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Sheraton Vancouver Wall Centre, Vancouver, BC

April 9-12, 2024

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ORAL PRESENTATIONS

Session A (Student competition)
Wednesday, April 10

A01
Health care resource use for acute respiratory syncytial virus paediatric hospitalization in Canadian infants: Immunization Monitoring Program ACTive (IMPACT) analysis

Nirma Khatri Vadlamudi[1,2], Kyle Gomes[1], Ethan Chow[1], Malou Bourdeau[3], Joanne Embree[4], Scott A Halperin[5], Taj Jadhavji[6], Joanne M Langley[5], Nicole Le Saux[7], Dorothy Moore[3], Shaun K Morris[8], Jeffrey M Pernica[9], Joan Robinson[10], Manish Sadarangani[1,2], Julie A Bettinger[1,2]

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OBJECTIVE: To evaluate differences in age-specific health-care resource use and hospitalization costs associated with respiratory syncytial virus (RSV) among healthy, full-term Canadian infants aged 0 to <12 months.

METHODS: Data assembled from active surveillance in 13 Canadian IMPACT hospitals on a random subgroup of infants hospitalized with laboratory-confirmed RSV during the 2018–2022 RSV seasons. We assessed disease severity indicators, including ICU admission, mechanical ventilation (MV), and health care resource use (length of hospital [LOS] stay, ICU stay, MV), stratified by two age groups (0 to <6 and 6 to <12 months). Hospitalization episode costs were computed by multiplying daily costs for pediatric ward or ICU stay by the number of days the services were used, adjusted to 2022 Canadian dollars.

RESULTS: Of 1,147 laboratory-confirmed RSV hospitalizations among 0 to 11 months infants, 618 (53.9%) were males, 963 (83.9%) were <6 months of age, 293 (25.5%) were admitted to ICU, and 75 (6.5%) required MV. ICU admission and MV proportions were significantly higher in those aged 0 to <6 months compared with those 6 to <12 months (28% versus 13% and 8% versus 1%) ($p < 0.001$). Mean LOS was 3.3 days (SD 2.2 d), ICU was 3.3 days (SD 2.2 d), and MV was 6.1 days (SD = 6.0 d). Mean LOS and ICU were comparable in both age groups. Infants aged 6 to <12 months required longer MV compared with those 0 to <6 months (mean 11.5 versus 6.0 days) ($p = 0.042$). Mean hospitalization costs showed no difference by age group. Mean costs were higher for patients requiring ICU/without MV (mean $25,900 [SD $11,800]) and for those needing ICU/with MV (mean $60,300 [SD $49,400]), compared to those without ICU (mean $7,540 [SD $5,210]) ($p < 0.001$), primarily due to extended overall LOS.

CONCLUSION: Our findings demonstrate substantial health care resource use and hospitalization costs associated with RSV in full-term, healthy Canadian infants <12 months of age. Consequently, this population should be prioritized for RSV prevention strategies.

A02
Clinical significance of cefazolin inoculum effect in methicillin-susceptible *Staphylococcus aureus* (MSSA) infections: A systematic review

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OBJECTIVE: There are rising concerns that cefazolin inoculum effect (CzIE) increases risk of cefazolin treatment failure in methicillin-susceptible *Staphylococcus aureus* (MSSA) infections. CzIE is defined as cefazolin minimum inhibitory concentration (MIC) $\leq$8 at 5×10^5 CFU/mL (standard-inoculum), with elevated MIC $\geq$16 at high-inoculum (5×10^7 CFU/mL). We conducted a systematic review to assess association of CzIE on mortality and treatment failure of cefazolin-treated MSSA infections.

METHODS: We searched OVID MEDLINE, EMBASE, Web of Science, medRxiv and bioRxiv from inception to April 12, 2023, using key words: *Staphylococcus aureus,* cefazolin, and acefazolin inoculum effect. Observational studies and randomized controlled trials (RCTs) in any language involving CzIE testing were included. Two blinded

authors screened abstracts and extracted data, and a third reviewer resolved any disagreements. Odds ratios (OR) were calculated for mortality and treatment failure between CzIE presence in patients with cefazolin-treated MSSA infections, without pooling due to study heterogeneity. For observational studies, risk of bias was assessed using Newcastle-Ottawa Scale.

RESULTS: Twenty-three studies were included—the median was 122 isolates per study (range: 17–690) and 23.3% of isolates were CzIE-positive (11.0%–58.8%). There was no significant difference in mortality due to CzIE, with ORs ranging from 0.73 to 19.8 in 4 studies. For treatment failure, ORs ranged from 0.26 to 13.0 across 5 studies; only one study showed statistically significant increase in treatment failure due to CzIE, OR 3.93 (95% CI 1.08 to 14.31; $p = 0.04$).

CONCLUSION: To our knowledge, this is the first systematic review assessing clinical impact of CzIE on cefazolin-treated MSSA outcomes. Limitations included few observational studies with small sample sizes reporting mortality and treatment failure, along with significant heterogeneity in defining outcomes and infection type. Lastly, only one study reported outcomes for anti-staphylococcal penicillins, limiting comparison of antimicrobials. Our findings currently do not support CzIE testing in clinical practice as means for predicting greater mortality.

A03

Rapid detection models of antifungal resistance in the pathogenic mold, *Aspergillus fumigatus* using clinical MALDI-TOF mass spectrometry data

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OBJECTIVE: The main objective of this study was to construct machine learning models using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) data, currently used in clinical microbiology for pathogen identification, to identify antifungal drug susceptibility in *Aspergillus fumigatus*, a highly clinically relevant pathogenic mold.

METHODS: MALDI-TOF MS data from 82 *A. fumigatus* isolates, using bioMérieux MS Prime, were prepared for analysis, according to established best practices. The isolates were categorized as resistant or susceptible using Clinical and Laboratory Standard Institute criteria on experimentally determined minimum inhibitory concentration (MIC) values for itraconazole, voriconazole, and amphotericin B. Protein spectra from the MALDI-TOF MS were employed for model training, validated through k-fold cross validation.

RESULTS: Correct discrimination of isolates resistant to amphotericin B from susceptible ones using an epidemiological cut of 2 mg/L (CLSI M57S) achieved 83.51% and 86.77% accuracy by applying diagonal linear discriminant analysis and random forest models, respectively, to the MALDI-TOF-MS-derived protein spectra. Interestingly, the most informative peaks present and optimal number of peaks to use differed between these models. Ongoing research involves testing additional diverse classification models and repeating the analysis for itraconazole and voriconazole resistance. Comparative assessment of model performance and peak importance both between and within antifungal susceptibility types may reveal new biomarkers associated with resistance.

CONCLUSION: MALDI-TOF MS combined with peak analysis is a promising method for antifungal resistance detection in *A. fumigatus*. As the current clinical detection methods necessitate several days' growth in the presence of a specific antifungal, implementing an MS-typing method using pure culture samples already employed for routine species identification could expedite turnaround times, improving patient outcomes. More broadly, novel resistance biomarkers have the potential to lay a foundation for research into novel antifungal drug targets and cryptic resistance mechanisms. Although more research is needed, MALDI-TOF MS coupled with machine learning shows great potential for rapid antifungal detection in *A. fumigatus*.

A04

Designing a multiplex typing PCR assay for assessing in-hospital outbreaks of *Clostridioides difficile*

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OBJECTIVE: Identifying potential outbreaks of *Clostridioides difficile* infection in a timely manner is essential to limiting the spread of the disease. The objective of this study was to design a multiplex polymerase chain reaction (PCR) assay to determine multi-locus sequence type (MLST) as a

rapid method of identifying potential relatedness of samples without the need for whole-genome sequencing.

METHODS: Samples from colonized and infected inpatients in Hamilton, ON, Canada, with *C. difficile* identified through molecular means (PCR and loop-mediated isothermal amplification [LAMP]), were cultured and sequenced. Genomes were constructed and MLST was determined. breseq and subsequently gdtools were then used to find all genome-wide polymorphisms unique to the four most prevalent MLSTs present in our dataset. These polymorphisms were then used to design PCR primers specific for each MLST.

RESULTS: Forty-four samples were successfully sequenced and had MLST identified. MLST1 (NAP1), as well as the top three most prevalent MLSTs found in Hamilton (2, 42, and 58, representing 15%, 15%, and 8% of samples, respectively), were selected as targets of identification by the multiplex PCR assay. Several loci are present in the *TcdB* gene that represent polymorphisms unique to MLST1/NAP1/ribotype 027 strains. TcdB sequences are >99% identical across NAP1 sequences, meaning that these loci represent excellent candidates for PCR sites specific for NAP1 strains. Candidate sites are being tested experimentally using samples with known MLST to confirm sensitivity and specificity of the assay to determine potential relatedness of samples.

CONCLUSION: The rapid turnaround that will be afforded by this new screening method will enable hospitals to quickly assess potential relatedness of samples without using whole genome sequencing. Samples that do not share a MLST with each other are likely not related and, thus, do not represent a potential outbreak. Those that do share MLSTs with each other may represent related samples and should be further investigated by sequencing methods.

ORAL PRESENTATIONS

Session B
Thursday, April 11

B01
Candida auris in Canada, 2012 – Oct 2023

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OBJECTIVE: *Candida auris* is an emerging yeast that is associated with high rates of antifungal resistance and health-care-associated outbreaks. We carried out genomic characterization of all known cases of *C. auris* in Canada to monitor its emergence.

METHODS: All isolates of *C. auris* submitted to Canadian provincial public health laboratories were forwarded to the Public Health Agency of Canada for whole genome sequencing (WGS). For the subset of cases that were also identified through the Canadian Nosocomial Infection Surveillance Program (CNISP; $n = 10$), enhanced epidemiological and patient data were collected.

RESULTS: Fifty isolates of *C. auris* from 51 cases were identified from January 2012 to October 2023. Isolates were obtained through surveillance testing from axilla and/or groin ($n = 13$) and from a variety of other specimen types such as blood, ear, respiratory tract, urine, and wounds ($n = 38$). Of 15 cases with known travel status, 11 (73%) reported international travel and receipt of health care in India ($n = 5$), the United States ($n = 4$), South Africa ($n = 1$), and Hong Kong ($n = 1$), or they reported no travel ($n = 4$). Canadian isolates of *C. auris* fell within four major genomic clades (clades I-IV). One-third of cases were multidrug resistant (resistant to fluconazole and amphotericin B). Fluconazole-resistant isolates contained known mutations in the ERG11 target protein. So far, all Canadian isolates were susceptible to echinocandins and lacked FKS1 hotspot mutations. Although isolates could be very clonal, for example, Canadian isolates from clade I differed by an average of 79 SNVs, epidemiologically linked isolates within clade I differed by only 1-19 SNVs.

CONCLUSION: WGS was useful for outbreak investigations of *C. auris* by demonstrating genetic linkage of isolates with known epidemiological links. Given the rapid emergence of *C. auris* in neighboring United States, there is a window of opportunity to prepare for a potentially similar emergence in Canada.

B02

Congenital syphilis in Canada: Clinical and health-care related diagnosis and treatment findings of a Canadian Paediatric Surveillance Program Study (June 2021 – May 2023)

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OBJECTIVE: The incidence of congenital syphilis (CS) is at an unseen high in Canada. A countrywide in-detail description of the affected newborns and their birthing parents has not been previously published. We aim to provide a national picture of the clinical presentation, diagnostic procedures, treatment, and severe outcomes in the affected newborns, as well as the diagnosis and care provided to their birthing parents.

METHODS: CS cases were elicited from paediatricians through the Canadian Paediatric Surveillance Program from June 2021 to May 2023. Data were collected voluntarily through a case-survey and analyzed using descriptive statistics to examine socio-demographic, clinical, laboratory, treatment, and prenatal variables.

RESULTS: In total, 245 cases were reported from 7 provinces and territories, 71% from the prairies; 33 cases were reported as confirmed, and 212 were reported as probable. In 88% (215), treatment was initiated during the first week of life, while 8 were >1 month old. Most infants had no physical exam findings of CS (139, 57%). Among symptomatic cases, prematurity and rash accounted for 30% (72) and 10% (25), respectively. Anaemia and thrombocytopaenia were rare. Long-bone abnormalities were detected in 24% (55/232). Neurosyphilis was reported in 19 cases. There were 2 neonatal deaths. The median age of birthing parents was 27 years, and 31% resided rurally. No prenatal care was reported in 25% (62) of birthing parents, and only 25% (61) reported at least one visit per trimester. Of 151 birthing parents with positive prenatal syphilis screen, 20% (30) did not receive treatment. Prenatal treatment was initiated <4 weeks predelivery in 38% (46/122).

