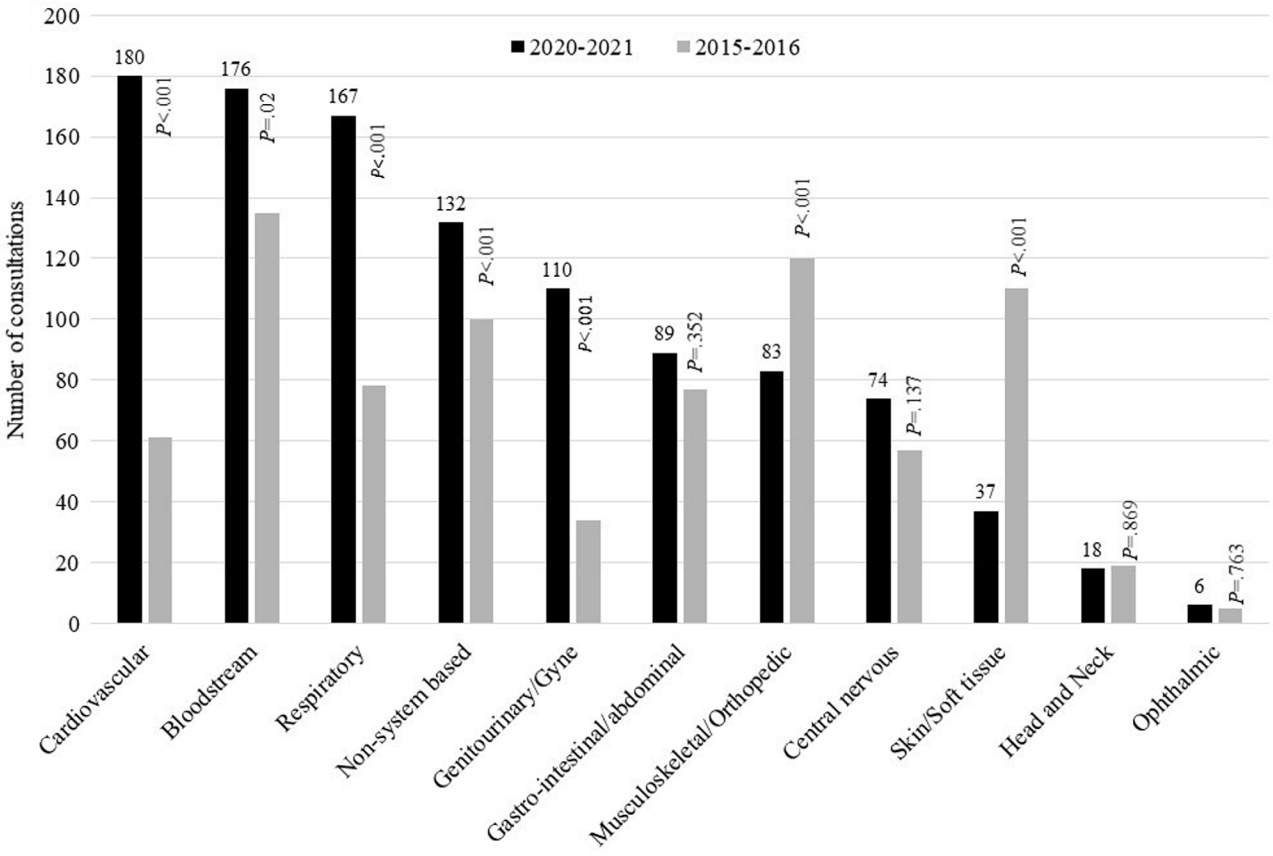

Figure SP09-1: Consultation by organ system

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OBJECTIVES: Little data exist about the nature and variety of infectious diseases (ID) consultations seen by subspecialty trainees. These data can inform the transition to a national competence-based curriculum for Canadian ID trainees, currently planned for 2024.

METHOD: We compared data collected by one PGY-4 adult ID subspecialty trainee in each of the 2015–2016 and 2020–2021 academic years as they rotated through three tertiary care hospitals. Reason for consultation, referring service, and date of consultation were documented. Coronavirus disease 2019 (COVID-19) status was also documented in 2020–2021. Data was then compiled according to top reason for consultation by hospital site, consultation by organ system and referring service, as well as total number of consultations by site.

RESULTS: A total of 897 consultations were seen in 2020–2021, representing an overall increase of 12% ($p = 0.02$) from the 2015–2016 academic year. There was an average of 4.5, 6.2, and 8.1 consultations per day at each respective site. Overall, the most common reason for consultation was bloodstream infections, but there was otherwise site-specific variation. Despite high numbers of consultations related to COVID-19 and related infections, there remained a wide breadth of exposure to various clinical syndromes (Figure SP09-1). Some gaps identified in the 2020–2021 academic year include exposure to travellers as a result of travel restrictions related to COVID-19, immunocompromised hosts, and viral hepatitis.

CONCLUSION: ID subspecialty trainees see a diversity of consultations at tertiary care academic centres. This data set is limited to two 1-year collection periods by individual trainees and does not consider exposures from longitudinal clinics, elective or selective rotations, or supplemental exposures in the subspecialty rotations of the PGY-5 year. A national database of these experiences could be considered to further characterize the educational experience of Canadian adult ID trainees.

SP10

Validation of an 8-plex real-time reverse transcription polymerase chain reaction assay for the detection of multiple respiratory viruses

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OBJECTIVES: To improve the efficiency of the clinical workflow in our laboratory, we developed and validated a fully automated multiplex assay to identify common viral pathogens associated with seasonal respiratory infection. A two-tube assay was designed for the detection of (1) severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza A, influenza B, and respiratory syncytial virus (RSV) and (2) parainfluenza 1-4 (PIV 1-4), metapneumovirus (hMPV), adenovirus (AdV) and picornavirus (rhino/enterovirus).

METHOD: Negative specimens obtained from patients included nasopharyngeal swabs in transport media, and bronchoalveolar lavages were spiked with known positive representative samples and used in our validation study. Samples were extracted using the Microlab STARlet IVD platform (Hamilton Company, Reno, Nevada). Real-time reverse transcription polymerase chain reaction (RT-PCR) was performed using the LightCycler (LC) Multiplex RNA Virus Master Mix (Roche Diagnostics, Indianapolis, Indiana) on a Roche LC480 II (Roche Diagnostics). An internal control (RNAseP) was included in tube 1. Winterplex Modular kits (TIB MOLBIOL, Berlin, Germany) for sarbecovirus E-gene, influenza A, influenza B, and RSV were multiplexed with RNAseP primers and probe (IDT Integrated DNA Technologies, Coralville, Iowa) in tube 1. Tube 2 combined separate LightMix Modular kits of PIV 1-4, hMPV, AdV, and Picornavirus (TIB MOLBIOL).

RESULTS: The accuracy was 99.77% for influenza A, influenza B, and RSV and 99.31% for SARS-CoV-2. The accuracies for tube 2 for PIV 1-4, hMPV, AdV, and picornavirus were 96.79%, 99.46%, 100%, and 97.87%, respectively. No cross-reactivity was observed. Precision was calculated from triplicates over 5 days. All targets had a coefficient of variation <5%.

CONCLUSION: The multiplex assay described here performed well, allowing for simultaneous detection of multiple seasonal respiratory viruses in a single RT-PCR assay. Implementation of this assay into the clinical workflow fostered expedited testing and reporting of seasonal respiratory viruses. Automation of the extraction and liquid handling components of the assay decreased hands-on time.

SP11

Age-associated seroprevalence of antibodies against six human coronaviruses: Population-based sero-surveys in 2013 and 2020

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OBJECTIVES: Older adults are disproportionately affected by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and are at higher risk of severe coronavirus disease 2019 (COVID-19); children often exhibit milder disease or are asymptomatic. Prior exposure to endemic human coronaviruses (HCoV) may modulate the response to SARS-CoV-2 infection and contribute to age-related observations. We assessed the relationship between anti-HCoV antibodies with age and their cross-reactivity with SARS-CoV-2 epitopes.

METHOD: We utilized 895 archived anonymized sera (ages 0–99) from sero-surveys conducted before the emergence of SARS-CoV-2 (May 2013; n = 407) and before widespread community circulation (May 2020; n = 488) in the same geographic region. Fifty sera, sex-balanced per 10-year age band, were sought among individuals ages ≤10 to ≥80 years, supplemented as indicated by sera from March and September 2020. Sera were tested using the Meso Scale Diagnostics (MSD; Rockville, Maryland) electrochemiluminescent multiplex immunoassay to quantify immunoglobulin G (IgG) antibodies against the spike proteins of HCoV-229E, HCoV-HkU1, HCoV-Nl63, HCoV-OC43, and SARS-CoV-1 and the spike protein, nucleocapsid, and receptor binding domain (RBD) of SARS-CoV-2. SARS-CoV-2 sero-positivity status was defined by positivity on two or more targets.

RESULTS: Anti-spike antibodies to all four endemic HCoV were acquired by age 10 years. Twenty of 407 (5%) sera in 2013 and 8/488 (2%) sera in 2020 were considered sero-positive for SARS-CoV-2 on the basis of MSD. Notably, antibodies against the SARS-CoV-2 RBD target were detected in 329/407 (81%) of 2013 sera and 91/488 (19%) of 2020 sera. Among the SARS-CoV-2 overall sero-negative population, age was correlated with anti-HCoV antibody levels and these, notably 229E and HKU1, were correlated with cross-reactive anti–SARS-CoV-2 RBD titres. Overall, SARS-CoV-2 sero-positive individuals showed higher titres to HCoV generally.

CONCLUSION: Most people have an HCoV priming exposure by age 10 years, with IgG levels remaining stable thereafter on a population level. Anti–HCoV antibodies may cross-react with SARS-CoV-2 epitopes. These immunological interactions warrant further investigation with respect to their implications for COVID-19 immune response and clinical outcomes.

SP12

Identification and characterization of bacteriophages isolated from sewage samples against two clinical strains of multi-drug-resistant *Escherichia coli*

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OBJECTIVES: This study aims to identify and characterize bacteriophages isolated during screening from interior British Columbia's municipal and hospital sewage samples against clinical multi-drug-resistant (MDR) bacterial strains.

METHOD: Five clinical MDR bacterial strains (*Escherichia coli [E. coli* #1, *E. coli* #2, *E.coli* #3]; *Pseudomonas aeruginosa [PA* #3]; and *methicillin-resistant Staphylococcus aureus* [*MRSA* #4]) were selected as potential hosts for the isolation and propagation of bacteriophages in the sewage samples collected from wastewater treatment plants in Kamloops, Vernon, and Kelowna (British Columbia). Traditional double-layer agar method was used to screen, purify, and propagate bacteriophages from sewage against the clinical MDR hosts. Subsequent subculturing of the host bacteria was performed with the addition of the relevant antibiotic (ciprofloxacin) to ensure bacterial growth occurred under the selective pressure. The phage concentrates were prepared using crossflow ultrafiltration to obtain the final products with ~10^9 PFUs/mL. Characterization was performed using transmission electron microscopy (TEM) and genome sequencing (MiSeq).

RESULTS: Bacteriophages isolated from sewage samples (Kelowna City, Kelowna Hospital, and Kamloops City) were successful in infecting two clinical strains of MDR *Escherichia coli (E. coli* #1 and *E. coli* #3). Phages against these strains of *E. coli* consistently showed productive lysis and appearance of plaques on a confluent bacterial lawn. Plaques produced by all three phage concentrates were clear and around 3–5 mm in diameter. No plaques were produced by phages when screened against *PA* #3, *MRSA* #4 and *E. coli* #2. Genomic analysis (MiSeq) and TEM of the isolated bacteriophages are under investigation.

CONCLUSION: Bacteriophages isolated in this study (designated as EC1KELHOS, EC1KELCTY, and EC3KAMCTY) could be potential candidates for use in phage therapy. This project's contribution will immensely help the growing field of phage research, because there is still an abundance of uncharacterized bacteriophages that could be used as an alternative solution to battle MDR bacteria.

SP13

Perspectives of health care professionals on infection prevention and control practices during the COVID-19 pandemic

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OBJECTIVES: To describe challenges and facilitators in the adoption of infection prevention and control (IPC) practices among health care professionals (HCPs) during coronavirus disease 2019 (COVID-19).

METHOD: In this qualitative study, individual semi-structured interviews with HCPs were conducted from June to October 2021 in four units of a pediatric tertiary care center in Montreal.

RESULTS: Six nurses, five staff physicians, one resident physician, four patient care attendants or orderlies, and one housekeeping staff were interviewed. Participants noted that many IPC measures had been implemented since COVID-19 onset, including the use of personal protective equipment (PPE), amplification of already-established protocols (eg, supervision of donning and doffing), reinforcement of basic IPC principles (eg, hand hygiene), and new workplace restrictions (eg, physical distancing, no drinking at nursing stations). A major identified barrier included frequent changes and resulting confusion and stress regarding the most accurate practices. Tensions between personnel regarding IPC protocols and modifications were reported, highlighting the importance of centralizing information, including IPC recommendations. Perceived lack of efficacy and physical discomfort in relation to PPE (eg, fogging vision due to eye protection, facial discomfort from N95 masks, and overheating with gown use) were also barriers to adherence. Main facilitators included communication with IPC teams and proactive attitudes among staff. Regular communications with IPC personnel and the availability of a designated IPC contact were mentioned as key facilitators. Many interviewees expressed contributions of teams to IPC practices, including initiatives among the various hospital departments. Adaptability of personnel, responsibility toward respective teams and patients, and HCP engagement to reduce spread of COVID-19 were important strengths identified.

CONCLUSION: Frequent and clear communications between IPC and hospital teams are a significant aspect of the adoption of IPC practices. Despite challenges faced by HCPs, adaptability and engagement were identified as important strengths of HCPs that positively contributed to IPC throughout the COVID-19 pandemic.

SP14

Nosocomial infections in patients with COVID-19 supported by extracorporeal membrane oxygenation

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OBJECTIVES: Extracorporeal membrane oxygenation (ECMO) has been widely used in the care of patients with respiratory failure resulting from coronavirus disease 2019 (COVID-19). Nosocomial infections are common complications in patients receiving ECMO but remain poorly characterized, especially among patients with COVID-19. We aimed to characterize nosocomial infections in COVID-19 ECMO-supported patients and to determine their impact on patient outcomes.