CONCLUSION: While most CS cases are diagnosed at birth without symptoms of infection, prematurity, skin and bone abnormalities are not uncommon on presentation. This clinical countrywide picture demands public health attention and action to ensure access to prenatal care and inclusion for all pregnant individuals.

B03

Mailed antibiotic prescribing feedback to primary care physicians: A factorial randomized controlled trial

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OBJECTIVE: To evaluate whether providing family physicians with feedback on their antibiotic prescribing compared to that of their peers reduces antibiotic prescriptions.

METHODS: We performed a pragmatic physician randomized controlled trial of an audit and feedback (A&F) mailed letter to family physicians compared to no letter (4:1 allocation). We embedded within the intervention arm a 2 × 2 factorial trial evaluating 1) case-mix adjusted versus unadjusted comparators, and 2) emphasis, or not, on harms of antibiotics. Eligible physicians who did not opt out received a mailed letter in January 2022 with peer comparison antibiotic A&F of prescriptions to patients aged ≥65 years. The primary outcome was antibiotic prescribing rate (APR) per 1,000 patient visits at 6 months postintervention analyzed using Poisson regression adjusted for baseline APR.

RESULTS: 5,046 physicians were included. Baseline APR rates were comparable between the arms. At 6 months, mean (SD) APR was 59.4 (42.0) in the control arm and 56.0 (39.2) in the intervention arm (adjusted relative rate (RR) 0.95 (95% CI 0.94 to 0.96). Antibiotic prescribing for viral illnesses (RR 0.89 [95% CI 0.86 to 0.92]), prolonged duration prescriptions defined as >7 days (RR 0.85 [95% CI 0.83 to 0.87]), and broad-spectrum prescribing (RR 0.94 [95% CI 0.92 to 0.95]) were also significantly lower in the intervention arm compared to control arm. Results were consistent at 12 months post intervention. No significant effect was seen for including emphasis on harms messaging. We observed a small increase in antibiotic prescribing with case-mix adjusted reports (RR 1.01 [95% CI 1.00 to 1.03]).

CONCLUSION: Peer comparison A&F letters significantly reduced overall antibiotic prescribing with no benefit of case-mix adjustment or harms messaging. Antibiotic prescribing A&F is a scalable and effective intervention and should be a routine quality improvement initiative in primary care.

Trial registration: NCT04594200

B04

Macrolide and fluoroquinolone-resistant *Mycoplasma genitalium* in Canada, 2018–2023

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OBJECTIVE: *Mycoplasma genitalium* (Mgen) is one of the leading causes of nongonococcal, persistent urethritis in men, and commonly causes cervicitis and urethritis in women. Severe infections can lead to pelvic inflammatory disease, preterm birth, and female infertility. Mgen infections are widespread, with a prevalence of 4.2%–9.6% in some Canadian studies of STI clinic attendees. Overall prevalence is unknown, as Mgen is not notifiable in Canada, and there is no established surveillance program. Antimicrobial resistance (AMR) is of particular concern, as Mgen has developed resistance to both azithromycin and moxifloxacin, the currently recommended therapeutics.

METHODS: Between 2018 and 2023, 2,039 Mgen-positive urogenital specimens were tested from 8 provinces in Canada. Polymerase chain reaction and Sanger sequencing were performed on these specimens to detect mutations associated with macrolide (23S rRNA A2058/A2059) and fluoroquinolone (*gyrA* 95/99/108 and *parC* 83/87/97) resistance.

RESULTS: Of 2,039 specimens collected in 2018–2023, 37.2% (n = 758) were from females, 60.8% (n = 1,240) from males, 2 were gender diverse, and 39 were unspecified. Of specimens with AMR results, 67.9% (1,354/1,993) contained single nucleotide polymorphisms associated with macrolide resistance across all years, with 80.6% (216/268) resistance in 2023. The most common mutations were A2058G (n = 655) and A2059G (n = 587). Fluoroquinolone resistance-associated mutations were found in 18.8% (348/1,851) of specimens across all years, with 27.3% (71/260) resistance in 2023. The most common mutations were *parC* S83I (n = 254) and *gyrA* M95I (n = 32). Both macrolide and fluoroquinolone-associated resistance markers were found in 16% (296/1,851) of specimens, while 29.3% (543/1,851) were susceptible to both.

CONCLUSION: While true prevalence cannot be determined without a surveillance program, the high proportion of antimicrobial-resistant specimens received from 2018 to

2023 is of great concern. Enhanced surveillance of AMR-Mgen is necessary to identify clusters, inform treatment guidelines, and mitigate the impact of resistant Mgen.

POSTER PRESENTATIONS

Wednesday, April 10

WP001 - WITHDRAWN

WP002

Antimicrobial stewardship quality improvement intervention for *Enterococcus Bacteremia*

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OBJECTIVE: Primary Objective: To determine acceptance rates of suggestions made by antimicrobial stewardship program (ASP) pharmacists in patients with enterococcal bacteremia. Secondary Objective: To describe the types of suggestions made by ASP stewardship pharmacists.

METHODS: A pharmacist-led antimicrobial stewardship service implemented in September 2020 at four Canadian tertiary care centres involved an ASP pharmacist reviewing patients with enterococcal bacteremia for compliance with treatment guidelines/quality performance measures and providing recommendations to the admitting service on weekdays. An infectious diseases (ID) physician was available for consultation at the pharmacist's discretion. Suggestions were noted as fully or partially accepted and implemented or rejected. Patients with positive blood cultures for *Enterococcus* species were identified prospectively using microbiology laboratory-generated daily reports. Key stewardship suggestions included: usage of anti-enterococcal therapies, repeat blood cultures documenting clearance of bacteremia, screening echocardiography for infective endocarditis, and formal ID consultation. An informational backgrounder published in January 2022 was used to support guideline adherence.

RESULTS: From September 2020 to September 2023, the ASP pharmacy team made 190 evidence-based recommendations for 100 patients with Enterococcus bacteremia. 68 and 24 were completely and partially accepted, respectively, for an overall acceptance rate of 92/100 (92%) in patients with suggestions. The most frequent recommendations were ID consultation (43%), assessment/diagnostic tests (24%), and antimicrobial changes (23%).

CONCLUSION: ASP-led intervention for patients with enterococcal bacteremia, in conjunction with clinician education, improves quality performance measures. Targeting this patient population would represent an excellent opportunity for other ASPs to optimize care.

WP003

Evaluating the feasibility of a reflex testing algorithm for *Neisseria gonorrhoeae* culture and NAAT co-testing requests

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OBJECTIVE: Multidrug-resistant (MDR) *Neisseria gonorrhoea* (GC) is an increasing public health threat. Diagnostic assessment for GC typically includes collecting two specimens: one for GC culture to guide treatment and monitor MDR emergence, and another for rapid and sensitive nucleic acid amplification testing (NAAT). This approach challenges resource stewardship as most collected specimens will be NAAT negative, eliminating the need for GC culture. This study evaluated a reflex testing algorithm, attempting a GC culture only for anatomic sites with a positive NAAT result. GC viability was assessed to confirm whether a culture deferral before a positive NAAT result was available is a reliable approach.

METHODS: Results from Dynacare requisitions, including both GC NAAT and culture requests, from January 1, 2020, to June 30, 2023, were retrieved and summarized by anatomic site for analysis. GC viability was assessed by contriving 10 isolates into residual cervical specimens in Copan Transystem M40 Amies media and incubating at room temperature (RT) for up to 72 hours.

RESULTS: During the study, 1,205 unique individuals met the inclusion criteria for GC NAAT and culture cotesting. Among these, 1,143 showed no detectible GC by either method. 62 exhibited detectable GC by either NAAT or culture, with 38/62 positive by both NAAT and culture, 15/62 positive by NAAT only, and 9/62 positive by culture only. In every case, NAAT-negative and culture-positive specimens from the same individual were obtained from two distinct anatomic sites, suggesting localized infection only. Stability studies revealed consistent isolation of viable GC from

residual cervical specimens up to 48 hours at RT (10/10), decreasing to 7/10 at 72 hours.

CONCLUSION: No cases of GC culture-positive and NAAT-negative individuals were found at the same anatomic site. GC culture was reliable up to 48 hours after collection, suggesting the feasibility of a reflex testing algorithm.

WP004

Characterization of daptomycin use in leukemia bone marrow transplantation, intensive care, and solid organ transplant patients at a Canadian tertiary hospital

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OBJECTIVE: To characterize the use of daptomycin in the leukemia/bone marrow transplant (LBMT), intensive care unit (ICU), and transplant services at our hospital and to identify opportunities to promote optimal prescribing of daptomycin.

METHODS: This was a retrospective chart review of all adult inpatients admitted under the LBMT, ICU, and transplant services who received daptomycin from January 1, 2018, to December 31, 2021.

RESULTS: We identified 249 courses of daptomycin in 210 patients. During the 4-year period, we confirmed the use of daptomycin has increased (301 courses in 2018 versus 415 courses in 2021). The most common type of infection requiring daptomycin was bacteremia ($d = 154$, 62%), and the most common pathogen identified was VRE ($d = 135$, 54%). Forty-three percent of daptomycin courses were consistent with formulary restriction criteria. Reasons for not meeting criteria included no positive culture ($d = 53$, 21%), other gram-positive infection susceptible to alternatives ($d = 45$, 18%), and a nonbacteremia VRE infection susceptible to alternatives ($d = 26$, 10%). Most daptomycin courses were classified as empiric therapy ($d = 154$, 62%), with only 32% ($d = 49$) of those cases consistent with formulary restriction criteria.

CONCLUSION: Daptomycin use at our hospital has increased in recent years. With less than 50% compliance in our daptomycin restrictions, education and antimicrobial stewardship opportunities exist to promote optimal prescribing of daptomycin.

WP005

Crafting double-drug antibiograms for enhanced antimicrobial precision

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OBJECTIVE: Broad-spectrum empiric antimicrobial therapy is crucial for patients presenting with febrile neutropenia. Antibiograms typically provide susceptibility coverage for single drugs. The study analyzed antimicrobial susceptibility data for double-drug combinations and compared them to local hospital guidelines for treatment of febrile neutropenia.

METHODS: Susceptibility data for 2018 to 2022 blood culture isolates from a cancer hospital serving a large urban area were presented in an antibiogram following 2022 CLSI M100/M39 guidelines. Susceptibility to piperacillin-tazobactam and tobramycin, meropenem and tobramycin, ceftazidime, and tobramycin, piperacillin-tazobactam and ciprofloxacin, meropenem and ciprofloxacin, and ceftazidime and ciprofloxacin combinations were compared against recommendations for empiric treatment from local hospital-based guidelines.

RESULTS: Gram-negative isolates had an associated 68% weighted average susceptibility to piperacillin-tazobactam. When paired with tobramycin or ciprofloxacin, the percent susceptibility rose to 91% and 88%, respectively. A similar increase was seen for ceftazidime, where there was 66% susceptibility to the drug alone, which increased to 91% and 88% when paired with tobramycin and ciprofloxacin, respectively. Percent susceptibility for meropenem stayed relatively stable at 96% when considered alone or when paired with ciprofloxacin, and 97% when paired with tobramycin. Gram-positive isolates did not show changes in susceptibility with the combinations studied. Local hospital febrile neutropenia hospital guidelines vary with one hospital recommending treating with piperacillin-tazobactam alone and another recommending treatment with a combination of piperacillin-tazobactam with tobramycin or with meropenem alone.

CONCLUSION: For gram-negative blood isolates from cancer hospital patients, the efficacy of piperacillin-tazobactam and ceftazidime is increased when paired with tobramycin or ciprofloxacin. Meropenem alone demonstrated high percentage of susceptibility. Centres suggesting the use of piperacillin-tazobactam alone should recognize the limitations of its coverage and the added coverage provided by combination treatment. It is valuable for institutions to incorporate combination drug susceptibility data into their antibiograms to help guide empiric recommended treatments.

WP006

Evaluation of antibiotic prophylaxis for perioperative infections in vascular surgery: A retrospective analysis at Vancouver General Hospital

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OBJECTIVE: To assess the concordance of antimicrobial prophylaxis practices with national and local guidelines in patients undergoing vascular surgery at Vancouver General Hospital (VGH). Additionally, we sought to identify the incidence and rationale for extended postoperative antimicrobial usage, along with potential risk factors associated with postoperative complications following vascular surgery.

METHODS: A retrospective chart review was conducted on a randomly selected sample of 100 patients (aged ≥18 years old) who underwent vascular surgery in a non-ICU setting at VGH between November 1, 2022, and October 31, 2023. Electronic patient records provided data on baseline characteristics, surgery types, antibiotic choices, duration of antibiotic therapy, length of hospital stay, and postoperative complications. The analysis involved descriptive statistics and consultations with the statistician.

RESULTS: Our findings revealed that 56% (56/100) of cases adhered to national and local guidelines for antimicrobial prophylaxis in vascular surgery, while 44% (44/100) deviated from these recommendations. Nonconcordance to antimicrobial prophylaxis was predominantly observed in cases lacking specific surgery guidelines, use of higher than standard doses, and unnecessary prophylaxis in procedures, such as AV fistula, angioplasty, and endarterectomy. Notably, the guidelines at VGH lacked specificity for various vascular surgery types when compared to more comprehensive guidelines in Alberta and Toronto. Despite limited evidence supporting postoperative doses, 75% of patients (75/100) received either preoperative and postoperative doses or postoperative doses alone for antimicrobial prophylaxis.

CONCLUSION: Ensuring the conformity of vascular surgery antibiotic practices with local and national guidelines is crucial for effective hospital antibiotic stewardship. This project highlighted the need for more comprehensive local guidelines. Rationalizing preoperative and postoperative antimicrobial use, guided by evidence, and enhancing guidelines can optimize care, alleviate antimicrobial resistance, and reduce postoperative complications.

WP007

Guideline adherence of antibiotic prescriptions for urinary tract infections in a paediatric emergency department

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OBJECTIVE: Urinary tract infections (UTIs) are common bacterial infections in children. To limit antimicrobial resistance (AMR), it becomes imperative to adhere to local prescription guidelines, thus ensuring effective treatment. We evaluated the appropriateness of antibiotic prescriptions for UTIs in a paediatric emergency department (ED) by identifying protocol deviations.

METHODS: Charts of patients diagnosed with a UTI at a tertiary care paediatric ED between January and December 2022 were randomly sampled for evaluation. The primary outcome was the percentage of appropriate empiric prescriptions, defined on the basis of compliance with hospital guidelines (antibiotic class and dose). Independent variables included age, sex, medical history (urinary tract abnormalities, prior UTIs, vesicoureteral reflux), travel history, allergies, maximum temperature, urine sampling methods, laboratory results, and identified bacterial strains. Each chart review was standardized, and interrater reliability was established for 5% of participants. Ambiguous diagnoses were reviewed by an emergency paediatrician

and a paediatric infectious diseases/medical microbiologist. The primary analysis determined the percentage of appropriate prescriptions for cystitis and pyelonephritis. To obtain a narrow 95% confidence interval (±5%) for an estimated 50% appropriateness, 385 charts were needed.

RESULTS: Of the 449 reviewed charts, 358 were eligible. The median age was 34 months, 253 (70.7%) were females, and 96 (26.8%) were diagnosed with cystitis. Overall, 75 prescriptions (20.9%) were deemed inappropriate, with a higher proportion observed in cystitis cases (61.5%) compared to pyelonephritis (6.1%). Most inappropriate prescriptions were solely due to the chosen antibiotic class (61 cases, 81.3%).

CONCLUSION: We found 79.1% of antibiotic prescriptions for UTIs to be appropriate in this paediatric ED. However, 61.5% of the prescriptions for cystitis were inappropriate. This study highlighted multiple opportunities for more stringent adherence to guidelines to reduce inappropriate antibiotic use, and it identifies specific situations well suited for improved antibiotic stewardship.

WP008

S. aureus skin and soft tissue (SSTI) isolate sensitivities in northern Manitoba and northwestern Ontario communities seen in the context of empiric therapeutic decision making

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OBJECTIVE: Oral clindamycin plus an IV/oral cephalosporin is a commonly used initial empiric therapy for SSTI in northern Manitoba (MB) and northwestern Ontario region communities, in which previous studies have demonstrated MRSA prevalence. We reviewed *Staphylococcus aureus* SSTI isolate sensitivity data in the context of local clinical practice.

METHODS: SSTI specimen isolates of *S. aureus* were analyzed from 20 reserve communities in northern MB (which refer to HSC Winnipeg Laboratory, January–December 2022) and 28 in Sioux Lookout (SL) region (which refer to SL Meno Ya Win Health Centre Laboratory, April 2021 to December 2023).

RESULTS: *S. aureus* was cultured from 965 and 1,586 SSTI specimens from MB and SL communities, respectively. All isolates from both regions were vancomycin sensitive. For MB, 50% of isolates were MRSA, with sensitivities: clindamycin 78%, TMP-SMX 99%, and tetracycline 99%. For SL isolates, 36% were MRSA, with sensitivities: clindamycin 89%, TMP-SMX 98%, and tetracycline 98%. Primary health care workers (HCWs) in both regions use a variety of sources to guide clinical practice. Intravenous vancomycin is normally restricted to initiation of therapy, with additional use requiring transfer to a referral centre.

CONCLUSION: Regional differences were observed in SSTI MRSA isolate sensitivity to clindamycin and are relevant to clinical practice. The development of local agreed upon treatment guidelines informed by laboratory, clinical and epidemiologic data, as well as the sharing of experience and practice across comparable health care settings, are encouraged to support evidence-based decision making.

WP009

Improving aminoglycoside resistance surveillance and stewardship efforts through nomenclature harmonization with the Comprehensive Antibiotic Resistance Database

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OBJECTIVE: Multidrug-resistant pathogens continue to challenge aminoglycoside antibiotics with the spread of genetic elements encoding aminoglycoside-modifying enzymes (AMEs). Unfortunately, these enzymes have a discordant naming history that further complicates treatment plans and surveillance efforts. In collaboration with the Comprehensive Antibiotic Resistance Database (CARD), we are undertaking the management and adoption of a single AME nomenclature. We will abide by the guidelines first proposed in the late-1970s, while incorporating additional rules accounting for the scale at which sequencing technology permits AME discovery.

METHODS: We have completed a literature review to collect cell-based and biochemical data supporting the characterization of AMEs identified to date. CARD will utilize these data in the development of a software to guide researchers in the classification of new and existing AME variants. Additionally, CARD will provide software

to evaluate AME benchmarks and recommend available namespace, resolve conflicts, or suggest additional analyses, if applicable.

RESULTS: After conducting a full review of the AME terminology in the antibiotic resistance ontology (ARO), CARD has updated the ARO to categorize AMEs with the aforementioned nomenclature guidelines. Where possible, this includes resolution of conflicting allele names, although there are several outstanding for which community feedback is required. The revised ontology is reflective of AME biochemistry and phenotype, with strict definitions for each allele family based on antibiotic susceptibility testing. Planning of a web interface to assist authors in naming and analyzing proposed novel AMEs is under way.

CONCLUSION: Going forward, novel published AMEs will only be included in CARD if, or once, they have a unique proper name. There remains an ongoing process to review existing AMEs and resolve naming conflicts, for which CARD will engage authors and the research community for feedback. Overall, clearer naming conventions will allow clearer communication for tracking and understanding AMEs from the clinical and One Health perspective.

WP010

Bridging the gap: Unveiling the crucial role of *Mycobacterium* antibiograms in antimicrobial precision

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OBJECTIVE: Antibiograms focus on nonmycobacterial bacteria, leaving *Mycobacterium* species underserved. Despite ATS/ERS/ESCMID/IDSA guidelines for treating nontuberculous mycobacterial pulmonary disease, susceptibility testing is recommended for targeted therapy. This study collated mycobacteria susceptibility in an antibiogram format for a hospital network and compared results against existing treatment guidelines.

METHODS: Antibiotic susceptibility data for mycobacteria isolated from all specimen types from 2018 to 2022 at four major academic hospitals were collected. The provincial reference centre speciated these isolates, and broth microdilution was completed at the national microbiology laboratory. Employing CLSI guidelines (M39-Ed5), results were analyzed for an antibiogram, then compared against established guidelines for generalizability.

RESULTS: A total of 48 mycobacteria had susceptibility testing completed between 2018 and 2022. *M. avium* isolates ($n = 26$) had 100% susceptibility to clarithromycin, 0% to amikacin, and untested susceptibility against rifampicin and ethambutol. ATS/ERS/ESCMID/IDSA guidelines suggest treating with a combination of drugs for *M. avium* with macrolide, rifampicin, ethambutol, and amikacin; antibiogram data suggest clarithromycin is the most suitable choice with unclear additional coverage with the addition of rifampicin and ethambutol and no role for the addition of amikacin. *M. abscessus* isolates ($n = 7$) had 100% susceptibility to amikacin, 57% to clarithromycin, 43% to linezolid, and 0% to imipenem, while tigecycline and clofazimine were untested. Guidelines for *M. abscessus* recommend parenteral drugs like amikacin, imipenem, or tigecycline, and orally administered azithromycin, clofazimine, or linezolid. Susceptibility data suggest amikacin as having the best empiric coverage followed by clarithromycin and linezolid, with no role for imipenem, and an unclear role for clofazimine and linezolid. *M. xenopi* and *M. kansasii* had insufficient isolates for conclusive susceptibility data.

CONCLUSION: Small numbers of mycobacteria isolated and tested for susceptibility limit extrapolation from antibiogram data. Notwithstanding this limitation, institutions should encourage susceptibility testing of mycobacteria and monitor susceptibility data, recognizing that published treatment guidelines may not reflect local susceptibility patterns.

WP011

Implementation of an antimicrobial stewardship intervention to improve management of bacteriuria and candiduria in hospitalized adults

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OBJECTIVE: Implement and evaluate a multifaceted antimicrobial stewardship (AMS) intervention on antimicrobial prescribing for bacteriuria and candiduria.

METHODS: A multifaceted, theory-informed AMS intervention that included virtual education and unit-level audit and feedback was developed and delivered by our research team. Our team included clinicians with expertise in infectious diseases and antimicrobial stewardship. A synchronous case-based virtual education session for health care providers was delivered October 26 and November 1, 2022. Audits were completed retrospectively using administrative records for patients with a positive urine culture on hospitalist units (HUs) at 4 community hospitals in Nova Scotia (NS). Antimicrobial prescribing appropriateness was assessed by pharmacists and an infectious diseases physician on the research team. An on-site clinical pharmacist champion delivered feedback to multidisciplinary HU teams providing direct care to patients every 1–2 months for 1 year. Appropriateness of antimicrobial prescribing was compared before (November 1, 2021, to October 31, 2022) and after (November 1, 2022, to October 31, 2023) implementation of the intervention using Chi-squared analysis. A time series analysis is under way.

RESULTS: During the study period, 27.5% of 3,426 urine cultures completed on study patients were reported positive. Preimplementation, 318 patient encounters were included, and 302 encounters were included postimplementation. Overall appropriateness of antimicrobial prescribing and use of antimicrobials for asymptomatic bacteriuria (ASB) before and after implementation of the intervention showed little change (55.9% versus 56.3%; p = NS) and (60.3% versus 57.6%; p = NS), although intervention impact varied by hospital. Two study sites showed a 10.7%–15.7% decrease in the proportion of patients with ASB receiving an antimicrobial, while 2 study sites showed a similar increase in antimicrobial use for ASB.

CONCLUSION: Inappropriate antimicrobial prescribing for bacteriuria and candiduria remains common in NS. Further research is needed to define facilitators and barriers to successfully implement interventions to improve antimicrobial prescribing in this population.

WP012

Decreasing antibiotic use in infants is correlated with a declining asthma incidence rate at the population level, 2000–2019

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OBJECTIVE: Asthma is the most prevalent chronic disease of childhood and a leading cause of hospitalization. Our prior study, conducted between 2000 and 2014, revealed an association between antibiotic use before the age of 1 and incidence of asthma diagnosis aged 1–4 years. In this study, we extend our analyses from 2000 to 2019, exploring this association at the local health area level and assessing the impact of number of antibiotic courses.