METHOD: We conducted a retrospective cohort study of adult patients admitted to our centre for COVID-19 from March 1, 2020, to June 30, 2021 who received ECMO. We identified bloodstream infections and ventilator-associated pneumonias and described their epidemiology and

microbiology. The cumulative burden of antimicrobial use and the specific management of bloodstream infections were determined. A multivariable time-dependent Cox proportional hazards model was constructed to evaluate the impact of bloodstream infections on mortality, controlling for age, receipt of COVID-19–specific therapies, and new renal replacement therapy.

RESULTS: We identified 136 patients who received ECMO for COVID-19 pneumonia during the study period. Bloodstream infections and ventilator-associated pneumonias occurred among 59.6% (81/136) and 68.4% (93/136) of patients, respectively. The incidence of bloodstream infections was 29.5 per 1,000 ECMO days, and the likelihood of having a bloodstream infection at 14 days of ECMO cannulation was 48.3%. *Staphylococcus aureus,* enterococci, and Enterobacterales were the most common causes of bloodstream infections, and *S. aureus, Klebsiella* spp, and *Pseudomonas aeruginosa* made up the majority of ventilator-associated pneumonias. Mean antibiotic use was 1,031 DOTs per 1,000 ECMO days (SD 496 DOTs per 1,000 ECMO days). There was no association between bloodstream infections and mortality (adjusted hazard ratio 1.14, 95% CI 0.63 to 2.06).

CONCLUSION: Nosocomial infections are common among COVID-19 ECMO-supported patients. Efforts to optimize their diagnosis, prevention, and management should be prioritized.

SP15

Genomic epidemiology of COVID-19 farm outbreaks throughout a Canadian province, March 2020–December 2020

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OBJECTIVES: Traditional epidemiological methods and whole-genome sequencing (WGS) were used to analyse coronavirus disease 2019 (COVID-19) farm outbreaks that occurred throughout a Canadian province to understand transmission.

METHOD: We obtained epidemiological information for COVID-19 cases related to outbreaks in agricultural settings from the provincial database of COVID-19 cases and conducted WGS analysis. We used the genome sequences of community control cases residing in the same public health unit with collection dates 2 weeks before and after the first and last cases, respectively.

RESULTS: We analyzed seven farm outbreaks (March 2020–December 2020); outbreaks ranged from 15 to 126 associated cases. The number of outbreak-associated cases sequenced per outbreak ranged from 4 to 53 , two outbreaks had <10 cases sequenced, and outbreaks had 6%–82% sequencing completeness. Outbreak-associated sequences in four of seven outbreaks had 0–2 pairwise single nucleotide polymorphism (SNP) differences between any two cases within the outbreak, and three of seven outbreaks had 0–4, 0–17, and 0–31. Outbreak-associated sequences had 7–23 pairwise SNP differences with Wuhan-Hu-1 reference. Phylogenetic analysis showed three of seven outbreaks with two distinct clades, whereas four of seven outbreaks were composed of a single clade. Farm outbreaks with two phylogenetic clades occurred in large outbreaks ranging from 60 to 126 outbreak-associated cases. Phylogenetic analysis demonstrated tight clustering of outbreak-associated cases with 0–3 community sequences within the cluster. No variants of concern were identified because the farm outbreaks occurred before their prevalence in the province. The two outbreaks with the highest genetic diversity occurred when community transmission was high (41.7 per 100,000 and 269.3 per 100,000, respectively).

CONCLUSION: Few reports have investigated COVID-19 farm outbreaks using genomic sequencing. We found evidence of multiple introductions on farms. When levels of community transmission are elevated, outbreak genetic diversity increases. Genomic sequencing allows for improved understanding of transmission of COVID-19 in agricultural settings, where several factors make farmworkers vulnerable to COVID-19.

SP16

Optimizing real-time viability PCR for Shiga toxin–producing *Escherichia coli* : Propidium monoazide can be light activated before being added to samples

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OBJECTIVES: Front-line laboratories are moving away from using culture to diagnose bacterial gastroenteritis. Although polymerase chain reaction (PCR)–based assays are

faster and more sensitive, this shift means that the presence of dead organisms could be mistaken for a real infection. Viability quantitative PCR (qPCR) assays address this issue by using light-activated propidium monoazide (PMA) to bind "free" DNA, which allows for the selective detection of intact organisms. This study aimed to optimize PMAxx (a more efficient form of PMA) treatment for heat-killed Shiga toxin–producing *Escherichia coli* (STEC) cells. The effectiveness of different PMAxx concentrations and the effect of adding dimethyl sulfoxide (DMSO) was compared. Using these optimized conditions, we determined whether PMAxx could be light activated before sample addition.

METHOD: Various PMAxx concentrations (50, 75, and 100 µM) with and without DMSO were used on heat-killed STEC. Regular treatment was performed according to the manufacturer's instructions. This involved adding PMAxx to the sample, a 10-minute dark incubation, then light activation. The pre-activation condition differed by activating the PMAxx before sample addition and subsequent dark incubation. All steps were conducted at room temperature, and light activation was achieved using the PMA-Lite™ LED Photolysis Device (Biotium, Fremont, California) for 15 minutes. Cells were washed and lysed before qPCR was conducted.

RESULTS: Compared with untreated cells, regular treatment with 75 µM of PMAxx was found to produce a significantly higher cycle threshold (Ct) value. The addition of 20% DMSO to the PMAxx solution further increased Ct values, so this combination was used for subsequent experiments. Pre-activated PMAxx (with 20% DMSO) provided a change in Ct value similar to that of regular activation.

CONCLUSION: Pre-activated PMAxx with 20% DMSO showed promising effectiveness with heat-killed cells and is poised for use with complex samples that would otherwise interfere with light activation. This technique will be utilized as we develop a direct-from-stool viability qPCR assay.

SP17

Epidemiology of candidemia in a Canadian tertiary pediatric hospital: An 11-year review

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OBJECTIVES: Candidemia is a significant cause of morbidity and mortality in the pediatric population. Understanding the local epidemiology of candidemia is essential in aiding clinicians in their empiric therapy choices and implementation of measures to reduce the risk of disease. This study examined the epidemiology over an 11-year period at a Canadian tertiary care pediatric hospital.

METHOD: A retrospective chart review was conducted of children with positive blood culture for *Candida* species between January 1, 2007, and December 31, 2018. Demographic characteristics, *Candida* species, underlying medical diagnoses, risk factors for candidemia, follow-up investigations and interventions, and outcome data were included in the analysis.

RESULTS: A total of 61 candidemia episodes were included in the final analysis. The most frequent species were *Candida albicans* (54%), *C. parapsilosis* (18%), and *C. glabrata* (8%). Mixed candidemia was noted in 8% of episodes. The annual incidence rate of candidemia varied, ranging from 3.9 to 9.5 episodes per 10,0000 patient admissions. The most common risk factors for candidemia included presence of central venous catheter (95%) and receipt of antibiotics in the past 30 days (92%). The majority of patients received an abdominal ultrasound (89%), ophthalmology consult (86%), and echocardiogram (70%), regardless of age. Line removal was performed in 79% of episodes ($n = 58$). Evidence of disseminated fungal disease on abdominal imaging was observed in 10% of episodes (all in non-neonates; specifically, 4 receiving immunosuppressants, 1 with gastroschisis, and 1 with a gastrointestinal perforation). The overall 30-day mortality rate was 8%.

CONCLUSION: The rates of candidemia fluctuated from year to year during our study period. *C. albicans* was the most commonly isolated species overall. Abdominal imaging should be considered in all patients with relevant risk factors, including immunosuppression or underlying gastrointestinal abnormalities.

SP18

Population-based outpatient antimicrobial use in Newfoundland and Labrador

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OBJECTIVES: Canada does not have standardized antimicrobial use (AMU) surveillance. Population-based provincial data on outpatient AMU has not been reported from Newfoundland and Labrador, and current national surveillance contains selected pharmacies only. We used provincial pharmacy network data to describe outpatient AMU.

METHOD: All outpatient antimicrobial prescriptions were captured from a provincial pharmacy network between June 2017 and June 2021, representing use among outpatients and long-term-care facilities. Patient identifiers were removed. Prescriptions for parenteral and topical antimicrobials, antivirals, and antifungals were excluded. Ethics approval was not required.

RESULTS: We analyzed 1,586,534 outpatient antibiotic prescriptions given to 394,708 unique individuals by 3,431 prescribers. The AMU rate was 757 prescriptions/1,000 inhabitants/year (7,392 defined daily doses [DDD]/1,000 inhabitants/y). Mean prescription duration was 10.4 days (SD 11.9). A total of 1,095,611/1,586,534 (69.1%) prescriptions were from the World Health Organization AWaRe "Access" category. The prescription rate decreased from 878/1,000 inhabitants/year to 564/1,000 inhabitants/year (–35.8%; $p < 0.00001$) over the study period, and mean DDD rate decreased from 8,589 DDD/1,000/year to 5,684 DDD/1,000/year (–33.8%; $p < 0.00001$). The highest-use antimicrobials were amoxicillin (1,544 DDD/1,000/y), doxycycline (877 DDD/1,000/y), and ciprofloxacin (685 DDD/1,000/y). Prescribers wrote a mean of 102 (SD 248) prescriptions/year, and three prescribers wrote >2,500 prescriptions/year. Of inhabitants, 9,203/394,708 (2.3%) received four or more prescriptions/year.

CONCLUSION: AMU rate in Newfoundland and Labrador is 25% lower than previously described in national surveillance (9,857 DDD/1,000/y). Coronavirus disease 2019 was associated with a significant reduction in AMU. Targets for stewardship intervention include prolonged duration, high-rate prescribers, and high-rate inhabitants. Further research is needed to assess the appropriateness of prescriptions according to diagnosis.

SP19

Validation study of a quality score to reject low-quality wound swab specimens using three processing methods

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OBJECTIVES: Separating true infection from contamination or colonization of wound swab cultures can be difficult. Using a quality score (Q score) during specimen processing may allow rejection of low-quality wound swabs whose culture results may be misleading, potentially reducing unnecessary antimicrobial prescribing. It is unclear whether processing method affects the proportion of rejected wound swabs. The primary objective was the comparison of the proportion of wound swabs rejected by Q score using three processing methods.

METHOD: Superficial and deep wound swabs from any anatomical site were included; sterile operating room swabs were excluded. The standard laboratory method with a 5-second manual vortex, an automated 5-second vortex on WASP (Copan Diagnostics, Murrieta, California), and a 10-second manual vortex were used to process swabs. Gram stains were prepared and assigned a Q score by medical laboratory technologists. Pairwise continuity-corrected McNemar's tests were used to compare the proportion of swabs rejected by each processing method.

RESULTS: A total of 102 patient wound swabs were included, and four operative specimens were excluded. The proportion of swabs rejected by Q score (Q score = 0) was 24.5%, 37.3%, and 57.8% for the standard, WASP, and manual processing methods, respectively. There were statistically significant differences in the proportion of wound swabs rejected by Q score when comparing standard and WASP processing methods ($p = 0.03496$), standard and manual methods ($p < 0.0001$), and WASP and manual methods ($p = 0.00196$).

CONCLUSION: Between 24% and 57% of wound swabs may be rejected using a Q score. Although the 10-second manual vortex rejected the most specimens, it also produced the highest number of rejected swabs whose cultures ultimately isolated clinically significant pathogens. A processing method that rejects fewer specimens upon application of the Q score, such as a manual or automated 5-second vortex, may thus be ideal.

SP20

Non-enteric adenovirus serotypes associated with acute gastroenteritis in pediatric patients

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OBJECTIVES: Human adenovirus (HAdV), particularly enteric-HAdVs (HAdV-F40/41), is a common cause of acute gastroenteritis (AGE); however, limited data are available regarding the association of non-enteric HAdVs and AGE in children. We investigate the genotype distribution, prevalence, and clinical impact of non-enteric HAdVs in children aged ≤12 years in the southern Ontario region.

METHOD: We analyzed 655 children (aged ≤12 y) presenting with AGE. We compared HAdV genotype distribution with children with confirmed respiratory HAdV infection matched for age, gender, and time of collection. We further examined HAdV patients (n = 7), with matched respiratory and stool specimens, presenting with AGE.

RESULTS: We detected HAdV in 68/655 (10.4%) children with AGE. The predominant genotypes were HAdV-F41 (n = 28; 45.2%), HAdV-C1 (n = 13; 21%), and HAdV-C2 (n = 11; 17.7%). The most reported symptoms were diarrhea (n = 45; 77.6%), fever (n = 12; 20.7%), and vomiting (n = 12; 20.7%). Children with non-enteric HAdV infections were significantly more likely to have abdominal pain, blood in stools, sepsis, or weight loss than children with HAdV-F41 (p = 0.008; OR 13.1, 95% CI 1.9 to 146.1). Six of seven patients with matched respiratory and stool specimens had matching genotypes from both sources.

CONCLUSION: Our results suggest non-enteric HAdVs may be causal of AGE in the absence of other enteric pathogens. The utilization of HAdV assays limited to F40/41 could lead to missed diagnoses and an overall underestimation of the burden of HAdV-associated AGE.

SP21

Modified two-tiered testing enzyme immunoassay algorithm for serologic diagnosis of Lyme disease

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OBJECTIVES: Lyme disease (LD) is endemic in Nova Scotia, and serology is available for testing. The standard two-tier testing (STTT) algorithm for LD serology has poor sensitivity for detection of early localized infection (>50%) but high sensitivity (>99%) for late infection. Recently, the Food and Drug Administration has approved a modified two-tier testing (MTTT) algorithm using two enzyme immunoassays (EIAs), which has been endorsed by the Centers for Disease Control and Prevention and the Infectious Diseases Society of America. We recently validated MTTT using a whole-cell EIA followed by C6 peptide EIA, and compared with STTT, MTTT identified 25% more cases of early LD with a specificity of 99.6%. Recently, the C6 EIA has been discontinued, prompting validation of two new EIAs for the MTTT.