METHODS: Our province-wide study utilized community antibiotic prescription data from PharmaNet and asthma diagnoses from the Chronic Disease Registry. A negative binomial quantile regression model was employed to estimate the association between the average antibiotic prescription rate in the first year of life and asthma incidence at 1–4 years of age, stratified by periods between 2000 and 2014 and 2015 and 2019.

RESULTS: Between 2000 and 2014, the adjusted incidence rate ratio (aIRR) for asthma in children aged 1–4 was 1.75 ($p < 0.001$), with a 31% decrease in asthma incidence and a 62% reduction in antibiotic prescribing. From 2015 to 2019, asthma incidence dropped by an additional 15%, accompanied by a 38% decline in antibiotic prescribing. The aIRRs for asthma fell to 1.11 ($p < 0.55$). The proportion of infants exposed to antibiotics decreased from 66% in 2000 to 30% in 2014 and further to 20% in 2019. For 4+ antibiotic courses, aIRRs predicting asthma were 1.66 ($p < 0.001$) between 2000 and 2014 and 1.33 ($p < 0.04$) from 2015 to 2019.

CONCLUSION: A significant association between antibiotic prescription and asthma incidence was observed from 2000 to 2014. This association was observed to have weakened in the period from 2015 to 2019, except for the groups that had 4+ antibiotic courses. A weakening association may result from a reduction in those exposed to multiple prescriptions.

WP013

The impact of CLSI M100E33 Enterobacterales aminoglycoside breakpoint changes on available treatment options for β-lactam-resistant organisms in Canada

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OBJECTIVE: The Clinical and Laboratory Standards Institute (CLSI) has recently revised the long-held susceptibility breakpoints for aminoglycosides (AMG) in 2023. The impact of these changes on Canadian institutions remains unexplored. We described trends in Enterobacterales AMG resistance data from our institution, particularly for extended β-lactam-resistant organisms for which limited treatment options are available.

METHODS: We retrospectively analyzed the first isolate per patient per year from January 1, 2022, to December 31, 2022, at an academic acute care hospital. Susceptibility of each isolate to AMGs was interpreted using the 2022 and updated 2023 breakpoints. Relevant changes in the percent of isolates susceptible (%S) to a given antibiotic were summarized for the Enterobacterales and for isolates identified as producing select β-lactamase enzymes.

RESULTS: A total of 2,650 unique Enterobacterales isolates were identified. While overall changes in susceptibility for Enterobacterales in aggregate were small, a moderate decrease in susceptibility to amikacin and tobramycin among Class A ESBL-expressing Enterobacterales was noted (Table WP013-1). Carbapenemase-producing Enterobacterales (CPE) were found to have significant resistance to all AMGs at baseline.

Table WP013-1: Changes in susceptibility for Enterobacterales.

All Enterobacterales ($N = 2650$)	CLSI 2022 %S	CLSI 2023 %S	Change in %S
Amikacin	99.80%	99.00%	− 0.80%
Gentamicin	94.60%	94.40%	− 0.20%
Tobramycin	94.40%	92.80%	− 1.50%
Enterobacterales expressing AmpC ($N = 136$)			
Amikacin	99.30%	97.80%	− 1.50%
Gentamicin	89.70%	89.70%	0.00%
Tobramycin	93.40%	91.20%	− 2.20%
Enterobacterales expressing ESBL ($N = 221$)			
Amikacin	99.10%	92.70%	− 6.40%
Gentamicin	73.30%	73.30%	0.00%
Tobramycin	64.70%	61.50%	− 3.20%
Enterobacterales expressing carbapenemases ($N = 4$)			
Amikacin	50.0%	50.0%	0.0%
Gentamicin	25.0%	25.0%	0.0%
Tobramycin	0.0%	0.0%	0.0%

CONCLUSION: With increasing AMG resistance in Enterobacterales, even modest changes in CLSI breakpoint values may put Canadians at risk if novel antimicrobial agents are not available. AMG activity against Enterobacterales is variable, although amikacin remains the most active agent. Additionally, baseline AMG resistance is significant in CPE and should be considered when choosing empiric therapy, particularly in patients with CPE risk factors.

WP014

In vitro antibacterial activity of some plant infusions against biofilm-forming methicillin-resistant *Staphylococcus aureus*

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OBJECTIVE: The objective of the study was to investigate the antibacterial and anti-biofilm properties of plant infusions *Entada abysinnica* (leaves), *Croton macrostachyus* (leaves), *Bridelia speciosa* (seeds, bark), and *Aframomum melegueta* (leaves, seeds, and stem) collected in Southwestern Nigeria against a panel of three strains of biofilm-forming MRSA.

METHODS: The plant infusions were extracted using a heat-assisted ultrasound method, and the bacterial species were standardized in relation to the McFarland standard. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of the plant infusions were determined by the broth dilution method, and the anti-biofilm assay of the most potent plant infusion was performed.

RESULTS: Four medicinal plants producing seven infusions (different parts of some plants were used) were investigated for their antibacterial activity using the broth microdilution method and an anti-biofilm assay. They include *E. abysinnica*, *C. macrostachyus*, *B. speciosa*, and *A. melegueta*. The MIC results showed that they exhibited antibacterial activity against MRSA at varying concentrations. The antibacterial activity of the plant infusions ranged from 0.156 mg/mL to 5.0 mg/mL, and the MBC ranged from 0.625 mg/mL to 5.0 mg/mL. The infusions of *B. speciosa* (bark) and *A. melegueta* (seeds) showed the best activity, while their seeds and stem showed weak activity, respectively. On the basis of the MIC/MBC ratio, the infusions of these plants were determined to be bactericidal and bacteriostatic in nature. The anti-biofilm assay showed that the infusions of *A. melegueta* (seeds) and

B. speciosa (bark) fairly inhibited the growth of MRSA in the preformed biofilm matrix.

CONCLUSION: These four medicinal plants may represent a good source of alternative antibacterial agents. Many scientific studies have reported their antibacterial activities, and they have a long history of use in folklore medicine, hence drawing the attention of scientists globally who daily explore their antibacterial potential.

WP015

Antimicrobial susceptibility of *Neisseria gonorrhoeae* isolates in Yaoundé, Cameroon

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OBJECTIVE: Gonorrhea and antimicrobial resistance (AMR) in *Neisseria gonorrhoeae* are public health problems globally. Quality-assured AMR data from Africa, particularly Central-Western Africa, is mainly lacking. The objective of this study is to investigate the resistance to therapeutically relevant and/or used antimicrobials in *N. gonorrhoeae* isolates from 2009 to 2014 in Yaoundé, Cameroon, and recommend revisions of the National Sexual Transmitted Diseases (STD) treatment guideline in Cameroon.

METHODS: Gonococcal isolates ($n = 193$) cultured from outpatients, 129 (66.8%) males and 64 (33.2%) females, at different hospitals or health centres in Yaoundé, Cameroon from January 2009 to December 2014 were tested for susceptibility to seven antimicrobials using disc diffusion method (Etest to confirm suspected ceftriaxone resistance).

RESULTS: High resistance to benzylpenicillin (93.3%), tetracycline (58.5%), and nalidixic acid that reflects ciprofloxacin (17.6%; increasing from 3.8% to 50% during 2009–2014) were observed. However, the resistance level to ceftriaxone, azithromycin, spectinomycin, and chloramphenicol were low (i.e., 0%, 2.6%, 3.1%, and 7.3%, respectively). Overall, 80.3% of isolates were producing penicillinase.

CONCLUSION: Multidrug-resistant gonorrhea is a major public health concern internationally, and quality-assured gonococcal AMR surveillance is crucial globally. In Africa, particularly central-western Africa, appropriate AMR surveillance for gonococci has mainly been lacking. Our current results will inform revisions of the National STD Treatment Guideline in Cameroon, i.e., to replace ciprofloxacin with ceftriaxone as the recommended first-line treatment of urethral discharge. It is essential to further strengthen the surveillance of *N. gonorrhoeae* AMR in Cameroon, and most countries in the WHO African Region, which requires national and international support, including technical support, and political and financial commitment.

WP016

Off-label use of dalbavancin to improve treatment outcomes and reduce health care costs: A single-centre quality improvement initiative

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OBJECTIVE: Dalbavancin is approved for use in Canada for the treatment of skin and soft tissue infections (SSTIs), with increasing evidence of effectiveness for treating other serious gram-positive infections. However, its use in British Columbia is currently cost-prohibitive. We present a single-centre quality improvement case-series of dalbavancin use in infections other than SSTIs in socially marginalized patients. Our goal was to facilitate access to this novel antimicrobial to improve treatment outcomes and identify potential health system savings.

METHODS: We established an unrestricted hospital-specific rapid access compassionate provision program for dalbavancin from Paladin Labs, Inc. Patients were considered for treatment with dalbavancin at the discretion of an Infectious Diseases Specialist if they had susceptible gram-positive infections. Patients provided informed verbal consent. Data was collected via retrospective chart review. All patients were offered outpatient Infectious Diseases follow-up. We compared cost savings using a cost calculator developed by Paladin Labs, Inc.

RESULTS: Between September 2022 and 2023, six patients received dalbavancin for blood stream and musculoskeletal infections. The most common indications for use included allowing early discharge from hospital and improved treatment adherence. Three patients had infection cure, and three patients were presumed to have infection cure but were lost to outpatient follow-up. One patient in our study died, unrelated to the dalbavancin-treated condition. There were no reported adverse events. There were significant cost

savings when comparing dalbavancin to standard of care treatment, primarily driven by reduced inpatient hospital days.

CONCLUSION: Dalbavancin may improve treatment adherence and outcomes for socially marginalized patients with serious gram-positive infections, while saving healthcare costs by facilitating earlier discharge from hospital. Our preliminary experience highlights the need for additional controlled studies to evaluate expanded indications for dalbavancin, as well as innovative approaches to increase access and facilitate coverage for novel antibacterial agents in our cost-constrained health system.

WP017

Phage science, therapeutics, and research: The Public Health Agency of Canada's new Phage Therapy Program

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OBJECTIVE: In response to the increased prevalence of antimicrobial resistance seen throughout the country, the Public Health Agency Canada (PHAC) has funded a 5-year pilot project to support phage therapy within Canadian clinics. The new Phage Science, Therapeutics, and Research (PhageSTAR) unit within the One Health Division of the National Microbiology Laboratory Branch aims to establish a phage library and screening processes to facilitate personalized phage mixtures tailored to isolates from individual patients' infections.

METHODS: The PhageSTAR program will be implemented over a multi-year timeline, beginning with a comprehensive effort to create a phage library and to validate high-throughput screening methods with a goal of leveraging in silico prediction. Environmental samples from ongoing national programs, notably wastewater, will be used to isolate additional phages targeting priority pathogens, such as *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella pneumonia*. Once established, clinicians will then be able to submit clinical isolates for screening against the phage library to identify a combination of phages, which can be formulated for patient administration.

RESULTS: The PhageSTAR program has just launched, and we are beginning engagements with stakeholders.

CONCLUSION: The program seeks to lessen the burden of antimicrobial resistance on the health care system and prolong the lifespan of antibacterials currently in circulation. The target of this program is to have successfully facilitated the treatment of 4 Canadians through phage therapy by the end of 2025 while establishing strong collaborations with both domestic and international partners. Furthermore, by engaging in both the regulatory and biopharmaceutical processes required for the creation of these therapeutics, the PhageSTAR pilot aims to significantly advance phage therapy and phage science for clinicians, researchers, and the biopharmaceutical industry alike.

WP018 - WITHDRAWN

WP019

Ceftobiprole usage in Canada: Final results from the CLEAR Registry

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OBJECTIVE: We report the final results for ceftobiprole usage in Canada from the national CLEAR (Canadian LEadership on Antimicrobial Real-life usage) Registry.

METHODS: The CLEAR Registry is coordinated by the Canadian Antimicrobial Resistance Alliance (CARA). It is a national, ethics-approved, voluntary study using a Web-based research data management program (REDCap), which allows clinicians across Canada to share their experiences when treating patients with ceftobiprole using an online survey: https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=A8EHM8JJRF.