METHOD: From March to July 2020, all positive or indeterminate LD serology specimens identified with the Zeus C10/VlsE EIA (Zeus Scientific, Branchburg, New Jersey) were tested with the Zeus whole-cell EIA (ie, MTTT algorithm), in addition to being referred to the National Microbiology Laboratory for immunoblot testing (ie, STTT algorithm). Clinical information was obtained from the ordering physicians to determine whether the patient's clinical presentation was consistent with LD.

RESULTS: Of 2,196 specimens tested for LD, 142 were positive by WCS EIA in the MTTT. Clinical information was obtained for 87 of these patients, and 8 were considered false positives with no clinical syndrome compatible with LD. However, 73 patients had early localized/early disseminated LD, and 20 did not have positive immunoglobulin M or G IBs, suggesting the MTTT had an increased sensitivity of 25% over the STTT. Considering that only 8 of 2,196 would be considered false positive, the specificity is 99% (95% CI 99% to 99%).

CONCLUSION: The MTTT improved the sensitivity for detection of early LD and has equivalent specificity to the STTT. On April 1, 2021, the MTTT method was implemented for the serologic diagnosis of LD in Nova Scotia.

SP22

Procedure development for biofilm growth from multi-drug-resistant clinically isolated bacteria

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OBJECTIVES: This study focuses on determining the optimal growth conditions for clinically isolated multi-drug-resistant (MDR) bacterial biofilms in order to begin screening alternatives to antibiotics that can inhibit biofilm growth.

METHOD: Adapting the protocol from the Innovotech Inc. MBEC Assay Procedural Manual 2.1 (Innovotech Inc., Edmonton, Alberta), 96-well MBEC Assay Biofilm Inoculator plates were used to grow MDR *Escherichia coli, Pseudomonas aeruginosa*, and methicillin-resistant *Staphylococcus aureus* (MRSA) biofilms. The 96-well plates were inoculated with suspensions diluted to an approximate cell density of 1.0×10^5 CFU/mL. Bacteria were each cultured in three different media, at different conditions. After incubation, biofilm growth was both qualitatively and quantitatively observed, and the optimal growth condition was determined.

RESULTS: With the conditions and equipment in the laboratory, it was determined that Tryptone Soya Broth produced the biofilms that best covered the pegs. In addition, incubating the bacteria at 37°C, 65% humidity, and 110 rpm for 16 hours consistently produced biofilms with an appropriate cell density for screening biofilm inhibitors. After this procedure, a biofilm density of 1.5×10^5 CFU/mL was obtained for *E. coli*, 8.8×10^4 CFU/mL for *P. aeruginosa*, and 2.7×10^5 for MRSA. Minimum biofilm eradication concentration assays will be ongoing to begin assessing the efficacy of novel biofilm inhibitors. Although viable cell count and turbidity measurements will be used to determine the potency of these inhibitors, scanning electron microscopy will be used to characterize the antibiofilm effects at the matrix level.

CONCLUSION: We successfully developed a protocol to reliably and efficiently culture MDR biofilms in the lab setting. This study will allow us to further screen potential anti-biofilm compounds, thus expanding the options for drug discovery against MDR bacterial infections.

SP23

Investigating the seroprevalence of hepatitis C virus in Alberta provincial correctional facilities: A retrospective cross-sectional study

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OBJECTIVES: Hepatitis C virus (HCV) is a blood-borne infection that is commonly spread through shared drug use equipment. People who are incarcerated (PWAI) are at high risk for HCV and are a priority group for HCV micro-elimination efforts. In 2019, universal opt-out screening for sexually transmitted and blood-borne infections was implemented in all provincial correctional facilities upon entry, and PWAI can additionally request testing during the incarceration period. We sought to identify the seroprevalence of HCV among PWAI in Alberta provincial correctional facilities.

METHOD: Blood samples from PWAI were sent to the Alberta Public Health Laboratory for HCV antibody screening. HCV testing data from January 1 to December 31, 2020 were extracted from the Public Health Laboratory Information System, and results from all adult provincial correctional facilities were analyzed. Seroprevalence was defined as the proportion of PWAI with reactive HCV antibody results out of all PWAI tested.

RESULTS: In total, 2,290 PWAI were tested for HCV, and the overall seroprevalence was 15.1%. The seroprevalence was highest in Lethbridge Correctional Centre (13/46; 28.3%), followed by Calgary Correctional Centre (21/100; 21.0%), Fort Saskatchewan Correctional Centre (52/311; 16.7%), Medicine Hat Remand Centre (4/27; 14.8%), Edmonton Remand Centre (187/1,289; 14.5%), Calgary Remand Centre (47/327; 14.4%), Peace River Correctional Centre (20/185; 10.8%), and Red Deer Remand Centre (0/5; 0.0%); was higher among women (77/419; 18.4%) than men (269/1,871; 14.4%); and was highest in PWAI aged 51 years or older (30/77; 39.0%), followed by those aged 41–50 years (94/308; 30.5%), 31–40 years (136/852; 16.0%), and 16–30 years (86/1,053; 8.2%).

CONCLUSION: HCV seroprevalence in the province is disproportionally higher among PWAI than among the general population (0.7%). Seroprevalence rates among male and female provincial PWAI align closely with federal estimates. Strategies to engage PWAI in treatment during incarceration and upon release will be imperative for achieving HCV micro-elimination goals in this population.

SP24

Self-collection and asymptomatic testing affect the positive predictive value of SARS-CoV-2 rapid antigen detection tests

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OBJECTIVES: Many rapid antigen-detection tests (RADTs) have been developed to screen for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; coronavirus disease 2019 [COVID-19]) infection. Although less accurate than molecular tests (ie, reverse transcription polymerase chain reaction [RT-PCR]), RADTs offer flexibility in deployment and faster turnaround times, and they may be implemented along with laboratory testing. The efficacy of these RADTs varies widely, influenced by the specific RADT kit and adherence to manufacturer's instructions. A prior study at the Eastern Ontario Regional Laboratory Association (EORLA) demonstrated near-perfect positive predictive value when RADT tests were conducted by trained laboratory professionals. As these tests become increasingly available, we aim to study real-world factors that affect the positive predictive value of COVID-19 RADTs, including the impact of self-collection and symptomatic versus asymptomatic testing.

METHOD: We retrospectively analyzed data from individuals with a positive RADT who subsequently underwent confirmatory RT-PCR testing between June 12, 2021, and December 28, 2021, at COVID-19 assessment centres in Ottawa, Ontario; RT-PCR testing was performed at EORLA.

RESULTS: Of 259 positive RADTs, 187 (72.2%) were confirmed to be positive by RT-PCR. Testing performed at a pharmacy or medical clinic had a higher positive predictive value than self-collection among asymptomatic individuals (73.7% versus 27.3%; $p = 0.02$). Testing among symptomatic individuals also had a significantly higher positive predictive value than that among asymptomatic individuals (86.1% versus 41.5%; $p = 1.7e\text{-}11$). There was no significant difference based on known COVID-19 contacts.

CONCLUSION: Many real-world factors affect the positive predictive value of RADTs. We found the positive predictive value of RADTs to be lower in the context of self-collection and asymptomatic screening. Further study and public awareness of these factors will guide the successful implementation of RADTs within the greater public health system.

SP25

Optimizing cefazolin use in obstetrical patients with beta-lactam allergy undergoing caesarean section

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OBJECTIVES: Cefazolin is the antibiotic prophylaxis of choice for caesarean section but is often avoided in patients reporting a beta-lactam allergy. The Allergy Clarification for Cefazolin Evidence-based Prescribing Tool (ACCEPT) was developed to quickly determine whether a patient with beta-lactam allergy can safely receive cefazolin. We conducted an interrupted time-series analysis to evaluate the impact of ACCEPT on peri-operative antibiotic use in patients with reported beta-lactam allergy undergoing caesarean section.

METHOD: ACCEPT was developed through consensus by allergists, anesthesiologists, and infectious diseases specialists and implemented over a 2-month period (December 1, 2018, to January 31, 2019). A segmented regression on monthly cefazolin use among patients with reported beta-lactam allergy undergoing caesarean section was conducted during the baseline (January 1, 2018–November 30, 2018) and intervention (February 1, 2019–December 31, 2019) periods. The frequency of peri-operative allergic reactions was also collected during both periods.

RESULTS: Of the 3,128 eligible women who underwent a caesarean section, 282 (9%) reported a beta-lactam allergy. The most common beta-lactam allergens were penicillin (64.3%), amoxicillin (16%), and cefaclor (6%). The most frequently reported allergic reactions were rash (38.1%), hives (21.4%), and unknown (11.6%). Use of cefazolin increased from 55% during the baseline period to 86% during the intervention period. Segmented regression analysis confirmed a statistically significant increase after implementation (incidence rate ratio 1.62, 95% CI 1.19 to 2.21, $p = 0.002$). There was one peri-operative allergic reaction in the baseline period and two during the intervention period.

CONCLUSION: Implementation of a standardized peri-operative allergy and antibiotic assessment tool with obstetrical patients with reported beta-lactam allergy resulted in an increase in peri-operative cefazolin use. Use of this simple tool has the potential to increase efficiencies surrounding peri-operative cefazolin antibiotic administration and reduce surgical site infection rate.

SP26

Antimicrobial susceptibility patterns in urinary tract infection isolates across Canadian hospitals: Results from CANWARD 2009–2019

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OBJECTIVES: Urinary tract infections (UTIs) represent a significant global health concern. This study investigated the in vitro susceptibility patterns of UTI pathogens across Canada from 2009 to 2019.

METHOD: A total of 6,641 UTI isolates were submitted to the CANWARD surveillance study's coordinating laboratory in Winnipeg, Manitoba, from January 2009 to December 2019. The Clinical and Laboratory Standards Institute (CLSI) broth microdilution method was utilized for all agents except fosfomycin (agar dilution). Minimum inhibitory concentrations were interpreted by CLSI M100 breakpoints (31st edition, 2021).

RESULTS: The top five isolated UTI pathogens across the past 10 years were *Escherichia coli* (54.0%), *Klebsiella pneumoniae* (9.8%), *Enterococcus faecalis* (9.2%), *Proteus mirabilis* (4.0%), and *Pseudomonas aeruginosa* (3.3%). The activity of commonly tested agents is presented in Table SP26-1. ESBL rates for *E. coli* and *K. pneumoniae*, respectively, have increased from 3.0% to 14.2% and 3.1% to 21.1%. Methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant enterococci rates have also increased from 35.7% to 50.0% and 3.4% to 5.6%, respectively.

CONCLUSION: Among first-line agents recommended for the treatment of uncomplicated UTI, the majority of *E. coli* isolates collected in 2019 were susceptible to nitrofurantoin and fosfomycin. In 2019, trimethoprim–sulfamethoxazole was susceptible to <70% of *E. coli* and <80% of *K. pneumoniae* isolates. Nitrofurantoin remained highly active (97.1% susceptible) against *E. faecalis* in 2019.

Table SP26-1: Antimicrobial susceptibilities for the three most commonly isolated UTI pathogens from 2009 to 2019

	MIC.(µg/mL) / % Susceptible				
Organism/Year	**AMC**	**CIP**	**FOS**	**NIT**	**SXT**
E. coli/2009	8/94.0	>16/78.5	4/99.4	32/98.5	>8/75.7
E. coli/2019	16/74.7	>16/67.3	4/98.8	32/95.7	>8/68.5
No. of isolates	2509	2389	1927	2270	2388
K. pneumoniae/2009	8/95.3	0.5/85.9	64/NA	128/10.0	>8/87.5
K. pneumoniae/2019	32/82.8	16/81.6	64/NA	128/39.5	>8/78.9
No. of isolates	424	433	179	268	433
Enterococcus spp[1] /2009	1/NA	>16/43.2	128/NA	32/94.1	0.5/NA
E. faecalis/2019	1/NA	>16/76.5	128/NA	16/97.1	0.5/NA
No. of isolates	381	402	160	253	40

AMC = amoxicillin-clavulanate; CIP = ciprofloxacin; FOS = fosfomycin; NIT = nitrofurantoin; SXT = trimethoprim-sulfamethoxazole; NA = not applicable.
[1] *In 2009,* Enterococcus *spp were not speciated*

SP27

Sepsis among critically ill people: An observational study of anatomical site of infection and microbiological diagnosis

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OBJECTIVES: Sepsis affects many patients requiring the intensive care unit (ICU) and imposes a large mortality and cost burden on the health care system. Despite this, we do not fully understand the microbial ecology or prevalence of specific infection sites. Our primary objective is to describe the site of infection and microbiological diagnosis in a cohort of patients admitted to the ICU with sepsis.

METHOD: We performed a secondary analysis of a cohort of adult patients with sepsis admitted to a Canadian general systems ICU. Patients were originally enrolled in a prospective, adaptive time series evaluating antimicrobial stewardship, procalcitonin, and rapid blood culture identification. From this cohort, anatomical site of infection and microbiological diagnosis were ascertained. Sepsis was defined by the third international consensus definition; site of infection was defined

by adapted Centers for Disease Control and Prevention–National Healthcare Safety Network surveillance definitions. A descriptive analysis was performed.

RESULTS: A total of 442 patients were included in this analysis. The median patient age was 60 years (IQR 50–69); 43% were female. Median Sequential Organ Failure Assessment score on ICU admission was 9 (IQR 6–12). Of the cohort, 15% did not have infection as the underlying diagnosis despite meeting sepsis criteria upon ICU admission. For those deemed to have an infection (n = 372), pulmonary infections were most common (55%), followed by intra-abdominal (20%), skin or soft tissue (9%), genitourinary (8%), bloodstream (3%), bone and joint (2%), cardiovascular (2%), and central nervous system (1%) infections. A microbiological diagnosis was found in 74% of patients: 39% polymicrobial, 11% *Escherichia coli,* 10% *Staphylococcus aureus,* 8% respiratory viruses, 4% *Streptococcus pneumoniae,* and 28% other organisms

CONCLUSION: In our cohort, most ICU patients admitted with sepsis had pulmonary infection. Intra-abdominal, skin or soft tissue, and genitourinary infections were also common. Of our patients, 74% had one or more causative organisms identified on microbiological testing, higher than generally found in prior literature.