RESULTS: Final results for 100 patients (as of December 1, 2023) are presented. The most common infections treated

were endocarditis (39% of patients), bone/joint infection (24%), hospital-associated bacterial pneumonia (8%), community-acquired bacterial pneumonia (8%), acute bacterial skin and skin structure infection (ABSSSI; 8%), and device-related infection (6%). 94% of patients had bacteremia, and 32% started or completed treatment in an intensive care unit. Ceftobiprole was used primarily as directed therapy, and MRSA (95%) was the most common pathogen. Ceftobiprole was used with daptomycin (46% of patients), or vancomycin (20%), daptomycin and vancomycin (5%), or as monotherapy (23%). Ceftobiprole was used following clinical failure of previous antimicrobial therapy (73%), resistance to initially prescribed antimicrobials (12%), or adverse effects associated with previously used antimicrobials (13%). The most common ceftobiprole dosages were 500 mg Q8h (67%), 500 mg Q12h (12%), and 250 mg Q24h (12%). Treatment duration was generally >10 days (66% of patients) with microbiological success in 96% and clinical success in 85% of patients. Overall mortality was 11%, and infection-related mortality was 8%. Five percent of patients reported an adverse effect, with one resulting in drug discontinuation.

CONCLUSION: In Canada, 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 shows an excellent safety profile.

WP020

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

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OBJECTIVE: We report results from the national CLEAR Registry on ceftolozane/tazobactam (C/T) use in Canada to treat hospital-acquired bacterial pneumonia (HABP), ventilated hospital-acquired bacterial pneumonia (vHABP), and ventilator-associated bacterial pneumonia (VABP).

METHODS: A C/T usage questionnaire was developed with input from physicians/pharmacists across Canada. The CLEAR Registry uses the Web-based research data management program REDCap (https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=WHWT7RDK7X) to facilitate clinicians voluntarily entering details of their clinical experiences using C/T.

RESULTS: Data were available for 54 patients. C/T was used to treat VABP (46.3%), vHABP (31.5%), and HABP (22.2% of patients). 7.4% of patients had bacteremia; 81.5% were in the ICU. C/T was used as directed (79.6%) and empiric therapy (20.4%) for documented/eventually documented *Pseudomonas aeruginosa* infections (98.1% of patients). C/T susceptibility testing was performed on isolates from 90.7% of patients. C/T was used in combination with another antimicrobial active versus gram-negative bacilli in 35.2% of patients (IV or aerosolized aminoglycosides [47.4%], IV or aerosolized colistin/polymyxin B [21.1%], fluoroquinolones [15.8%], and carbapenems [10.5%]). C/T was used primarily because of resistance to previously prescribed antimicrobials (94.4%). The most common dosages of C/T were 2 g (1 g) Q8H and 2 g (0.5 g) Q8H, with the dosage regimen customized in all patients based on their creatinine clearance. Treatment duration was primarily >10 days (44.4% of patients) with 50.0% microbiological success and 61.2% clinical success. Overall, 30-day mortality was 20.4%. 7.4% of patients had adverse effects with one patient requiring drug discontinuation.

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

WP021

How and why clinicians use IV fosfomycin in Canada: Results from the national CLEAR (Canadian LEadership on Antimicrobial Real-life usage) registry

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OBJECTIVE: Data on the use of IV fosfomycin in Canada are limited. We report the use of IV fosfomycin in Canadian patients using data captured by the CLEAR Registry.

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

RESULTS: Data were available for 77 patients (as of December 4, 2023). Infections treated included: bacteremia/sepsis ± a documented site of infection (26.0% of patients), complicated urinary tract infection (17.9%), ventilator-associated bacterial pneumonia (17.9%), hospital-acquired bacterial pneumonia (14.9%), complicated intra-abdominal infection (8.9%), bone/joint infections (4.5%), community-acquired bacterial pneumonia (4.5%), and endocarditis (3.0%). IV fosfomycin was used to treat gram-negative (92.2%) or gram-positive (7.8%) infections. The most common pathogens treated were carbapenem-resistant Enterobacterales (CRE) (45.3%), MDR *Pseudomonas aeruginosa* (19.4%), extended-spectrum β-lactamase (ESBL)-producing Enterobacterales (10.4%), vancomycin-resistant *Enterococcus faecium* (VRE) (5.1%), and MRSA (2.6%). IV fosfomycin was used primarily as directed therapy (86.8% patients) and typically prescribed as part of combination therapy (87.2%). Fosfomycin was prescribed due to resistance to other antimicrobial agents (73.7%), clinical failure of previous therapy (17.1%), or adverse effects associated with use of previous agents (9.2%). Microbiological success (pathogen eradicated/presumed eradicated) occurred in 78.1% and clinical success (clinical cure/improvement) in 62.9% of patients; 13.0% of patients died due to their infection. Adverse effects were not documented in 70.7% of patients, and no patient discontinued therapy due to adverse effects.

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

WP022

IV dalbavancin usage in Canada: Results from the CLEAR Registry

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OBJECTIVE: We report the results for dalbavancin usage in Canada from the national CLEAR (Canadian LEadership on Antimicrobial Real-life usage) Registry.

METHODS: The CLEAR Registry is coordinated by the Canadian Antimicrobial Resistance Alliance (CARA). It is a national, ethics-approved, voluntary study using a Web-based research data management program (REDCap), that allows clinicians across Canada to share their experiences when treating patients with dalbavancin using an online survey: https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=TPMWJX98HL.

RESULTS: The results for 19 patients (as of December 4, 2023) are presented. The most common infections treated were acute bacterial skin and skin structure infection (ABSSSI; 68.4% of patients), bone/joint infection (15.8%), endocarditis (10.5%), and bloodstream/vascular infection (5.3%). Dalbavancin was used both as directed therapy (73.7%) and empiric therapy (26.3%). MRSA was

the most common identified pathogen (57.9%), followed by unknown (26.3%) and *Streptococcus* spp in (15.8%). Dalbavancin was used in an outpatient treatment setting (e.g., emergency department) (57.9%), an inpatient treatment setting (e.g., hospital ward) (31.5%), an OPAT clinic (5.3%), or in an infectious disease clinic (5.3%). Dalbavancin was primarily used because of the convenience of a single-dose treatment (84.2%) or following clinical failure of previous antimicrobial therapy (15.8%). Dalbavancin was primarily used alone (84.2%), and most commonly using a single 1,500 mg dose (73.7%). Microbiological success (pathogen eradicated or presumed eradicated) occurred in 100% of known cases, while clinical success (cure and/or improvement) occurred in 100% of known cases. No adverse events were reported.

CONCLUSION: In Canada, IV dalbavancin is used as both directed and empiric therapy to treat a variety of on-label and off-label infections. It is primarily used because of its convenience as a single-dose treatment regimen, in both outpatient and inpatient settings. Dalbavancin use is associated with high microbiological and clinical cure rates along with an excellent safety profile.

WP023

In vitro activity of cefditoren, a new-to-Canada oral third-generation cephalosporin, against community-acquired respiratory tract, skin/soft tissue, and urinary tract infection pathogens isolated from Canadian patients: CANWARD 2015–2020

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OBJECTIVE: Cefditoren pivoxil is an oral third-generation cephalosporin under review by Health Canada. We compared the in vitro activities of cefditoren and other oral antimicrobials against respiratory, skin/soft tissue and urinary pathogens causing infections in Canadian patients collected by the CANWARD study from 2015 to 2020.

METHODS: We studied 1,021 clinical isolates. Antimicrobial susceptibility testing was performed with cefditoren and eight oral comparator antimicrobials using custom-designed microbroth dilution panels as per CLSI methods (M07, 11th edition, 2018).

RESULTS: The activity of cefditoren and selected comparators versus various pathogens and resistance phenotypes is depicted in Table WP023-1.

CONCLUSION: Cefditoren was 4–8 times more active than cefuroxime and amoxicillin/clavulanate versus *S. pneumoniae*, including PEN-I and PEN-R phenotypes. Cefditoren was 128–256 times more active than cefuroxime and amoxicillin/clavulanate versus *H. influenzae* and 16-32 times more active versus *H. parainfluenzae*. Ceftditoren was significantly more active than cefuroxime and amox-

Table WP023-1: Activity of cefditoren and selected comparators versus various pathogens and resistance phenotypes.

Pathogen/ Phenotype (*n*)	Cefditoren (MIC_{50}/MIC_{90}/range) µg/mL	Cefuroxime (MIC_{50}/MIC_{90}/range) µg/mL	Amoxicillin/Clavulanate (MIC_{50}/MIC_{90}/range) µg/mL
Streptococcus pneumoniae			
All (479)	≤0.015/0.06/≤0.015–1	≤0.25/0.5/≤0.25–8	≤0.06/0.25/≤0.06-–8
PEN-S (394)	≤0.015/≤0.015/≤0.015–0.12	≤0.25/0.5/≤0.25–2	≤0.06/≤0.06/≤0.06–0.12
PEN-I (64)	0.06/0.5/≤0.015–0.5	≤0.25/4/≤0.25–4	0.12/2/≤0.06–2
PEN-R (21)	0.5/1/≤0.015–1	4/8/4–8	4/8/1–8
Haemophilus influenzae			
BLN (30)	≤0.015/≤0.015/≤0.015–0.03	2/4/0.5–8	0.5/2/0.12–4
BLP (69)	≤0.015/≤0.015/≤0.015–0.25	1/2/≤0.25–4	1/4/0.12–4
Haemophilus parainfluenzae (48)	≤0.015/0.25/≤0.015–0.5	0.5/4/≤0.25–8	0.5/8/≤0.06–>32
Moraxella catarrhalis (95)	0.06/0.5/≤0.015–1	1/2/≤0.25–2	≤0.06/0.25/≤0.06–0.5
MSSA (70)	1/1/0.5–2	Not tested	0.5/2/0.12–2
Streptococcus pyogenes (30)	≤0.015/≤0.015/≤0.015	≤0.25/≤0.25/≤0.25	≤0.06/≤0.06/≤0.06
Streptococcus agalactiae (30)	0.03/0.06/≤0.015–0.06	≤0.25/≤0.25/≤0.25	≤0.06/0.12/≤0.06–0.12
Escherichia coli (150)	0.25/>8/0.12–>8	Not tested	8/16/1–32
Klebsiella pneumoniae (20)	0.25/>8/0.12—>8	Not tested	2/8/1–>32

PEN-S, penicillin-susceptible MIC ≤0.03 µg/mL; PEN-I, penicillin-intermediate MIC 0.06–1 µg/ml; PEN-R, penicillin-resistant MIC ≥2 µg/mL; BLN, β-lactamase-negative; BLP, β-lactamase-positive; MSSA, methicillin-susceptible *Staphylococcus aureus.*

icillin/clavulanate versus pathogens causing community-acquired respiratory tract infections.

WP024

Phage therapy in the management of urinary tract infections: A comprehensive systematic review

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OBJECTIVE: Urinary tract infections (UTIs) affect almost half a billion people each year. Increasing antibiotic resistance and limited therapeutic options have led to the exploration of alternative therapies for UTIs, including bacteriophage (phage) therapy. This systematic review aims at evaluating the efficacy of phage therapy in treating UTIs.

METHODS: A systematic review was conducted in conformity with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines and following Cochrane methodology. We employed a comprehensive search strategy for any language, any animal, and any publication date prior to the conclusion of our search on November 18, 2022. Eligibility screening and critical appraisal were performed by two independent reviewers, and a third reviewer resolved disagreements. Data extraction was completed with validation by an additional reviewer. Critical appraisal of case reports and case series was completed in accordance with Joanna Briggs Institute (JBI) guidelines. Randomized control trials underwent critical appraisal using the Critical Appraisal Skills Program (CASP) checklist.

RESULTS: A total of 55 in vivo and clinical studies were included from 1805 screened articles. Of the studies, 22% were published in a non-English language; 32.7% of included manuscripts were published before the year 1996. Subgroup analysis of phage therapy in human subjects identified more than 1400 unique UTIs treated with phage. Of those specified, ~79% showed marked clinical improvement/cure, with only 4% of those treated having no clinical improvement. When reported, adverse events occurred in 1.3% of treatments.