SP28

Identification of priority areas for emergency department antibiotic stewardship via audit of prescriptions for common childhood infections

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OBJECTIVES: Most antibiotics prescribed to children are provided in the outpatient and emergency department (ED) settings, yet these settings are seldomly engaged with formal antibiotic stewardship programs. We evaluated the duration of antibiotic therapy prescribed for common pediatric infections (acute otitis media [AOM], bacterial pneumonia, and urinary tract infection [UTI]), assessed concordance with Canadian Pediatric Society (CPS) guidelines, and quantified excess antibiotic exposure.

METHOD: Children prescribed antibiotics on discharge from a children's hospital ED between January 1, 2018, and December 31, 2021, with a diagnosis of AOM (in those age ≥2 y), bacterial pneumonia, or UTI were identified via electronic medical record. Antibiotic prescribing for each infection was characterized with descriptive statistics, and antibiotic exposure exceeding the minimum duration suggested by the CPS (eg, >7 d for UTI) were quantified per 1,000 infection-visits. Pareto charts were used to investigate prescriber-level excess antibiotic prescribing.

RESULTS: A total of 10,832 antibiotic visits were identified (AOM, n = 4,883; bacterial pneumonia, n = 3,007; UTI, n = 2,942). Antibiotic prescriptions were frequently longer than the lower limit of the CPS guideline range for bacterial pneumonia (54%) and UTI (44%). Children aged ≥2 years treated for AOM received the recommended 5-day duration only 53% of the time. Evaluation of antibiotic-days prescribed in excess of the CPS recommended minimum duration revealed large potential cumulative reductions in antibiotic exposure per 1,000 infection-visits for AOM (1690 antibiotic-days), pneumonia (1,627 antibiotic-days), and UTI (1,334 antibiotic-days). Excess prescribing for any one of the studied infections did not predict excess prescribing for the other infections studied.

CONCLUSION: This study characterizes the potential impact that duration-focused ED antibiotic stewardship activities may have in reducing population-level antibiotic exposure of children seeking care for common childhood infections. It also identifies priority infections for ED antibiotic stewardship programs to target and highlights provider-level variation in prescribing practices.

SP29

ProbeTools: Hybridization probe design for targeted genomic sequencing of diverse and hypervariable viral taxa

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OBJECTIVES: Sequencing viruses in clinical specimens is hampered by excessive background genomic material from hosts. Hybridization probes are widely used for targeted genomic

enrichment in many fields, but their application to clinical virology has been limited; designing broadly inclusive probe oligos against rapidly evolving and diverse viral taxa is a major obstacle. To address this challenge, we created ProbeTools, a general-purpose bioinformatics package for designing and assessing hybridization probes that target hypervariable genomes. We validated its performance by designing a surveillance panel for avian influenza viruses (AIVs), which are among the most diverse RNA viruses, making them an appropriately challenging test case. AIVs are also a perennial zoonotic threat, so effective probe panels are valuable genomic surveillance tools for outbreak prevention and pandemic preparedness.

METHOD: ProbeTools was used to design a panel of 3,600 hybridization probes targeting the hemagglutinin (HA), neuraminidase (NA), and matrix (M) genome segments. ProbeTools was also used to predict coverage of 36,313 AIV reference sequences *in silico*. Panel performance was further assessed in vitro on a representative collection of 23 egg-cultured AIVs, including examples of all avian-origin HA and NA subtypes isolated from wild birds, poultry, and humans.

RESULTS: *In silico* assessment by ProbeTools showed broad coverage of HA, NA, and M segments (90% of reference sequences had 90.8%, 95.1%, and 99.9% of their bases covered, respectively). This translated to effective capture in vitro on egg-cultured AIVs: 64 of 69 HA, NA, and M segments had more than 96% of their bases enriched. In vitro results were also used to validate ProbeTool's *in silico* coverage assessment algorithm; predictions were 89.2% concordant with results.

CONCLUSION: ProbeTools generated an effective AIV panel that can be deployed for genomic surveillance. Success against hypervariable AIVs demonstrates that the ProbeTools design and prediction algorithms are suitable for targeting other challenging viral taxa of clinical importance.

SP30

Microbiological characteristics of *Actinotignum schaalii*, an emerging cause of urinary tract and skin and soft tissue infections: A retrospective population-based cohort study

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OBJECTIVES: *Actinotignum schaalii* is a small, non-motile, non–spore-forming gram-positive bacilli and an emerging cause of urinary tract and skin and soft tissue infections. It is under-diagnosed because it is difficult to identify using standard culture or phenotypic methods. We conducted a longitudinal study to describe the incidence and microbiological characteristics of *A. schaalii* with the adoption of advanced microbiological diagnostics.

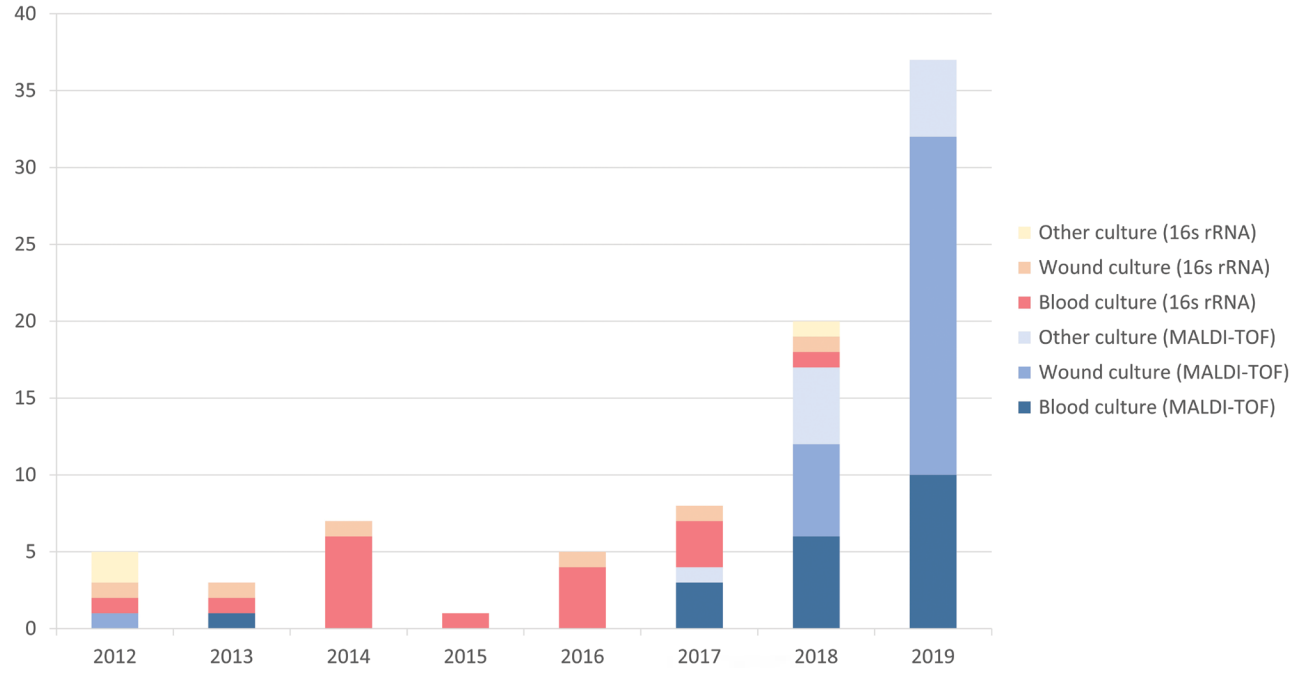

Figure SP30-1: Actinotignum schaalii infections over time by specimens and diagnostic methods

METHOD: All positive cultures from the hospital and ambulatory settings with *A. schaalii* were analyzed over 8 years in a large Canadian health region. Blood cultures were incubated in the BacT/Alert VirtuO instrument (bioMérieux, Marcy-l'Étoile, France), and other specimens were processed using standardized microbiology methods. Definitive identification was performed with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, 16S rRNA gene sequencing, or both. Incidence rate was calculated by dividing positive cultures by the mid-year population annually. Time to definite identification (TTDI) was defined as being from time processed to definite identification.

RESULTS: A total of 86 unique *A. schaalii* cultures were identified; 37 (43.0%) were from blood; 35 (40.7%), from deep wound and abscess; and 6 (7.0%), from urine cultures. *Of the total,* 34 (30.2%) isolates were polymicrobial and were largely from deep wound specimens (26/34; 76.5 %). The median TTDI was 242.9 hours (IQR 124.7–285.5) during the first year of the study period and significantly decreased to 65.6 hours (IQR 43.4–83.1) for the last year. The overall period incidence rate was 5.68 (95% CI 4.57 to 6.98) per 1,000,000 person-years and statistically significantly increased from 2.94 (95% CI 1.08 to 6.53) for the first year to 18.45 (95% CI 13.12 to 25.16) per 1,000,000 person-years for the last year.

CONCLUSION: We identified an increased incidence rate and faster TTDI over time possibly attributable to improved diagnostics. *A. schaalii* infections may still remain underdiagnosed due to variability in detection based on infection site, particularly in laboratories without advanced identification methods. Given the potential pathogenicity, *A. schaali* must be considered and assessed on the basis of the clinical context.

SP31

Economic burden of malaria in a centralized laboratory system from 2013 to 2017: Making a case for publicly funded pre-travel clinics

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OBJECTIVES: Malaria remains a leading cause of morbidity and mortality globally. Although Canada has a low malaria incidence, there has been a steady rise in cases since 2000. Few studies have ascertained the economic burden associated with malaria, particularly in the context of a high-income country. This study aims to describe the health care utilization and health system costs for those diagnosed with malaria within a large Canadian urban center.

METHOD: We used a prior case–control study of symptomatic individuals who tested for malaria between 2013 and 2017. Patients were linked to physician claims and inpatient (DAD) and outpatient (NACRS) databases using unique identifiers. We identified patients diagnosed with malaria using relevant codes from the *International Classification of Diseases,* 9th and 10th revisions. Physician-related costs were identified using physician billing data, inpatient malaria-related costs were estimated using a case mix costing approach, and outpatient cost estimates were derived from Comprehensive Ambulatory Care Classification System. Average malaria-related costs are described using 2021 Canadian dollars.

RESULTS: A total of 5,436 unique patients were tested for malaria over the study period, and 673 positive malaria cases were diagnosed overall. Overall malaria-related utilization consisted of 100 inpatient visits and 525 outpatient visits. On average, 135 malaria patients were diagnosed annually between 2013 and 2017 (range 124–139 per year). The total malaria-related health system cost over the study period was C$1.9 million, with an average cost of C$373,498 per year, driven predominantly by inpatient stays.

Table SP31-1: Malaria-related costs by year: mean costs in 2021 Canadian Dollars, (N)* represents the number of patients seen

Year	MEDDS (Claims) Mean per person per year	Inpatient (DAD) mean per person per year	Outpatient (NACRS) mean per person per year
2013	$230.17 (76)	$14420.95 (17)	$609.11 (111)
2014	$325.51(64)	$12415.93 (17)	$573.17 (107)
2015	$435.29 (78)	$14008.70 (24)	$732.56 (97)
2016	$348.44 (91)	$14630.28 (18)	$778.76 (106)
2017	$294.98 (78)	$13547.29 (24)	$740.72 (104)

CONCLUSION: High health care costs are associated with the diagnosis and management of malaria and are largely driven by inpatient stays, which may reflect more severe disease states. Because pretravel clinics are not currently publicly funded, this may be an important public health intervention to reduce future hospitalizations and the high economic burden associated with malaria on the public health care system.

SP32

Use of revised Clinical and Laboratory Standards Institute cefazolin breakpoints for urinary samples at a regional reference laboratory

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OBJECTIVES: Published Clinical and Laboratory Standards Institute breakpoints for certain antibiotics may be used in the context of uncomplicated urinary tract infections (uUTIs). These breakpoints are higher than for other infections; therefore, an antibiotic could be considered susceptible for uUTIs even if they are resistant for complicated UTIs (cUTIs). We assessed urine cultures (UCs) for differences in cefazolin susceptibility using uUTI breakpoints versus systemic breakpoints for Enterobacteriaceae. We also aimed to assess the potential clinical impact of these differences.

METHOD: We retrospectively reviewed the antimicrobial susceptibility profiles of previously collected UCs growing *Escherichia coli* (EC), *Klebsiella pneumoniae* (KP), or *Proteus mirabilis* (PM) from a tertiary care hospital. Susceptibilities of isolates from July 1, 2020, to Dec 13, 2021, were compared using uUTI and systemic breakpoints for cefazolin. Fifty patients from July 2019 were categorized as having uUTI, cUTI, or other or asymptomatic bacteriuria by chart review and had cefazolin susceptibility compared as above.

RESULTS: From July 1, 2020, to December 13, 2021, 5,041 and 1,259 urine cultures that grew EC and KP, respectively. A total of 71% (n = 3,567) of EC and 77% (n = 973) of KP isolates were cefazolin susceptible when using systemic breakpoints. Both percentages increased to 85% (EC, n = 4288; KP, n = 1,072) when using uUTI breakpoints. From the July 2019 subset, 66% (33/50) of UCs were from cUTIs, and only 8% (4/50) were from uUTIs. Among the isolates from uUTIs, 75% (3/4) were susceptible when using systemic breakpoints, and 100% were susceptible when using uUTI breakpoints. Among the cUTI isolates, 50% (18/36) were susceptible when using systemic breakpoints and 78% (28/36) when using uUTI breakpoints.

CONCLUSION: Use of uUTI-specific breakpoints resulted in more susceptible isolates of EC, KP, and PM, potentially allowing for treatment with narrower-spectrum antibiotics. However, laboratories must balance this benefit with the potential risks of using uUTI breakpoints if the majority of patients have cUTIs.

SP33

Detection of SARS-CoV-2 from combined nasal–rectal swabs

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OBJECTIVES: This study evaluated the utility of combined nasal–rectal (N–R) swab specimens used to screen new admissions for methicillin-resistant *Staphylococcus aureus* (MRSA) to simultaneously test for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

METHOD: This study was conducted at two acute-care hospitals between March 2020 and February 2021, the period in which the original Wuhan strain was predominantly circulating. An ESwab™ kit (COPAN, Murrieta, California) containing two flocked swabs with liquid amies medium is used to screen for MRSA. One swab is used to circle inside and around the nares, and the second swab is used to sample the sides of the rectum and perianal area. In total, 180 N–R swabs were screened for SARS-CoV-2 by reverse transcriptase polymerase chain reaction; 80 were from inpatients with no clinical suspicion of coronavirus disease 2019 (COVID-19), and 100 were from inpatients with lab confirmed COVID-19 (detection of SARS-CoV-2 from a nasopharyngeal specimen). Retrospective chart reviews were conducted on lab-confirmed COVID-19 study inpatients.

RESULTS: SARS-CoV-2 was not detected in any N–R swabs collected from inpatients with no clinical suspicion of COVID-19. SARS-CoV-2 was detected in 39% of N–R swabs from lab-confirmed COVID-19 study inpatients. The most frequently reported symptoms in lab-confirmed COVID-19 study inpatients were fever (69.3%), dyspnea (61.3%), and cough (58.7%). A minority of lab-confirmed COVID-19 study inpatients reported gastrointestinal symptoms such as nausea (17.3%), diarrhea (14.7%), and vomiting (13.3%). No association between severity of illness and the detection of SARS-CoV-2 in N–R swabs was observed.

CONCLUSION: Combined N–R swabs can be used to detect SARS-CoV-2; however, N–R swab specimens performed

poorly compared with nasopharyngeal swab specimens. Despite low sensitivity, N–R swabs may be useful in certain circumstances (such as if nasopharyngeal swab supply is limited), but they are insufficient as the sole specimen for the diagnosis of SARS-CoV-2.

SP34

Post–COVID-19 syndrome: A prospective cohort study

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OBJECTIVES: A Canadian provincial registry was created in 2019 to track the clinical features, treatment response, and post-infection outcomes of infected patients. An integrative classification for post–coronavirus disease 2019 (COVID-19) symptoms has been proposed in present literature, but this has yet to be validated. We report prospectively collected multi-centre data to describe the long-term post-infection symptoms that constitute the post–COVID-19 syndrome and determine baseline patient characteristics that predict development of this syndrome.

METHOD: In collaboration with public health, patients were contacted, enrolled, and verbally consented over phone from March 12, 2020, to August 14, 2021. Baseline patient characteristics and follow-up on symptoms post-recovery were obtained. Univariate analysis was performed, using sign test for continuous variables and χ^2 test or Fisher exact test for categorical variables. The odds of developing post–COVID-19 syndrome were calculated using simple and multivariable logistic regression models with a stepwise method using likelihood ratio testing.

RESULTS: A total of 277 patients were included in this study, with 115 (41.5%) experiencing post–COVID-19 symptoms. Patients with post–COVID-19 symptoms tended to be female, White, and obese; to have more affluent housing and rheumatological comorbidities; to snore; to experience symptoms during infection; or to be admitted to the hospital. Fatigue, dyspnea, and anosmia were the most common post–COVID-19 symptoms reported. Dyspnea (adjusted OR 2.50, 95% CI 1.04 to 6.09) and anosmia (adjusted OR 3.12, 95% CI 1.40 to 7.13) during infection were independent predictors for the development of any post–COVID-19 symptoms around weeks 11–12 post-recovery.

CONCLUSION: Our results showed that symptoms of dyspnea and anosmia experienced during infection were significant independent predictors for the development of any post–COVID-19 symptoms. Our work provides additional insight on the relationship between patient baseline characteristics and post–COVID-19 symptoms and will help with the development and validation of a universally recognized and robust classification for post–COVID-19 syndrome.

SP35

Bacteroides fragilis group antibiotic susceptibility testing and reporting and impact on prescribed therapy

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OBJECTIVES: Susceptibility testing on anaerobic isolates, including the *Bacteroides fragilis* group, is not routinely performed on non-blood specimens in our laboratory. Our study aim was to understand rates of resistance among *B. fragilis* group isolates through retrospective susceptibility testing and to compare resistance patterns and empiric antibiotic selection with patient outcomes with the objective of determining whether routine anaerobic susceptibility testing is needed.

METHOD: We performed retrospective testing of 141 isolates for susceptibility to piperacillin–tazobactam, metronidazole, meropenem, and clindamycin and created a summary of antimicrobial susceptibility compared with previous antibiogram data. A detailed chart review was performed, comparing empiric antibiotic selection data with susceptibility patterns and clinical outcomes for each patient, to determine whether the lack of upfront susceptibility data affected patients.

RESULTS: Our percentage susceptibility to piperacillin–tazobactam was 93%, higher than the 87% previously reported in our local antibiogram. Isolates had 100% susceptibility to metronidazole. Empiric antibiotic selection was appropriate in

82.4% of cases. Of initial antibiotic regimens, 3.8% were affected by resistance. Only one patient in our study decompensated as a result of treatment with a non-susceptible antibiotic and may have benefited from upfront susceptibility data. There were nine cases of discordant antibiotic use (no anaerobic coverage, resistance, or no antibiotics). Of these, one patient improved despite resistant *B. fragilis* group, and five achieved surgical cure. The remaining three patients on discordant antibiotic therapy were not cured; however, none of these patient outcomes would have been influenced by prospective susceptibility data.

CONCLUSION: Given our study analysis, it remains reasonable laboratory practice to not perform routine susceptibility testing and reporting for anaerobes in non-blood cultures. Instead, providers should be counselled to add anaerobic coverage to antibiotic regimens in which anaerobes, particularly the *B. fragilis* group, are cultured and to request further microbiology testing from the laboratory.

SP36

Two bugs for the price of one: Detection of co-infection of Lyme disease patients with *Anaplasma phagocytophilum* in Nova Scotia using PCR testing on serum rather than whole blood samples

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OBJECTIVES: *Anaplasma phagocytophilium* is an emerging pathogen in Canada that is primarily transmitted by blacklegged ticks (*Ixodes scapularis*) in central and eastern Canada. In Nova Scotia, the agent of Lyme disease, *Borrelia burgdorferi,* is the most commonly observed pathogen in blacklegged ticks, and the prevalence of *A. phagocytophilum* has been relatively low (<5%). However, a recent increase in the number of anaplasmosis cases in Nova Scotia may suggest that this pathogen is more common than previously identified. Using residual sera from *B. burgdorferi* sero-positive specimens collected in 2021, we sought to determine the frequency of co-infection with *A. phagocytophilum*. We also assessed the suitability of serum as a diagnostic specimen for the detection of *A. phagocytophilum*.

METHOD: Sera (N = 500) were shipped to the National Microbiology Laboratory where DNA was extracted using Qiagen DNeasy® (Qiagen, Germantown, Maryland) extraction kits. Extracted DNA was tested for *A. phagocytophilum* using a real-time polymerase chain reaction (PCR) assay targeting the *msp2* gene. Samples that produced a cycle threshold (Ct) value of <40 were considered presumptively positive and underwent a second DNA extraction and testing with the *msp2* assay. If both extracts produced Ct values <40, samples were reported as positive for *A. phagocytophilum*. The strain of *A. phagocytophilum* present in the positive samples was determined using an in-house single nucleotide polymorphism assay.

RESULTS: In total, 11 samples (2.2%) had detectable *A. phagocytophilum* by PCR with Ct values ranging from 26.9 to 38.9. All positive samples were determined to contain the pathogenic strain (Ap-ha).

CONCLUSION: This study demonstrates that co-infection with *A. phagocytophilum* occurs in a small proportion of Lyme disease cases in Nova Scotia and that in the absence of whole blood, residual serum may be used to detect *A. phagocytophilum*. Development of a tick-borne disease panel to detect common tick-borne pathogens in Nova Scotia may be warranted.

SP37

Clinical characteristics associated with laboratory-confirmed influenza

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OBJECTIVES: To examine the symptoms of patients with laboratory-confirmed viral respiratory infection in an effort to investigate clinical features associated with influenza infection.

METHOD: A total of 141 midturbinate swabs and 162 nasopharyngeal swabs associated with a respiratory viral infection, as confirmed via multiplex reverse transcriptase polymerase chain reaction, were collected at two acute-care facilities located in Toronto, Ontario, Canada, between

November 2019 and April 2020. Clinical specimens were collected from 227 inpatients and 76 outpatients. Logistic regression models were constructed to examine associations between patient symptoms and influenza infection.

RESULTS: The prevalence of influenza infection was 31% (93/303). Respiratory viruses identified were influenza A (n = 74), influenza B (n = 19), respiratory syncytial virus (n = 69), human metapneumovirus (n = 24), parainfluenza virus (n = 30), enterovirus–rhinovirus (n = 60), adenovirus (n = 4), severe acute respiratory syndrome coronavirus 2 (n = 19), and seasonal coronavirus (n = 12). The median age of the study cohort was 76 years (interquartile range [IQR] 56–88) years; 170 (56%) patients were female, and the median Charlson Comorbidity Index score was 2 (IQR 1– 4). Among the hospitalized patients, 18% (40/227) were admitted to the intensive care unit, and 11% (24/227) died. Fever, cough, and myalgia were determined to be significantly positively associated with influenza infection as compared with patients without influenza infection via multivariable analysis.

CONCLUSION: These findings suggest that certain clinical characteristics can aid in the identification of influenza virus infection. Although clinical characteristics alone cannot be used to confirm or exclude the diagnosis of influenza, these findings support their use in patient management decisions and allocation of diagnostic resources.

SP38

Prospective audit and feedback of piperacillin–tazobactam prescriptions in two acute-care hospitals: Is there a role for intravenous amoxicillin–clavulanate?

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OBJECTIVES: Prospective audit and feedback (PAF) has been shown to decrease antimicrobial exposure and costs and improve patient outcomes. We evaluated inpatient piperacillin–tazobactam prescriptions for concordance with guidelines, cost avoidance associated with prescription optimization, and characterized the role of intravenous (IV) amoxicillin–clavulanate as a cost-neutral alternative to reduce antibiotic selective pressure on *Pseudomonas aeruginosa*.

METHOD: PAF was performed on 118 adult patients receiving piperacillin–tazobactam for more than 24 hours in two acute-care hospitals from May 17 to June 4, 2021, in Edmonton, Alberta. If a regimen was determined to be non-concordant with local guidelines, a recommendation was communicated to the attending team to optimize therapy. Cost avoidance was calculated by subtracting the cost of the new regimen from the cost of the original regimen.

RESULTS: Piperacillin–tazobactam prescriptions were considered non-concordant in 55% of cases, according to local guidelines. The most common indication for piperacillin–tazobactam use was respiratory infections (36%), followed by intra-abdominal infection (24%). IV amoxicillin–clavulanate was an appropriate alternative in only 6% (7/118) of piperacillin–tazobactam prescriptions, most commonly for intra-abdominal infections (86%). Ceftriaxone with or without metronidazole was the preferred antimicrobial regimen in 43% of the 65 non-concordant piperacillin–tazobactam prescriptions. Of the 30 antimicrobial stewardship recommendations made, 80% were accepted, resulting in an actual cost avoidance of $904. The total cost avoidance, had all recommendations been accepted over the 3-week period, was C$1,117, which extrapolates to C$19,362 annually.

CONCLUSION: Piperacillin–tazobactam was suboptimally prescribed in approximately half of the assessed prescriptions in which ceftriaxone with or without metronidazole was the preferred regimen. Targeted PAF resulted in the prescription of more narrow-spectrum agents with associated drug cost avoidance. IV amoxicillin–clavulanate was appropriate in only a small proportion of piperacillin–tazobactam prescriptions on the basis of local guidelines. Further investigation is required to clarify and expand its role.

SP39

Retrospective review of urine culture colony count cut-offs and urinary tract infection diagnosis at a tertiary academic hospital network

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OBJECTIVES: Urinary tract infections (UTIs) account for up to 40% of hospital-associated infections and have significant morbidity, mortality, and associated health care costs. Definitive identification (ID) and antimicrobial susceptibility testing (AST) is triggered at our centre for organisms at concentrations of $\geq 10^4$ colony-forming units per milliliter (CFU/mL). The proportion of these specimens that reflect asymptomatic bacteriuria versus true UTI remains unclear. The primary objective of this study was to assess the utility of a concentration cut-off of $\geq 10^5$ CFU/mL compared with $\geq 10^4$ CFU/mL for identification of true UTIs.

METHOD: Inclusion criteria involved patients aged ≥18 years, culture concentration of $\geq 10^4$ CFU/mL, and inpatients. Samples were excluded if more than two uropathogens were identified, charts were incomplete, and they were collected via cystoscopy. Microbiological investigation was completed using the WASPLab™ system (COPAN Diagnostics, Murrieta, California) and chromogenic media (Orientation Agar, BD, Franklin Lakes, New Jersey). Chart review extracted patient demographics, primary hospital diagnosis, urinalysis, urine culture results, and receipt of antibiotics. Yates-corrected χ^2 tests were used to compare the proportion of patients with UTIs using both cut-offs.

RESULTS: A total of 184 samples were identified for the 10^4–10^5 CFU/mL group and 49 for the $\geq 10^5$ CFU/mL group. The sample population was composed of 110 men and 123 women. Fifty-six patients were catheterized, and 128 were not. Ages ranged from 21 to 103 years. Patients with colony counts of $\geq 10^5$ CFU/mL were found to be 2.34 times more likely to have a clinically significant UTI than patients with colony counts of 10^4–10^5 CFU/mL (OR 2.34, $p = 0.0204$).

CONCLUSION: Adjusting the concentration cut-off for ID and AST to $\geq 10^5$ CFU/mL would reduce the treatment of clinically insignificant UTIs and the financial burden from unnecessary treatment and microbiological work-up. Future goals target adjusting the current protocols at our centre to complete full ID and AST for concentrations of $\geq 10^5$ CFU/mL and monitoring the clinical impact of this change.