CONCLUSION: More than 72% of the included articles reported microbiological and clinical improvements, yet there are only 5 randomized controlled trials included in the analysis. Case reports and case series information were frequently incomplete for analysis. Overall, this comprehensive systematic review identifies preliminary evidence supporting the potential of phage therapy as a safe and viable option for the treatment of UTIs.

WP025

A replica plating method for efficient, high-throughput screening of antibiotic gene clusters in bacteria uncovers a holomycin-like cluster in the clinical isolate *Pantoea agglomerans* 20KB447973

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OBJECTIVE: As antimicrobial resistance continues to outpace the development of novel therapeutics, the treatment of multidrug-resistant (MDR) infections continues to become more challenging. Natural products from bacteria are a major untapped source for novel antimicrobial scaffolds. Many of these products are encoded by biosynthetic gene clusters (BGCs), which can be identified using functional genomics. Although effective, these approaches are often labour-intensive, without robotics or automation. We developed a replica-plating approach to quickly screen for antibiotic production mutants from transposon mutant libraries to identify candidate antibiotic BGCs.

METHODS: In our mutant transfer technique, filter paper is used to transfer up to 200 mutants simultaneously onto a soft agar overlay containing a target microbe to identify antibiotic production mutants. These mutants can then be analyzed to identify disrupted genes and antibiotic BGCs. We first tested and optimized this technique by successfully reidentifying three previously identified BGCs in *Pantoea*. We then used this technique to uncover the gene cluster responsible for producing an unknown broad-spectrum antibiotic from the clinical isolate *P. agglomerans* 20KB447973.

RESULTS: Analysis of the predicted gene cluster in *P. agglomerans* 20KB447973 showed similarity to previously identified gene clusters for the broad-spectrum dithiolopyrrolone antibiotic, holomycin. This study is the first to report a holomycin-like BCG in *Pantoea*. We also identified

the production of a second antibiotic, pantocin A, in *P. agglomerans* 20KB447973. Analysis of the spectrum of activity of the holomycin-like antibiotic from *P. agglomerans* 20KB447973 showed activity against members of the Enterobacteriaceae, Erwiniaceae, and Streptococcaceae, including clinically relevant pathogens like *Klebsiella pneumoniae* and *Escherichia coli*.

CONCLUSION: Our findings demonstrate the usefulness of our replica-plating mutant transfer method in exploring unknown antibiotic BCGs. Adoption of this technique by others could allow for quick and simple exploration of potentially novel antimicrobial BCGs within laboratory strain collections, advancing the search for novel antimicrobials to fight MDR pathogens.

WP026

Epidemiology of *Streptococcus pneumoniae* serotypes 15A, 15C, 16F, 23A, 23B, 24F, 31, and 35B, causing invasive pneumococcal disease (IPD) in Canada: Coverage of V116, a new 21-valent conjugate pneumococcal vaccine in the SAVE Study, 2018–2021

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OBJECTIVE: V116 is a 21-valent pneumococcal conjugate vaccine being developed specifically for adults. V116 covers serotypes first included in PCV13 (3, 6A, 7F, 19A), PCV15 (22F, 33F), PCV20 (8, 10A, 11A, 12F), and PPSV23 (9N, 17F, 20A) vaccines, as well as 8 unique serotypes (15A, 15C, 16F, 23A, 23B, 24F, 31, 35B). We assessed serotype coverage of V116 in adult patients and isolate demographics for the 8 unique serotypes in V116 in Canada.

METHODS: The SAVE study, in collaboration with PHAC-NML, collected IPD isolates from Canadian provincial public health and hospital laboratories. Serotype was determined by Quellung reaction, and broth microdilution AST was performed by CLSI methods.

RESULTS: From 2018 to 2021, the SAVE study collected 5,189 isolates from adult patients aged ≥18 years. For patients aged 18–49 years, V116 covered 72.3% of isolates (963/1,332) compared with 82.8% for PPSV23 and 69.2% for PCV20. In patients aged 50–64 years, V116 covered 76.2% of isolates (1,294/1,696) compared with 75.1% for PPSV23 and 60.2% for PCV20. In patients aged ≥65 years, V116 covered 78.2% of isolates (1,689/2,161) compared with 62.4% for PPSV23 and 52.4% for PCV20. The 8 V116-unique serotypes accounted for 11.7%, 15.4%, and 25.1% of isolates from patients aged 18–49, 50–64, and ≥65 years, respectively. For adults ≥50, V116 covered 75.9% (530/698) of isolates in Western Canada, 77.2% (2,200/2,851) in Central Canada, and 82.1% (253/308) of isolates in Eastern Canada. V116 unique serotypes demonstrated resistance to clarithromycin (13.5%), clindamycin (24.5%), doxycycline (14.8%), and penicillin (5.5%).

CONCLUSION: In 2018—2021 in Canada, V116 covered more IPD serotypes than PCV20 for all adults, and more IPD serotypes than PPSV23 in patients aged ≥50 years. In this timeframe, the 8 V116-unique serotypes accounted for 25% of isolates from patients aged ≥65 years. Common MDR isolates causing IPD, including serotypes 19A and 15A, are covered by V116.

WP027

Comparison of PCV-20 and PPSV-23 vaccine coverage of *Streptococcus pneumoniae* (SPN) serotypes in Canada: The SAVE Study, 2018–2021

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OBJECTIVE: A polysaccharide vaccine covering 23 pneumococcal serotypes (PPSV-23) has been licensed in Canada since 1983. In 2022, Health Canada licensed a conjugate vaccine covering 20 pneumococcal serotypes (PCV-20). The two formulations cover 19 common serotypes, with serotype 6A unique to PCV-20 and serotypes 2, 9N, 17F, and 20 unique to PPSV-23. Some clinicians recommend PCV-20 replace PPSV-23 because of similar formulation and because conjugate vaccines are more effective at preventing both invasive pneumococcal disease (IPD) and community-acquired bacterial pneumonia than polysaccharide vaccines. The objective of this study was to compare PCV-20 and PPSV-23 coverage of recent Canadian SPN isolates collected by the SAVE study.

METHODS: From 2018 to 2021, the SAVE study, in collaboration with the PHAC-NML, collected 5,854 IPD isolates

from Canadian provincial public health and hospital laboratories. Serotypes were determined by the Quellung reaction and broth microdilution antimicrobial susceptibility testing performed by CLSI methods.

RESULTS: Of the 5,854 isolates, 3,443 (59.1%) were covered by PCV-20 compared to 4,121 (73.3%) by PPSV-23. The isolates covered by PPSV-23 included 388 (6.6%), 235 (4.0%), and 71 (1.2%) with serotype 9N, 20, and 17F, respectively. For isolates from those aged 50–64 ($n = 1,696$) and ≥65 ($n = 2,161$), PPSV-23 covered 75.1% (1,273) and 62.5% (1,350) respectively, while PCV-20 covered 60.2% (1,021) and 52.4% (1,133), respectively. Isolates from all patients aged ≥50 ($n = 3,857$) included 591 (15.3%) with serotype 9N. Compared to PCV-20, PPSV-23 covered similar numbers of isolates resistant to chloramphenicol (188 versus 191 isolates, respectively), clarithromycin (976 versus 1,008), clindamycin (216 versus 229), doxycycline (357 versus 381), penicillin (93 versus 95), and trimethoprim-sulfamethoxazole (257 versus 267).

CONCLUSION: PPSV-23 covered a higher proportion of SAVE isolates compared to PCV-20, primarily due to serotypes 9N and 20, which represented ~11% of IPD isolates in Canada in 2018–2021. Both formulations covered similar numbers of isolates with AMR phenotypes.

WP028

A novel data structure for prediction of phenotypic antimicrobial resistance based on whole genome sequencing

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OBJECTIVE: Whole-genome sequencing (WGS) is revolutionizing microbiology, but WGS technologies for antimicrobial resistance (AMR) prediction for typical bacteria are not ready for clinical use. Multiple tools exist that can accurately find AMR genes, but there is a lack of standardization in interpreting and reporting this information. Current tools often present irrelevant or inaccurate AMR predictions in unintuitive formats. Our objective is to create a novel data structure for communicating phenotypic predictions of AMR based on WGS analysis in a format that is useful for clinical practice.

METHODS: Whole genomes from representative bacterial isolates were analyzed using the Resistance Gene Identifier software and formatted using hAMRonization specifications. Rules for phenotypic AMR predictions derived from the published literature were applied to these data, and CLSI M100 guidelines were referenced to derive a reporting structure. Predicted phenotype was compared with conventional phenotypic susceptibility testing done by VITEK 2.

RESULTS: We created a novel data structure for presenting phenotypic AMR predictions, which can be easily converted to a format useful to clinicians. This structure is organized antibiotic-first and only reports clinically relevant antibiotics. AMR determinants are listed for each affected antibiotic to allow for both 1:1 gene-antibiotic associations and complex rules that consider multiple genes. This structure is extensible to predictions based on gene expression or machine learning analysis. Additional columns with genotypic data or metadata produced earlier in the bioinformatics pipeline are included in the output file but are optional for the clinician. Reported antibiotics, interpretations, and comments can be modified by the user based on local practice and new evidence.

CONCLUSION: We created a data structure for reporting WGS predictions of AMR in typical bacteria, which can be incorporated into bioinformatics pipelines to create susceptibility prediction reports that are useful for clinicians and can be extended for future developments in AMR bioinformatics.

WP029

Assessment of hybrid assembly methods for accurate plasmid reconstruction in carbapenemase-producing organisms

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OBJECTIVE: Health-care-associated infections caused by carbapenemase-producing organisms (CPOs) are increasing in Canada, largely due to carriage of carbapenemase genes on highly transmissible plasmids. Identifying plasmid-mediated CPO transmission events in health care settings requires accurate characterization of CPO plasmids. Using both short-(Illumina) and long-read (Oxford Nanopore Technologies) sequencing platforms,

this study aimed to evaluate three hybrid plasmid assembly methods to identify the optimal approach.

METHODS: CPO reference strains from ATCC, with available whole genome sequences, were used as the "gold standard" to evaluate the accuracy of plasmid reconstruction methods. These ATCC strains were streaked on selective agar plates, and three colonies were resuspended in separate culture broths and grown overnight. DNA was extracted, and library DNA preparations were prepared in triplicate from each for Illumina and ONT sequencing platforms. Sequences were assembled using Unicycler (https://github.com/rrwick/Unicycler), Dragonflye (https://github.com/rpetit3/dragonflye), and Plassembler (https://github.com/gbouras13/plassembler). A plasmid was considered "recovered" if a single-contig, "circularized" plasmid assembly within ±5% of the size of the corresponding ATCC plasmid sequence was generated. The minimum-acceptable sequence accuracy of the resulting plasmid sequences required ≥95% sequence identity, relative to the ATCC plasmid sequence.

RESULTS: Plassembler performed the best compared to the other hybrid assembly methods. This assembler recovered 98% of the plasmids ranging from ≥100 kb to <10 kb in size, followed by Unicycler, which recovered 88.2% of the plasmids. Dragonflye performed well in recovering large- to medium-sized plasmids (10 kb to ≥100 kb) but could not recover plasmids <10 kb. Additionally, all hybrid assembly methods produced plasmid assemblies with ∼99% sequence identity relative to the ATCC plasmid sequences.

CONCLUSION: We demonstrate that Plassembler hybrid assembler method can reliably reconstruct single-contig, circularized plasmid assemblies with ≥99% sequence identity of the corresponding reference plasmid sequence. Moving forward, we recommend that Plassembler hybrid assembly method be used to reconstruct plasmid assemblies for CPOs.

WP030

Does increased vancomycin MIC increase the risk of complications in patients with methicillin-sensitive *Staphylococcus aureus* blood stream infections? A retrospective review

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OBJECTIVE: *Staphylococcus aureus* (SA) is a common cause of community and hospital-associated infections, including bloodstream infection (BSI). For methicillin-resistant *S. aureus* (MRSA) BSI, studies have demonstrated worse outcomes when the vancomycin minimum inhibitory concentration (MIC) is ≥1.5 mg/L. Limited studies in patients with methicillin-sensitive *S. aureus* (MSSA) BSI indicate that a higher vancomycin MIC is associated with treatment failure, suggesting that reduced vancomycin susceptibility is a marker for poorer prognosis. This study explored the outcome of patients with MSSA-BSI in relation to the vancomycin MIC.

METHODS: A retrospective chart review of 268 patients with MSSA-BSI admitted to the hospital between October 2015 and June 2018 was conducted. Patients were divided into low (<1.5 mg/L) or high (≥1.5 mg/L) vancomycin MIC groups. The primary outcome was all-cause mortality at 90 days after onset of the MSSA-BSI. The secondary outcomes were cure with or without complications. Additional information gathered included demographics, comorbidities, investigations, management, and antibiotic treatment.

RESULTS: Of the 268 patients, 102 (38.1%) were female, and the mean age was 61.3 years. The proportion of patients with a vancomycin MIC of <1.5 mg/L and ≥1.5 mg/L was 79.1% (212/268) and 20.9% (56/268), respectively. All-cause mortality at 90 days was 12.7% (27/212) and 17.9% (10/56), respectively. There was a trend toward improved cure without complications in the low versus high MIC group (53.3% [112/210] versus 42.6% [23/54] respectively), but this did not reach statistical significance.

CONCLUSION: MSSA BSI is a common cause of mortality and complications. In our study, elevated vancomycin MIC demonstrated a trend toward higher mortality and associated complications. A larger study will be necessary to determine whether this association is statistically significant.

WP031

Virulence actors and cellular interactions of *Staphylococcus aureus* in bovine mammary epithelial cells

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OBJECTIVE: This study aimed to investigate the interaction of *S. aureus* virulence factors in the adhesion and invasion of bovine mammary epithelial cells (MAC-T).

METHODS: Polymerase chain reaction (PCR) was performed to detect microbial surface components recognizing adhesive matrix molecules (MSCRAMMs), such as fbnA, fbnB, fib, clfA, clfB, can, eno, ebpS, and the agr cluster (I, II, III, IV) on 10 isolates from clinical mastitis (5 mild and 5 moderate) and 5 from subclinical mastitis. Subsequently, the cells were cultured in 24-well microplates, forming confluent layers. *S. aureus* cultures (1.5×10^6 CFU/mL) were inoculated in duplicate wells at 37°C/5% CO_2. After 3 hours, cells were detached with trypsin-EDTA, stopped with DMEM, and seeded on TSA plates. For invasion, bacterial suspensions were incubated, treated, and plated to check for intracellular bacteria. Triton X-100 was added to lyse cells, and dilutions were plated on TSA. Positive invasion results were determined by colony recovery and counting, relative to adhesion test values.

RESULTS: Our results indicated that subclinical strains exhibited a lower adhesion rate compared to clinical strains. Conversely, all subclinical strains were agr-negative and presented one MSCRAMMs gene, resulting in a higher invasion rate than moderate and mild clinical strains carrying agr type II and III genes and three or more MSCRAMMs genes.

CONCLUSION: These results emphasize that the presence of agr may favor the expression of MSCRAMs, increasing the adhesion capacity of the strain. Highlighting the intricate link between disease factors and clinical severity, stressing the importance of understanding bacterial genetic composition for predicting harm.

WP032

Characterization of enterotoxin-producing *S. aureus* isolated from the hands and nose of food handlers

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OBJECTIVE: In this study, we examined 27 *Staphylococcus aureus* isolates obtained from the noses and hands of food handlers.

METHODS: The isolates DNA was extracted and using polymerase chain reaction (PCR), the research targeted the protein A gene (*spa*) and 27 enterotoxin-producing genes, encompassing both classical SEs (*SEA*, *SEB*, *SEC*, *SED*, and SEE) and nonclassical ones (*SEG*, *SEH*, *SEI*, *SElJ*, *SEK*, *SEL*, *SEM*, *SEN*, *SEO*, *SEP*, *SEQ*, *SER*, *SES*, *SElU*, *SElV*, *SElW*, *SElX*, *SEY*, *SEZ*, *SEl01*, *SE02*, and *SEl26*).

RESULTS: The isolates were categorized into 14 spa typing groups, with 37% classified as t127, 11.1% as t002, 7.4% as t065, and the same percentage was found for t084. The remaining strains (44.5%) were distributed among 10 different spa groups. All strains carried at least 3 enterotoxin-producing genes, with *SEB* (96.3%), *SEX* (88.8%), and *SEW* (81.5%) being the most prevalent.

CONCLUSION: The diversity in spa groups suggests a widespread dissemination of *S. aureus* isolates among food handlers. Furthermore, the huge presence of enterotoxin-producing genes in all strains underscores the risk of food poisoning if proper hygiene measures are not observed during processing and handling.

WP033

Adhesion and invasion in Mac-T cells by *Escherichia coli* isolated from cows with clinical mastitis

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OBJECTIVE: This study aimed to evaluate the adhesion and invasion capabilities of *E. coli* isolates obtained from bovine mastitis cases, using three distinct isolates for each grade (mild, moderate, and severe).

METHODS: The cultivation of bovine mammary epithelial cells (Mac-T) occurred in 24-well microplates. Cultures of the nine isolates, incubated at 37°C/24 h in BHI broth, were diluted in Opti-MEM supplemented with 2% FBS, yielding a bacterial suspension containing 1.5×10^6 CFU/mL,

and it was added in duplicate to the wells, and the plate was incubated at 37°C/3 h at 5% CO_2. After being washed with PBS, the adhered cells were detached using trypsin. Concurrently, invasion tests were executed with adhesion tests. After 2 h with gentamicin, Triton X-100 0.1% was added to lyse the cells and release the invading bacteria. The invasion index was calculated on the basis of the recovery and enumeration of colonies, expressed as a percentage in relation to the values obtained in the adhesion test.

RESULTS: All isolates demonstrated the ability to adhere to Mac-T cells, with no significant differences observed in invasion rates among the various severity levels of the disease. However, upon individual analysis of each isolate, we observed a statistical difference between an isolate from mild mastitis and one from moderate mastitis, as well as between an isolate of moderate and one from severe grade.

CONCLUSION: On the basis of initial findings, it seems that invasion of host cells does not significantly contribute to the severity of mastitis induced by *E. coli*.

WP034

Reducing false positivity rates of *Neisseria gonorrhoeae* nucleic acid amplification testing using a two-stage molecular testing algorithm in a low prevalence population

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OBJECTIVE: Rates of *Neisseria gonorrhoeae* have increased across Canada to 81.1 per 100,000 population. Given the relatively lower prevalence in Nova Scotia at 9.0 per 100,000 population, *N. gonorrhoeae* testing includes an initial screen followed by confirmatory testing for positive or equivocal results. This study aimed to review the proportion of false positive screening tests in Nova Scotia among various anatomic sites.

METHODS: Specimens were initially tested for *N. gonorrhoeae* (and *Chlamydia trachomatis*) using the Aptima Combo 2 Assay on the Hologic Panther instrument. Specimens testing positive or equivocal for *N. gonorrhoeae* were confirmed using the Aptima *Neisseria gonorrhoeae* assay. Positive or equivocal screening tests for *N. gonorrhoeae* and confirmatory results were compared from swabs (throat, rectal, vaginal, or other) and urine were collected from January 2018 to December of 2023. A positive screen followed by a negative confirmatory test was considered a false positive, and the overall proportion of false positives was described by specimen type.

RESULTS: Of 1,287 confirmatory tests during this period, negative results were obtained on 58 occasions, equating to 4.5% of screening tests being falsely positive. Similar trends were seen over the years, with the highest overall proportion of false positives observed in the throat swabs at 6.27% (20/319), followed by vaginal swabs at 5.25% (16/305), urine at 4.47% (20/447) and rectal swabs at 0.53% (1/189). Only a small number of other swabs (9 cervical, 8 urethral, 5 penal, and 2 miscellaneous) screened positive for *N. gonorrhoeae*, and 4.17% (1/24) was a false positive.

CONCLUSION: False-positive test results for *N. gonorrhoeae* have significant implications, including patient stigma, unnecessary treatment of patients and close contacts, while leading to increased workload for physicians and public health. In areas with low *N. gonorrhoeae* prevalence, a two-stage molecular testing algorithm is useful in reducing false-positive results.

WP035

Genomic analysis of environmental and clinical isolates of *Vibrio parahaemolyticus* collected from 1999 to 2022 in the Pacific Coast

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OBJECTIVE: *Vibrio parahaemolyticus* (Vp) is a prominent cause of gastroenteritis in humans through the consumption of contaminated seafood. Although *tdh* and *trh* have traditionally been used as potential genomic indicators of virulence during risk assessment, some clinical isolates contain neither gene. We performed whole genome sequencing (WGS) of clinical and environmental Vp isolates in order to

1) identify genomic virulence predictors that could facilitate the molecular risk assessment of environmental isolates, and 2) identify genomic markers of antimicrobial resistance (AMR).

METHODS: WGS was conducted on 653 Vp isolates collected between 1999 and 2022: 310 clinical and 343 environmental. Abricate (using Virulence Factor Database) and AMRFinderPlus were used to identify genes associated with virulence and AMR, respectively. Chi-squared tests were used to identify significant proportions of virulence factors and AMR genes between clinical and environmental isolates. A genome-wide association study was conducted, and Fisher's exact test was conducted on each detected gene to compare their presence in clinical and environmental isolates.

RESULTS: A total of 13 (4.2%) clinical and 235 (68.5%) environmental isolates were negative for both *tdh* and *trh*. Multiple virulence factor genes were found in a significantly higher proportion in clinical isolates, including *tdh, trh*, v*crV*, *VopB*, *VP1611*, and *VopQ* ($p < 0.001$). Carbenicillin-hydrolyzing class A β-lactamase genes (*blaCARB-30* and *blaCARB-34*) were more commonly found in clinical isolates ($p < 0.001$). A genome-wide study demonstrated over 30 genes associated with type III secretion systems and urease enzymes found in a significantly higher proportion in clinical isolates ($p < 0.001$).

CONCLUSION: This study forms a baseline genomic understanding of Vp. Virulence factor and AMR genes that could potentially facilitate genomic risk assessment of environmental isolates were identified. The identification of virulence and AMR genes provides a basis for future in-depth pathogenicity and AMR investigations of Vp isolates. This knowledge is vital for enhancing the ability to predict, prevent, and manage Vp outbreaks.

WP036

Antimicrobial susceptibility patterns of Viridans Group Streptococci in a Canadian tertiary care centre

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OBJECTIVE: To describe susceptibility patterns of viridans group streptococci (VGS) between species and patient populations in a Canadian setting.

METHODS: A total of 624 patient specimens growing VGS were analyzed over 18 months. Susceptibility testing was performed using gradient diffusion for penicillin, ceftriaxone, and vancomycin. The number of susceptible and non-susceptible specimens were compared between VGS species and between patient populations using the chi-square test. Because of supply shortages, some penicillin-susceptible isolates were not separately tested for ceftriaxone and vancomycin ($n = 244$; 49.9%).

RESULTS: Overall, 584 specimens underwent susceptibility testing. The most frequently tested VGS species were the *Streptococcus anginosus* group (252 isolates; 43.2%), followed by the *S. mitis* group (214 isolates; 36.6%). There were 489 specimens susceptible to penicillin (83.7%). The *S. salivarius* group had the highest rate of penicillin nonsusceptible isolates (42% [95% CI 28 to 56]), followed by the *Streptococcus mitis* group (31.3% [95% CI 25.10 to 37.52]) compared to the *S. anginosus* group (2.4% [95% CI 0.50 to 4.28]) and the *S. bovis* group (1.7% [95% CI 0.00 to 4.98]). Only the *S. mitis* group demonstrated nonsusceptibility to ceftriaxone (3.9%). There were three isolates in the *S. anginosus* group and one isolate in the *S. salivarius* group that demonstrated MICs >1 to vancomycin. There was a higher incidence of nonsusceptible isolates to penicillin in the specimens from cancer wards (28.6% [95% CI 13.60 to 43.54]) versus specimens from non-cancer wards (15.5% [95% CI 12.45 to 18.51]); $p = 0.042$. Nonsusceptibility rates in paediatric versus adult patient specimens were 30.8% (95% CI 13.03 to 48.51) versus 15.6% (95% CI 12.58 to 18.60); $p = 0.058$.

CONCLUSION: There are significant differences in susceptibilities between VGS species, with high rates of penicillin nonsusceptibility in the *S. salivarius* and *S. mitis* groups. There was also a higher proportion of penicillin nonsusceptible isolates in specimens from cancer wards versus specimens from non-cancer wards. This study provides Canadian data that supports broader empiric gram-positive coverage for VGS infection, especially in septic and neutropenic patients.