SP40

Evaluation of the trends in antibiotic prescribing at a tertiary pediatric hospital in Calgary during pre– and peri–COVID-19 pandemic times

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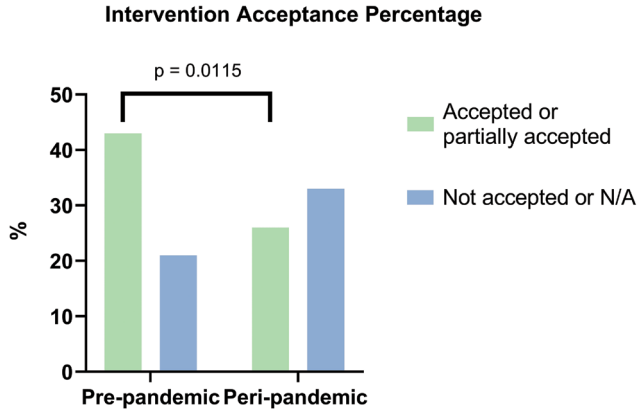

Figure SP40-1: Intervention acceptance results pre- and post-pandemic

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OBJECTIVES: Antibiotic stewardship is imperative in combating the ever-growing threat of antibiotic resistance. We evaluated the impact of the coronavirus disease 2019 (COVID-19) pandemic on antibiotic prescribing at a tertiary-care pediatric hospital. We conducted antimicrobial stewardship prospective audit and feedback (PAF) to evaluate changes in the timing and number of interventions and acceptance of interventions pre- and peri-pandemic and to describe notable trends in prescribing.

METHOD: PAF was performed on inpatient charts from November 23 to December 15, 2021. The number of reviews, type of interventions, timing for review and interventions, and outcomes were recorded. Interventions included virtual handshake stewardship and multidisciplinary notes with therapy guidance. Pre-pandemic data (3-wk blocks in 2017–2019) were compared against peri-pandemic data (2020–2021). Statistical analysis was done using Mann–Whitney and Fisher exact tests.

RESULTS: A total of 1,957 antimicrobial starts were reviewed, with PAF conducted for 746 charts, 313 3-day follow-ups, and 65 PAF interventions. There was no significant difference in the number of median daily chart reviews comparing pre-pandemic versus peri-pandemic: number of 3-day reviews (21.5 versus 13.0, $p = 0.0168$), total follow-ups (9.50 versus 13.0, $p = 0.0757$), and number of interventions (2.00 versus 3.00, $p = 0.0741$). The majority of interventions included narrowing of drugs and advising a stop date. Overall, 44.1% of interventions were accepted or partially accepted peri-pandemic compared with 67.3% pre-pandemic ($p = 0.0115$). Specific trends noted included the inappropriate use (ie,

prolonged duration) of pre- and post-operative prophylaxis in surgical patients.

CONCLUSION: As a result of the COVID-19 pandemic, communication between health care providers has shifted toward a virtual platform. Although this may help reduce potential exposures to COVID-19, it has eliminated the face-to-face interactions integral in handshake stewardship. This is important in fostering a collaborative and constructive relationship with prescribing physicians. Antibiotic stewardship during the pandemic requires adaption of current methods to develop longitudinal relationships, raise greater awareness, and support ongoing PAF interventions.

SP41

COVID-19 outbreak on an inpatient medical unit associated with geriatric chairs: Whole-genome sequence outbreak investigation

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OBJECTIVES: As severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has spread around the world, hospital outbreaks have been common and devastating. Understanding how SARS-CoV-2 is transmitted in these environments is critical to develop effective strategies to mitigate future outbreaks.

METHOD: To this end, we analyzed a hospital inpatient medical unit outbreak in Toronto, Ontario, Canada (November 22, 2020– January 4, 2021) through epidemiological mapping and whole-genome sequencing phylogeny. A maximum likelihood tree was inferred with IQ tree and bootstrap analyses performed for statistical support to study the relatedness of the outbreak cases and other contemporary cases.

RESULTS: The outbreak involved 8 patients and 10 staff resulting in 3 patient deaths. Phylogenetic trees showed that 14 of 15 outbreak-associated samples sequenced formed one clade with 0–1 single nucleotide polymorphisms (SNPs) and one staff sample was unrelated, with 18 SNPs difference compared with the outbreak clade. By analyzing the outbreak through both traditional outbreak investigation and whole-genome sequencing, we were able to show that patients in geriatric chairs at the nursing station were at high risk for both acquiring and transmitting coronavirus disease 2019 (COVID-19) to other patients and staff.

CONCLUSION: Because of the informal nature of certain interactions, such as having patients in geriatric chairs, transmission events related to these interactions can be missed as high-risk exposures during outbreak management. During times of high community incidence of COVID-19, strategies to support patients in their room, rather than at the nursing station, should be prioritized.

SP42

Development and evaluation of real-time PCR assay for the molecular detection of *Theileria* species

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OBJECTIVES: *Theileria annulatais* is a tick-borne hemoprotozoan parasite responsible for tropical theileriosis in bovine populations and substantial economic loss in the livestock sector. This study was performed to develop a real-time polymerase chain reaction (PCR) detection method and characterize phylogenetic profiles of *T. annulata* infection found in small ruminants from Khyber Pakhtunkhwa, Pakistan.

METHOD: DNA from ticks was extracted using the chloroform-phenol method at Quaid-i-Azam University, Islamabad, Pakistan. The real-time quantitative PCR (qPCR) primers and probes were designed to detect *Theileria* species to target the 18S rRNA gene. The qPCR assay was performed on an Applied Biosystems™ 7500 Fast Real-Time PCR System using the TaqMan™ Fast Advanced Master Mix (ThermoFisher Scientific, Waltham, Massachusetts). Synthetic gBlocks™ Gene Fragments (Integrated DNA Technologies, Coralville, Iowa) and clinical specimens were used for analytical and clinical validation to test specificity, sensitivity, PCR efficiency, precision, ruggedness, and accuracy. Ten-fold dilutions of gBlocks representing the 18S rRNA gene from different *Theileria* species were used for analytical validation, and DNA extracts from ticks were used for clinical validation. Positive *T. annulata samples* were confirmed using 18S rRNA Sanger sequencing on an Applied Biosystems™ 3130xl Genetic Analyzer using BigDye® terminator chemistry (ThermoFisher).

RESULTS: The PCR was properly designed and optimised with PCR efficiency between 91.7% and 97.48%. The reportable range of the assay is 10E1 to 10E9. The R^2 values are between 0.9825 and 0.9985, indicating a great linearity throughout the reportable range. The detection limit for *Theileria* species is between 10 and 100 copies per reaction. All the PCR positives were confirmed through sequencing, and results are 100% matched.

CONCLUSION: This newly developed qPCR assay is a reliable method for detecting *T. annulata* from clinical samples. It is also a great tool for epidemiological screening. Phylogenetic and sequence analysis data showed that *T. annulata* 18S rRNA isolates from Pakistan shared homology and phylogeny close to that of other isolates from Asia and Europe.

SP43

A commensal bacteria-derived protein protects mice from *Clostridioides difficile* disease *in vivo*

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OBJECTIVES: *Clostridioides difficile* (CD) infection (CDI) is mediated by toxin A (TcdA) and toxin B (TcdB) and has a recurrence rate of 25%. Preliminary findings from our lab show that a protein derived from gastrointestinal commensal bacteria is able to neutralize CD toxins *in vitro*. The objective of this work is to test the efficacy of our novel therapeutic, called SHU-1, in preventing disease in an established murine CDI model.

METHOD: To test the *in vivo* efficacy of SHU-1, 7-week-old C57/BL6 female mice were given a cocktail of antibiotics (colistin, gentamicin, kanamycin, metronidazole, vancomycin) followed by SHU-1 (400 ug; SHU-1 mice) or saline (CD or control mice) by oral gavage. SHU-1 and CD mice were then infected with CD (3.5×10^9 vegetative cells) and gavaged SHU-1 or saline every 24 hours for 3 days post-infection. Mice were weighed, and stool was collected daily. Cell rounding assays (NIH 3T3 fibroblasts) were performed on stool samples to measure toxin activity. Mice were euthanized at their humane endpoint or 72 hours post-CDI, and colons were stained with H&E to assess cellular infiltration and tissue damage.

RESULTS: CDI led to significant weight loss in both SHU-1 and CD mice in the first 48 hours ($p = 0.014$ and $p = 0.042$, respectively), which was not seen in control mice. Unlike SHU-1 mice, CD mice were sacrificed at 48 hours post-infection due to severe disease. SHU-1 mice experienced weight gain back to baseline weights between 48 and 72 hours. CD toxin activity was significantly higher in CD mice than in SHU-1 mice (39.9 versus 15.8%, $p < 0.001$), and H&E staining revealed no immune cell infiltration or colonic architectural destruction in SHU-1 mice, which was seen in CD mice.

CONCLUSION: These preliminary findings suggest that SHU-1 harbours anti-toxin activity *in vivo* and is a promising candidate for the treatment of CDI.

SP44

Evaluating swish and gargle saliva sampling compared with nasopharyngeal swabs to detect SARS-CoV-2 by PCR

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OBJECTIVES: We evaluated the use of saliva (swish and gargle; SG) for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) polymerase chain reaction (PCR) detection in outpatient settings because it could increase accessibility and uptake and minimize discomfort.

METHOD: We recruited outpatients who were tested for SARS-CoV-2 because of either symptoms compatible with or exposure to coronavirus disease 2019 cases. We collected paired nasopharyngeal swabs (NPSs) and saliva obtained by SG of normal saline (5 mL) during the same visit. Specimens were tested in parallel using real-time reverse transcription PCR. We performed SARS-CoV-2 variant of concern (VOC) testing on positive specimens. Participants completed a satisfaction survey for these two collection methods.

RESULTS: A total of 237 patients were included (154 adults, 83 children), of whom 32 patients tested positive for SARS-CoV-2 with both NPS and SG samples. Eight patients had discrepant NPS and SG results; 2 tested positive only with NPS and 6 only with SG. When NPS was used as the reference standard, the SG sensitivity and specificity were 94.1% (95% CI 80.3% to 99.3%) and 97.0% (95% CI; 93.7% to 98.9%), respectively.

When using SARS-CoV-2 infection as a reference, defined as NPS or SG positive, the sensitivity for SG was 95.0% (95% CI 80.1% to 99.4%); for NPS, it was 85.0% (95% CI 70.2% to 94.3%). The Cohen's κ agreement between SG and NPS was 0.87 (95% CI 0.78 to 0.96), indicating an almost perfect level of agreement. VOC results were available for 26 NPS—24 as Alpha (B.1.1.7), 1 as Gamma (P.1), and 1 as wild type. Our satisfaction survey showed that SG was an easy and quick method described as comfortable or very comfortable by 89.2% of the participants.

CONCLUSION: Saliva SG is statistically comparable with standard NPS to detect SARS-CoV-2 infection. Patient acceptability was higher for SG. Saliva SG should be considered as an equivalent alternative to NPS for SARS-CoV-2 detection in outpatients, especially when NPS are difficult to collect or in scarce supply.

SP45

Monitoring blood culture fill volumes in acute-care hospitals through audit and feedback

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OBJECTIVES: The most essential factor affecting the sensitivity of blood culture is an adequate volume of blood collected, between 8 and 10 mL per bottle in adults. An audit of blood culture volumes and practices, followed by education of and feedback to those who perform collection, was performed with the goal of achieving adequate volumes.

METHOD: Blood culture bottles were manually weighed for 2 weeks to validate the automated measurement of blood culture volume by BD BACTEC Epicenter module (BD, Franklin Lakes, New Jersey). Average volumes were generated across 19 months from two acute-care hospitals. A single-centre intervention was directed at phlebotomists, whereby an education session was provided that included instructions to make an end-volume mark as a visual cue to collect adequate volumes. Audit and feedback of bottle marking and volumes were then provided to collectors at regular intervals to monitor their performance over time.

RESULTS: Validation demonstrated comparability of automated (Epicenter) and manual (weighted) volumes, with means of 6.70 and 6.78, respectively. Pre-intervention mean blood culture volumes were 6.8 mL (SD 3.9) and 6.1 mL (SD 3.8) for all wards at two hospitals. In the phlebotomist-targeted intervention, the practice of bottle marking increased to a peak of 54% at 2 months post-intervention but declined in months 3 and 4 (ranging from 17% to 33%). This corresponded to increased mean blood culture volumes from 5.4 mL and 6.2 mL in the 2 pre-intervention months to 7.3 mL and 8.4 mL in the 2 months after the intervention, which declined to 6.3 mL and 6.8 mL at 3 and 4 months.

CONCLUSION: Our interventions of education, bottle marking, audit, and feedback in a phlebotomist-targeted pilot demonstrated short-term improvement in fill volumes at one site. These strategies along with many others will be needed to bring about sustainable clinical practice change (Khare et al. CID 2020).

SP46

Use of culturomics to characterize the gut microbiota of neonates in the NICU

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OBJECTIVES: The developing gut microbiota of neonates play an important role in long- and short-term health. Metagenomics is commonly used to characterize the gut microbiota; however, "culturomics," the use of specialized media in conjunction with metagenomics, has the potential to provide further insight into the isolation and identification of bacterial populations in the gut microbiota. This study aims to better characterize the gut microbiota of neonates in the neonatal intensive care unit (NICU) through high-throughput culturing methods.

METHOD: Using a culturomics approach, we isolated bacterial species from the stool of both low-birth-weight (LBW) and normal-birth-weight (NBW) neonates ($n = 6$) in the NICU who were unexposed to probiotics or antibiotics. Stool was cultured either immediately on eight different selective and differential media or preincubated in blood culture bottles with or without sheep blood and rumen fluid supplementation before culturing on agar. Isolates were

identified using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, 16S Sanger sequencing (V3–V4 hypervariable regions), or both.

RESULTS: Eighteen species of bacteria were isolated from neonatal stool, including those commonly isolated from the neonatal gut, coagulase-negative *Staphylococcus, Streptococcus*, and several members of the family Enterobacteriales. In addition, *Clostridium tertium, Clostridium aldenensis, Bacteroides vulgatus, Veillonella rogosae, Ralstonia solanacearum, and Pseudocitrobacter* spp were isolated. *Clostridium* spp, *Bacteroides* spp, and *Enterobacter* spp were recovered from the NBW group ($n = 3$) but not from the LBW group ($n = 3$). Enrichment allowed for the isolation of 10 bacterial species not identified in the unenriched conditions including *C. tertium, V. rogosae, R. solanacaerum,* and *Pseudocitrobacter.*

CONCLUSION: More than half of the bacterial species identified from neonatal stool were recovered only after pre-incubation in blood culture bottles. These studies will increase our understanding of the membership of the neonatal gut microbiota and provide insight into the role of fastidious bacteria not previously defined as playing a role in the neonatal gut microbiota and neonatal health.

SP47

Increased detection of *Lactobacillus* in urine specimens processed by the WASP versus traditional incubation

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OBJECTIVES: *Lactobacillus* is a common bacterial colonizer of the female genital tract, particularly in pre-menopausal women. It is generally considered to be a non-infectious bystander organism when identified in urine cultures, though can occasionally cause clinical infection in immunocompromised individuals. We noticed a significant increase in the detection of *Lactobacillus* spp that corresponded with the introduction of CHROMagar™ (CA; DRG International, Springfield, New Jersey) and WASP™ (COPAN Diagnostics, Murrieta, California) in our laboratory and compared it with urine specimens processed using traditional incubation techniques.

METHOD: Urine cultures were processed in the WASP using an 18-hour 37°C incubation on CA. Those identified as growing *Lactobacillus* spp were re-cultured on the WASP as above on both CA and blood agar (BA) and incubated for 18 and 48 hours in conventional incubators at 35°C in ambient air. Only those cultures growing *Lactobacillus* spp with or without normal urogenital flora (NUF) were included. Cultures with growth of common urinary tract pathogens were excluded from analysis. All isolates were identified using the VITEK MS.

RESULTS: Thirty-three specimens growing *Lactobacillus with or without* NUF were identified. On repeat culture, 32/33 specimens incubated on CA in the WASP re-grew *Lactobacillus* in 18 hours, and 13/33 re-grew it when a BA plate was incubated in the WASP. Using conventional incubators, 8/33 and 32/33 specimens grew *Lactobacillus* on CA when incubated at 18 and 48 hours, respectively, whereas, only 2/33 and 20/33 grew *Lactobacillus* on BA at 18 and 48 hours, respectively.

CONCLUSION: Urine cultures processed by the WASP system demonstrate an increased incidence of *Lactobacillus* growth. Although CA appears to better support their growth than BA, the optimal incubation conditions found in the WASP allow these organisms to readily grow in 18 hours compared with conventional incubation. New users of WASP systems should be aware of this phenomenon.

SP48

Different drugs, different sides: Injection use of opioids alone, and not stimulants alone, predisposes to right-sided endocarditis

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OBJECTIVES: Many studies suggest that infective endocarditis (IE) in people who inject drugs is predominantly right sided, whereas other studies suggest left-sided disease; few have differentiated by class of drug used. We hypothesized that on the basis of differing physiological mechanisms, opioids but not stimulants would be associated with right-sided IE.

METHOD: A retrospective case series of 290 adult (aged ≥18 y) patients with self-reported recent injection drug use, admitted for a first episode of IE to one of three hospitals

in London, Ontario, between April 2007 and March 2018, stratified patients by drug class used (opioid, stimulant, or both) and by site of endocarditis. Other outcomes captured included demographics, causative organisms, cardiac and non-cardiac complications, referral to addiction services, medical versus surgical management, and survival.

RESULTS: Of those who injected only opioids, 47/71 (69%) developed right-sided IE, 17/71 (25%) developed left-sided IE, and 4/71 (6%) had bilateral IE. Of those who injected only stimulants, 11/24 (46%) developed right-sided IE, 11/24 (46%) developed left-sided IE, and 2/24 (8%) had bilateral IE. Relative to opioid-only users, stimulant-only users were 1.75 time (95% CI 1.05 to 2.93; $p = .031$) more likely to have a left-sided or bilateral IE versus a right-sided IE.

CONCLUSION: Although injection use of opioids is associated with a strong predisposition to right-sided IE, stimulants differ in producing a balanced ratio of right- and left-sided disease. As the epidemic of crystal methamphetamine injection continues unabated, the rate of left-sided disease, with its attendant higher morbidity and mortality, may also grow.

SP49

A mandatory declination form program for influenza vaccination was highly effective in increasing vaccination rates during the COVID-19 pandemic

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OBJECTIVES: To examine the effectiveness of a mandatory influenza immunization declination form as a method to improve influenza vaccination rates among health care workers.

METHOD: Two public tertiary hospital systems instituted a policy of mandatory vaccination or completion of a declination form in 2020–2021 for credentialed staff (physicians, midwives, dentists) and trainees (CS+T) but not for other hospital staff (HS). An interrupted time-series regression model using data from the 2012–2013 through 2020–2021 influenza seasons was performed to compare vaccination rates when the mandatory influenza immunisation declination form was in place with other periods in which other methods were used, including mandatory vaccination or masking in 2013–2014 through 2017–2018.

RESULTS: There was a rise in the percentage of vaccination on institution of the vaccination or declination policy for CS+T (50.0%; 95% CI 22.8% to 77.3%; $p = 0.01$)] but not for HS (11.1%; 95% CI −14.6% to 36.7%; $p = 0.263$) among whom the policy was not applied. Vaccination in CS+T rose from 60% in 2019–2020 to 94% in 2020–2021 ($p < 0.001$). There was a trend for the % vaccination in the CS+T group to be higher during the period of vaccination or declination form than during the period of mandatory vaccination or masking (26.6%; 95% CI −2.6% to 55.8%; $p = 0.062$).

CONCLUSION: A policy of mandatory vaccination or completion of a declination form raised influenza vaccination rates to 94.1% among health care workers. This may help to preserve hospital capacity during the coronavirus disease 2019 pandemic.

SP50

Laboratory identification of hypervirulent *Klebsiella pneumoniae* in a low-prevalence area

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OBJECTIVES: Hypervirulent *Klebsiella pneumoniae* (hvKp) is an emerging microbial agent that causes tissue-invasive disease. Rapid identification of hvKp has been attempted in clinical laboratories through the string test; however, the correlation between string test positivity and hvKp disease remains unclear.

METHOD: From September 29, 2015, to May 31, 2019, all unique *K. pneumoniae* isolates from sterile sites were prospectively tested by the string test in a tertiary-care microbiology laboratory. Cases were patients with string test–positive isolates, and controls were patients with string test–negative isolates. Controls were matched to cases (2:1) on the basis of sex, age, hospital site, and ward of collection. Medical records were reviewed to redefine cases; cases were defined as having at least one site of non-bladder organ involvement. String tests were repeated from frozen isolates. Genomic analysis for K serotype, ybtA; clbA; iucA, iroB; and prmpA, prmpA2, and peg-344, including determination of

a genomic virulence score,[1] was completed. All statistical analyses were conducted using Stata/MP version 12 (StataCorp, College Station, Texas).

RESULTS: Of the 94 *K. pneumoniae* infections, 31 were identified as having tissue-invasive disease. In multivariable analysis, the string test (≥5 mm) was the only significant predictor for invasive disease (OR 5.00, $p = 0.007$); virulence score was not significantly associated ($p = 0.88$). The sensitivity (Sn) and specificity (Sp) of the string test were 52% and 81%, respectively, which increased to 58% and 87% when limited to community-acquired infections. The Sn and Sp of the virulence score were 25% and 87%, respectively. When the string test ≥ 5 mm and virulence score were considered together, the Sp rose to 94%.

CONCLUSION: Our findings suggest that the string test remains an effective tool for clinical laboratories to identify potential hvKp strains. Although a negative string test cannot rule out invasive disease, a positive string test, especially when used with a genomic virulence score, provides high specificity in ruling in hvKp strains.

[1] Lam MMC, Wick RR, Watts SC, Cerdeira LT, Wyres KL, Holt KE. A genomic surveillance framework and genotyping tool for *Klebsiella pneumoniae* and its related species complex. Nature Comm. 2021;12:4188. https://doi.org/10.1038/s41467-021-24448-3.

SP51

Elucidating determinants of respiratory health by virome assessment

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OBJECTIVES: Previous studies have suggested that early infection with herpesviruses, notably Epstein–Barr virus (EBV), have a protective effect against the development of childhood asthma, whereas infection with rhinovirus and respiratory syncytial virus have been associated with heightened risk. Conversely, infection with EBV and human adenovirus have been implicated in the development of sleep-disordered breathing (SDB). We sought to optimize and validate a pan-viral antibody detection method to describe how previous viral exposures are associated with the development of asthma and SDB in children.

Table SP51-1: Summary of validation panel by immunoglobulin target

Target and inclusion criteria	Positive	Negative
Immunoglobulin G		
EBV or CMV	20	20
HSV1, HSV2, VZV, parvovirus B19, HCV, HAV, or HIV	10	10
HAdV or RSV	12	0
Immunoglobulin M		
EBV or CMV	10	10

METHOD: VirScan is a serological profiling assay that identifies antibodies against a library of 206 viruses. This method displays epitopes representing entire viral proteomes on the surface of bacteriophages and identifies viruses captured by immunoglobulins G and M through next-generation sequencing. We linked clinical serology and polymerase chain reaction results to identify residual sera samples for validation and have titrated clinical samples to determine optimal antibody loading concentrations. We will further manipulate reaction conditions in library preparation steps to optimize this assay for high-throughput automation.

RESULTS: We determined that a 1:50 dilution of neat serum is ideal to avoid the Hook effect and have modified the bioinformatic pipeline for more stringent analysis. Table SP51-1 describes the validation panel assembled.

CONCLUSION: VirScan requires project-specific validation and optimization before its application with a longitudinal birth cohort. This work will elucidate the complex relationships between early-life viral infections and subsequent outcomes to generate critical data on the determinants of disease for asthma and SDB that can guide preventive strategies.

SP52

Examining the bacterial diversity of the nasal microbiota of SARS-CoV-2–infected individuals in comparison with other respiratory viruses

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OBJECTIVES: The nasal mucosa is a major site for respiratory virus entry. Epithelial cells lining the nasopharynx house a community of bacteria called the *nasal microbiota* (NM). The NM has been shown to protect against pathogen invasion and contribute to the mucosal immune response. Influenza A (flu-A) has been shown to modify the NM, resulting in enrichment of opportunistic pathogens such as *Streptococcus pneumoniae* and contributing to secondary bacterial infections. Here we evaluate the NM of individuals infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), flu-A, respiratory syncytial virus (RSV), and negative controls (NCs).

METHOD: RNA extraction was performed on nasopharyngeal swabs (NPSs) collected from patients using Maxwell whole blood RNA/DNA extraction kits. Specimens were tested for SARS-CoV-2/flu-A/B/RSV by reverse transcription polymerase chain reaction. Samples were sent for 16S rRNA Illumina Next Generation Sequencing (MiSeq). Analysis was performed using QIIME II, Microbiome Analyst, and PRISM9.

RESULTS: NPS from 45 SARS-CoV-2–, 40 flu-A–, and 26 RSV-positive and 45 NC individuals were evaluated. The NM of SARS-CoV-2 individuals demonstrated a marked increase in alpha and beta diversity (both ps < 0.001) and had a distinct bacterial profile compared with that of NCs. The NM of SARS-CoV-2 individuals had an increase in streptococci and staphylococci and depletion of *Bifidobacterium* and *Moraxella* compared with NCs (both ps < 0.001). Compared with flu-A and RSV patients, SARS-CoV-2 patients had enrichment of streptococci and depletion of *Haemophili* spp (p < 0.002). The abundance of streptococci and staphylococci in the NM did not correlate with SARS-CoV-2 cycle thresholds.

CONCLUSION: This study demonstrates that the NM of SARS-CoV-2–infected individuals had a distinct community from those infected with flu-A and RSV, although the abundance of specific bacteria did not correlate with SARS-CoV-2 viral loads. Our findings related to differences in bacterial abundance is likely the cause of changes in the NM metabolome observed in our previous studies and should be investigated for its impact on SARS-CoV-2 transmission potential.

SP53

Associations of SARS-CoV-2 variants, clinical characteristics, and hospitalization among COVID-19 patients from Toronto, Ontario, Canada

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OBJECTIVES: New variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) continue to emerge as the coronavirus disease 2019 (COVID-19) pandemic progresses. We sought to investigate associations between genomic and clinical characteristics of COVID-19 patients.

METHOD: A cohort of 1,984 adult outpatients and inpatients with laboratory-confirmed COVID-19 from five hospitals in the greater Toronto area were recruited from February 2020 to December 2021. Demographic and clinical data were obtained by chart review and participant interview. RNA from nasal specimens underwent whole-genome sequencing. SARS-CoV-2 genomes with a minimum of 100 times read-depth and 75% completeness were assigned lineages using Phylogenetic Assignment of Named Global Outbreak LINeages (PANGOLIN). Multivariable logistic regression models were constructed to investigate whether lineages, demographics, symptoms, and comorbidities were associated with hospitalization.

RESULTS: Overall, 22% (428/1,984) of cases had corresponding genomic and clinical data. The median age was 60 years (interquartile range 47–73) and 55% (236/428) were male. Thirty-four percent (154/428) were outpatients and 66% (283/428) were hospitalized, of whom 38% (78/283) were admitted to the intensive care unit. Predominant symptoms included cough in 65% (277/428) of patients, fever in 60% (257/428), and shortness of breath in 46% (196/428). Fifty-five unique lineages were identified; B.1 was the most prevalent at 17% (72/428). Thirty-two percent (135/428) of cases were variants of concern (VOCs); 36% (48/135) were Alpha (B.1.1.7), 3% (4/135) Beta (B.1.351), 22% (30/135) Gamma (P.1), and 39% (53/135) Delta (B.1.617.2 and its AY sub-lineages). Preliminary multivariable logistic regression analysis indicated infection with B.1.1.181, infection with B.1.1.7, male sex, age, fever, and hypertension were significantly associated with hospitalization.

CONCLUSION: We observed a heterogenous lineage distribution with 55 different lineages. Two lineages, including one VOC, were significantly associated with hospitalization. Emerging SARS-CoV-2 variants must continue to be monitored to understand effects on disease severity and outcomes.

SP54
WITHDRAWN

SP55
Optimizing the use of MALDI-TOF mass spectrometry for the detection of SARS-CoV-2 with pure cultured isolates and clinical nasopharyngeal and saliva samples

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OBJECTIVES: Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) is an important tool in clinical microbiology for the rapid and accurate identification of bacteria and fungi. Limited evidence suggests that MALDI-TOF may be used for the diagnosis of coronavirus disease 2019 (COVID-19), especially on the basis of detection of the spike protein. The objective of this study was to optimize MALDI-TOF pre-analytical processing and to investigate the performance of this optimized approach combined with machine learning for the detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

METHOD: Pure cultured SARS-CoV-2 isolates and clinical nasopharyngeal and saliva samples of SARS-CoV-2 were serially diluted and inactivated with heat, beta-propriolactone, acetonitrile, or isopropyl alcohol. The impact of additional filtration, protein solubilization, and extraction to further purify viral proteins of interest was studied. In addition, two matrices (4-alpha hydroxycinnamic acid and sinapinic acid) and two spotting techniques (standard and sandwich) were compared to evaluate for changes in spectra. Machine learning analysis was performed using a previously described pipeline.

RESULTS: Despite much higher viral concentrations in the cultured isolates, there was no significant difference in the quality or number of peaks between pure culture and clinical sample mass spectra. We were unable to observe peaks corresponding to those previously reported for SARS-CoV-2 spike proteins. The choice of sample type, matrix, spotting technique, and additional processing methods all demonstrated an impact on the peaks of observed spectra, but reproducibility was poor. Using an optimized processing protocol, the area under the receiver operating characteristic curve score ranged from 0.65 to 0.7 on our test set.

CONCLUSION: Several processing factors influence the quality of spectra for MALDI-TOF viral analysis. Despite pre-analytical optimization, MALDI-TOF for the diagnosis of SARS-CoV-2 did not perform as well as presented in earlier, small studies. Alternative diagnostic or processing strategies are needed to optimize MALDI performance for COVID-19 testing.

SP56
Trends in antimicrobial resistance among gram-negative organisms between January 2013 and December 2020

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OBJECTIVES: The rise of antimicrobial-resistant bacteria is a rapidly growing threat to human health. This study analyzes the trends in antimicrobial resistance among gram-negative organisms between January 2013 and December 2020.

METHOD: Antimicrobial susceptibility testing results from January 2013 through December 2020 from a tertiary-care microbiology laboratory servicing a multicultural city were analyzed for trends in resistance among Enterobacterales (average [avg.] 6,866/y), *Pseudomonas aeruginosa* (avg. 1,215/y),

and *Acinetobacter* spp (avg. 52/y). Among Enterobacterales, predominant species included *Escherichia coli* (avg. 4,693/year) and *Klebsiella pneumoniae* (avg. 1,178/year). For each category of organisms, an individual patient was represented only once per year. Following Canadian Public Health Laboratory Network and Canadian Association for Clinical Microbiology and Infectious Diseases recommendations, Enterobacterales isolates were classified as susceptible, multi-drug resistant (MDRO), or extensively drug resistant (XDRO), and *P. aeruginosa* and *Acinetobacter* spp isolates were classified as either susceptible or XDRO. Chi-square test for trends were completed using GraphPad Instat (GraphPad, San Diego, California).

RESULTS: The proportion of MDRO Enterobacterales increased significantly between 2013 and 2020, from 7.58% in 2013 to 10.48% in 2020 ($p < 0.0001$). Among the Enterobacterales, there was also a significant increase in MDRO *E. coli,* from 9.72% in 2013 to 13.21% in 2020 ($p < 0.0001$), as well as of MDRO *K. pneumoniae,* from 3.59% in 2013 to 7.28% in 2020 ($p < 0.0001$) and XDRO *K. pneumoniae,* from 1.55% in 2013 to 3.82% in 2021 ($p < 0.001$). Between 2013 and 2020, there was no significant change in the proportion of XDRO *Acinetobacter* spp, which ranged from 0% to 4.55% over the study period, or in that of XDRO *P. aeruginosa,* which ranged from 0% to 0.71%.

CONCLUSION: The proportion of MDRO Enterobacterales rose significantly between 2013 and 2020, affecting predominantly *E. coli* and *K. pneumoniae*. There is a need for continued surveillance and interventions to stem the ongoing rise in resistance, with particular attention to *E. coli* and *K. pneumoniae* organisms.

SP57

Evaluation of rapid pellet MALDI-TOF mass spectrometry identification from positive blood cultures

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OBJECTIVES: Bloodstream infections can cause significant mortality, particularly among those who are immunocompromised or in intensive care. Rapid and accurate identification of microbial pathogens from positive blood cultures informs therapeutic management and improves patient outcomes. In this study, we evaluated the accuracy of a rapid matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) identification method from cultured pellets of positive blood cultures (rPEL).

METHOD: We compared rPEL with traditional MALDI-TOF MS on overnight subcultures from positive blood culture vials to evaluate method accuracy. Monomicrobial positive blood cultures were collected from an acute-care hospital over 4 years (August 2017 to July 2021). rPEL was performed by centrifuging 10 mL of blood from the positive blood culture vial in a serum separator tube. The pellet was then inoculated to a chocolate agar plate and incubated for a minimum of 2 hours. VITEK MS (bioMérieux, Marcy-l'Étoile, France) was used for rPEL and final identification of routine overnight subcultures.

RESULTS: Of 8,167 positive blood cultures during the study period, 4,128 (50.5%) were new positive blood cultures for which rPEL was performed. Positive blood cultures with mixed Gram stain or no pellet growth were excluded from the analysis (16%; $n = 662$). On Gram stain, the remaining 3,466 positive blood cultures identified as gram positive (59.5%; $n = 2,063$), Gram negative (38.3%; $n = 1,327$), and yeast (2.2%; $n = 76$). A concordant rPEL occurred for 99.9% of isolates ($n = 3,464$). The two organisms (*Staphylococcus aureus* and *Microbacterium paradoxydans*) misidentified using rPEL were both identified as coryneform bacilli by VITEK MS after conventional growth conditions.

CONCLUSION: Overall, rPEL is a useful method that provides rapid and accurate organism identification for positive blood cultures that correspond with initial Gram stain results. In most cases, rPEL provided a result a minimum of 20 hours before traditional MALDI-TOF MS identification from positive blood culture subcultures. Future methods whereby mixed cultures could be processed could further improve patient management.

SP58

Prospective evaluation of immunity after COVID-19 vaccines (PREVENT-COVID) among older adults

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OBJECTIVES: There is a critical need to understand real-world population level coronavirus disease 2019 (COVID-19) vaccine immunogenicity, especially among older adults who are at increased risk of developing severe disease. We intend to (1) establish the immunogenicity of COVID-19 vaccines among adults and (2) explore vaccine-elicited protection against various severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral variants. In addition, we will investigate the influence of endemic coronavirus (HCoV) exposure and prior SARS-CoV-2 infection on the response to COVID-19 vaccines.

METHOD: This ongoing prospective observational study involves participants (N = 709) aged 50 years and older. To date, up to five dried blood spot samples per participant have been collected pre–COVID-19 vaccination (baseline) through 5 months post-completion of vaccine series. Quantitative detection of nucleocapsid (N)- and wild-type spike (S)–specific SARS-CoV-2 immunoglobulin G (IgG) antibodies was done using a multiplex anti-IgG assay developed by Meso Scale Diagnostics (Rockville, Maryland).

RESULTS: Preliminary findings demonstrate an increase in geometric mean concentration (GMC) of S-specific IgG antibodies from pre-vaccination (64.09 AU/mL) to 1-month after the first vaccine dose (1,239.06 AU/mL). An additional increase was observed at 1 month after the second vaccine dose (9155.81 AU/mL). At 5 months after the second vaccine dose, a modest decrease in the GMC of S-specific IgG antibodies (3,822.47 AU/mL) was observed. These results indicate a high level of S-specific SARS-CoV-2 IgG levels up to 5 months after vaccination compared with baseline concentration levels.

CONCLUSION: Preliminary immunogenicity findings suggest that the current provincial vaccination schedules and vaccine types administered induce a robust humoral immune response that is sustained for at least 5 months post two-dose COVID-19 vaccination series completion in participants aged 50 years and older. We intend to establish COVID-19 vaccine immunogenicity and protection using regression modelling adjusting for the effect of age, biological sex, prior HCoV exposure, and SARS-CoV-2 infection. Future work includes quantitation of ACE2 inhibiting antibodies of 10 SARS-CoV-2 lineages, including variants of concern.

SP59

Investigating the correlation between SARS-CoV-2 variants of concern and PCR cycle threshold values

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OBJECTIVES: Several severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOCs) have been identified. This study compared mean reverse transcription polymerase chain reaction (RT-PCR) test cycle thresholds (Cts) of different VOCs as a surrogate for VOC viral load over time.

METHOD: All specimens submitted for SARS-COV-2 testing to a tertiary-care microbiology laboratory in the Greater Toronto Area between February 4, 2021, and May 31, 2021 as part of the Ontario Provincial COVID-19 Diagnostic Network were studied. A VOC PCR-based screening assay developed by Public Health Ontario was used to classify positive cases into VOC types by presence or absence of N501Y and E484S mutations (baseline [N501Y and E484S negative], Alpha [N501Y positive], and Beta or Gamma [N501Y and E484S positive]). The mean Ct values of positive coronavirus disease 2019 (COVID-19) RT-PCR tests (lowest target when assays with multiple targets were used) were reviewed, and mean values for results consistent with the Alpha and Beta or Gamma VOC were compared with baseline values using the Kruskal–Wallis H-test (a non-parametric analysis of variance test).

RESULTS: Baseline COVID-19 cases (N501Y and E484S negative) between February 4, 2021, and May 31, 2021 had an average Ct value of 26.6 (n = 3,396), whereas COVID-19 cases with single positive N501Y (Alpha variant) or double positive N501Y and E484S (Beta or Gamma variant) mutations had average Ct values of 22.3 (n = 19,745) grouped together and 22.3 (n = 19,258) and 21.7 (n = 253) separately, respectively. The Kruskal–Wallis test showed a significant

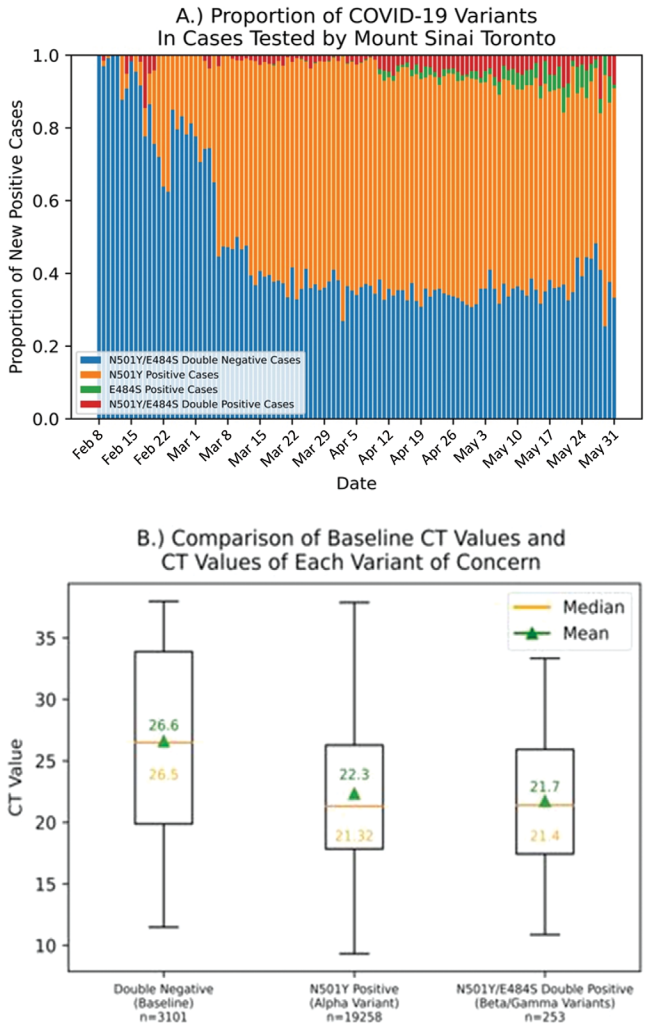

Figure SP59-1: (a) Proportion of COVID-19 variants in cases tested by Mount Sinai Toronto; (b) Comparison of baseline CT values and CT values of each variant of concern
CT = Cycle threshold, N/A = Not applicable

reduction in the Ct values of VOC results compared with baseline ($p < 0.001$).

CONCLUSION: The lower RT-PCR Ct values associated with the Alpha, Beta, and Gamma VOCs suggests that these SARS-CoV-2 VOCs are associated with higher viral loads in submitted specimens from infected patients compared with baseline SARS-CoV-2 isolates, which may be associated with higher infectivity. Review of the Cts for the Delta and Omicron VOCs is ongoing.

SP60

Assessing the limit of detection of *Candida auris* using Micronostyx Colorex Candida Plus agar and polymerase chain reaction

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OBJECTIVES: A sensitive and reliable testing procedure is necessary for the effective management of *Candida auris* infections and outbreaks. We aimed to determine the optimal screening procedure for *C. auris* in the clinical lab by assessing and comparing the limit of detection (LOD) of *C. auris* with culture-based methods using a Micronostyx Colorex Candida Plus Agar (M; Micronostyx, Ottawa, Ontario), ThermoFisher Auris Enrichment Broth (AEB; ThermoFisher, Waltham, Massachusetts), and BioGX (Birmingham, Alabama) *C. auris* research-use-only polymerase chain reaction (PCR) using EasyMag® (bioMérieux, Marcy-l'Étoile, France) extraction.

METHOD: Fresh nasal–axillary–groin–perineum–rectal swabs were spiked with a single *C. auris* isolate, and six 5-fold dilutions (from 250 CFU/mL to 0.08 CFU/mL) of each spiked sample were prepared. Each diluted sample was (1) directly inoculated onto M and incubated at 37°C for 48 hours; (2) extracted and tested directly by PCR; (3) inoculated into AEB and incubated at 250 rpm for 24 hours at 37°C, then tested by PCR; and (4) inoculated into AEB and incubated at 250 rpm for 48h at 37 °C before being tested by PCR. The limit of detection was calculated using the online Probit Analysis Tool for LOD data from Public Health Ontario.

RESULTS: The LOD of the various screening procedures were between 0.47 CFU/mL and 2.73 CFU/mL. The culture-based, direct-to-agar procedure had the highest LOD at 2.73 CFU/mL, followed by the direct PCR from specimen procedure with a LOD of 2.49 CFU/mL. Both the culture-based, AEB-enriched procedure and the PCR from AEB-enriched specimen procedure had the lowest LOD, at 0.47 CFU/mL.

CONCLUSION: Direct culture-based and PCR screening procedures showed similar LOD. AEB enrichment of specimens increased the sensitivities of both culture-based and PCR screening procedures compared with direct-from-specimen procedures.