WP037

Evaluation of the use of a VITEK MS MALDI research database in the identification of rare bacterial species in a clinical laboratory

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OBJECTIVE: MALDI-ToF is the primary method of bacterial identification in most clinical microbiology laboratories. Rare bacteria are often not included in MALDI clinical databases, requiring referral of these isolates to reference laboratories for final identification. The aim of this study was to evaluate the clinical utility of using a research MALDI database, Saramis 4.17, to provide a presumptive identification for hard to identify bacteria and ultimately to prevent delays in patient care.

METHODS: We included bacterial isolates from blood culture that did not yield a reliable identification from the clinical VITEK MS database from October 6, 2023 to January 5, 2024. Isolates were sent to the Public Health Ontario (PHO) Laboratory for external identification as per routine practice. The PHO-provided identification was compared to available organisms in both the current clinical and Saramis databases. Those isolates whose identification was only available in the Saramis database and not in the clinical database were then subcultured. The subcultured organisms were then run on the MALDI-ToF using the research database to determine whether the organism could be identified in our lab via this method.

RESULTS: Thirty-nine bacterial isolates were included. Five isolates had species identification only available in the Saramis database, 15 in both the clinical database and the Saramis database, and 20 species that were not available in either database. The turnaround time (TAT) of identification through use of a referral lab took a median of 9 days.

CONCLUSION: Twelve percent of hard to identify bacterial isolates from blood cultures are included in the VITEK MS MALDI Saramis 4.17 database, with the potential to reduce TAT. Use of the MS VITEK MALDI Saramis 4.17 database may be an effective strategy for the identification of a subset of less common bacterial species in a high-volume clinical microbiology laboratory.

WP038

Transmission dynamics and genotypic diversity of *Mycobacterium tuberculosis* in Colombian persons deprived of liberty

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OBJECTIVE: Between 2011 and 2017 in Central America, tuberculosis case notifications quadrupled in persons deprived of liberty (PDL). The changing understanding of the continuum of the *Mycobacterium tuberculosis* spectrum underscores the importance of molecular epidemiology to elucidate transmission in highly overcrowded settings. Our study aims to show the genotypic diversity of *M. tuberculosis* strains present in Colombian prisons and examine disease clusters and transmission dynamics of *M. tuberculosis*.

METHODS: Sixty-four PDL incarcerated in two male and two female Colombian prisons were followed for 2 years (monthly during anti-tuberculosis treatment, bimonthly for 6 months, and quarterly during the second year). Among them, 132 *M. tuberculosis* strains were obtained, and 49 isolates were determined to be in clusters based on 24-mycobacterial interspersed repetitive unit typing. Demographic information was collected from participants. Strains were sequenced with Illumina MiSeq, and phylogeny was determined using a single nucleotide variant calling method, the SNVPhyl pipeline. The phylogenetic results will then be analyzed in conjunction with patient data to identify case clusters and transmission events.

RESULTS: Among 49 *M. tuberculosis* strains, individual and clusters of tuberculosis diagnoses within the prisons were identified. These clusters indicate active transmission within prisons. We identified reinfections, such as person 250 with diagnostic and follow-up strains in one cluster and presenting with a different strain a year later acquired from person 475 while sharing a cell. We also identified relapses, such as person 367 presenting a year later with the same strain. Further analysis will include the temporal and spatial distribution of persons diagnosed with tuberculosis within each prison and the identification of any potential factors associated with these clusters.

CONCLUSION: Our data show active tuberculosis transmission within these prisons. In the future, whole genome sequencing as a tool for tuberculosis surveillance and transmission dynamics within prisons should be considered when developing infection control and prevention strategies.

WP039

A visual job aid improves filling of adult blood culture bottles in emergency departments

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OBJECTIVE: Optimal detection of bacteremia relies on filling blood culture bottles with 8-10 mL of blood. Filling bottles with <8 mL of blood may lead to falsely negative growth and failure to diagnose bacteremia, which has significant patient safety implications. Most bottles collected in our local emergency departments are underfilled. The objective of this quality improvement project was to improve filling of adult blood culture bottles in the emergency departments using a visual job aid.

METHODS: A job aid poster was created for education of blood culture collectors and was circulated with the help of a memo on June 1, 2023, to key stakeholders in the emergency departments. Monthly mean filling volumes and proportions of underfilled bottles (volume <8 mL) in each emergency department (ED) were calculated with MYLA software using fill volume data of adult bottles measured by the BACT/ALERT VIRTUO automated blood culture system. These key quality indicators were compared before (November 1, 2022, to April 30, 2023) and after (May 1, 2023, to October 31, 2023) intervention.

RESULTS: Before our intervention, mean filling volumes (95% confidence interval) were 6.9 (6.5–7.2) mL at ED #1, 5.5 (5.2–5.7) mL at ED #2, and 4.4 (4.2–4.5) mL at ED #3. After circulation of the job aid, mean filling volumes (95% confidence interval) increased to 8.2 (7.9–8.4) mL at ED #1, 6.9 (6.5–7.3) mL at ED #2, and 5.5 (5.2–5.7) mL at ED #3. This statistically significant increase was sustained for at least 6 months after distribution of the job aid. There was a corresponding decrease in the proportion of underfilled bottles at all sites.

CONCLUSION: The visual job aid and memo circulated on May 1, 2023, led to a significant and long-lasting improvement in filling volumes of adult blood culture bottles collected in the emergency departments. Additional interventions, such as audit and feedback of individual collectors, will be undertaken to further improve blood culture bottle filling.

WP040

Virulence factors in *Staphylococcus aureus* obtained from chronic venous ulcers

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OBJECTIVE: Chronic venous disease can cause ulcers in the lower limbs, leading to socio-economic impact and a decline in the individual's quality of life due to reduced social participation and limitations in professional activities. These lesions can become infected by endogenous microorganisms (fomites) or exogenous microorganisms (from health care professionals), and *Staphylococcus aureus* is frequently involved due to its ability to produce biofilm and toxins such as leukocidins (*pvl/lukMF/lukAB/lukDE/hlgA/hlgC*), modulins (*psmA/psmB/hld*), exfoliatins (*eta/etb/etc*), and hemolysins (*hla/hlb*). This study aimed to characterize *S. aureus* from ulcers regarding the presence of the mentioned genes and biofilm production.

METHODS: We used 40 isolates of *S. aureus* obtained from 24 patients with chronic venous ulcers (open ulcers lasting more than 6 weeks), exhibiting at least two NERDS criteria (N, nonhealing wounds; E, exudative wounds; R,: red bleeding wound surface granulation tissue; D, debris yellow or black necrotic tissue on wound surface; S, smell or unpleasant odor from the wound). This work was approved by the Research Ethics Committee FMB/UNESP no. 3.055.504.

RESULTS: All isolates were biofilm producers, and the genes assessed were present in most isolates. The genes *hld, hlgA, hlgC, psmA* were identified in all isolates, while *psmB, lukAB, lukDE* were present in 87.5%, and *hla* in 85% of the isolates. The *pvl* gene occurred in only 20% of the isolates, and none of them presented exfoliatin genes (*eta/etb/etc*). The number of genes per isolate ranged from 4 to 10, with 33 (82.5%) isolates having 8–10 genes, demonstrating the high virulence potential of this bacterium.

CONCLUSION: Several investigated toxins can alter local immunity by stimulating proinflammatory cytokines that hinder healing, promoting deterioration of granulation tissue, and exudate. Furthermore, the presence of biofilm makes the isolates more resistant to antimicrobials, contributing to the low healing rate of these lesions.

WP041

Assessing the risk of *Mycobacterium tuberculosis* transmission by tissue transplantation

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OBJECTIVE: In the United States, several cases of tuberculosis (TB) have been acquired via bone grafts prepared by tissue banks in 2021 and 2023. Compliance with the requirements set forth by the American Association of Tissue Banks (AATB) involves documenting an assessment and a justification as to why the collected tissues are not subject to the ban on tissue donation containing living cells from donors over 65 years of age. Héma-Québec carried out such a risk assessment.

METHODS: A nonsystematic literature review and risk analysis was carried to estimate the risk of TB transmission via tissue transplantation in Québec (Canada). The gray literature and the Medline database (via PubMed) were reviewed, considering the collected tissues, donor qualification measures, and tissue preparation processes in place at Héma-Québec. The risk analysis was based on a deterministic model in which the risk of transmission was estimated as the product of three main proportions: prevalence of active and latent tuberculosis infection in tissue donors, the efficacy of treatment reduction, and the probability of a TB-positive tissue capable of transmitting the infection.

RESULTS: Few cases of *Mycobacterium tuberculosis* transmission by tissue transplantation have been reported and confirmed. The risk of collecting tissues with viable cells from deceased donors can be mitigated by a careful donor selection policy that considers epidemiological and clinical risk factors and sets reasonable age limits for specific tissue types. Bioburden reduction measures (e.g., skin decontamination, antibiotic treatments of allografts containing viable donor cells, and the terminal irradiation of musculoskeletal tissues) also reduce the risk of transmission. Overall, the risk of acquiring TB through tissue transplantation was estimated at 1 per 2,369,805 transplantations. Additional sensitivity analyses, considering tissue-specific characteristics, are under way.

CONCLUSION: This study suggests that tissue transplantations are associated with a negligible risk of acquiring TB.

WP042

Enhanced *Caenorhabditis elegans* in vivo infection model for screening new antimicrobial compounds against gram-positive and gram-negative bacteria

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OBJECTIVE: An initial *Caenorhabditis elegans* nematode model used for screening infection and rescue from *Enterococcus faecalis* has been enhanced to serve as an in vivo model for screening antimicrobial compounds against a wide range of bacteria.

METHODS: L4 stage AU37 *C. elegans* were infected with gram ± strains (*Staphylococcus aureus, E. faecalis*, *Escherichia coli*, *Pseudomonas aeruginosa*) at various time points. Treated with conventional antimicrobials, the time point of maximum rescue was identified. The model's efficacy was evaluated by testing known antimicrobial-susceptible and -resistant compounds using controls where % worm rescue = 100 − (mean death rate of rescue/mean death rate of control).

RESULTS: Maximum rescue was demonstrated at 48 h between control and conventional antimicrobial worm rescue with a mean rescue rate (MRR) of 92.6% (SD 3.0%) for *S. aureus* treated with 10 μg/mL of vancomycin; at 72 h with 88.8% (SD 2.8%) for *E. faecalis* with 50 μg/mL gentamicin; at 4 h with 90.3% (SD 3.5%) for *E. coli* with 50 μg/mL gentamicin; and at 72 h with 84.7% (SD 7.3%) for *P. aeruginosa* with 12.5 μg/mL gentamicin. All p values were <0.0001 (treatment versus control for each strain). Additional evaluations with antimicrobial-susceptible compounds (6.25, 12.5, 12.5 and 12.5 μg/mL chloramphenicol, tetracycline, tetracycline, and amikacin) for each strain demonstrated MRRs equivalent to that of the conventional antimicrobials, with 92.0% (SD 5.4%) rescue for *S. aureus*, 90.7% (SD 3.9%) for *E. faecalis*, 95.9% (SD 2.6%) for *E. coli*, and 90.5% (SD 3.6%) for *P. aeruginosa*, respectively, with no statistically significant difference. Antimicrobials that exhibited resistance (6.25, 12.5, 12.5 and 12.5 μg/mL erythromycin, erythromycin, tetracycline, and chloramphenicol, respectively) had similar MRRs to their control groups.

CONCLUSION: These data show that our enhanced *C. elegans* model may serve as a reliable in vivo infection model for identification of new antimicrobial compounds.

Future directions include examining dose-response MRR and the mechanism of rescue against each pathogen.

WP043

Improved spore recovery from clinical samples for metagenomic sequencing

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OBJECTIVE: With the expansion of molecular sequencing for infectious disease surveillance, targeted enrichment of clinically relevant pathogens will be important to ensure these populations can be accurately monitored using these methods. Bacterial spores, such as those from *Clostridioides difficile*, are often harder to detect in molecular sequencing due to their resistant structure. Thus, there is a need for improved spore enrichment protocols to allow for better recovery of spores and more accurate metagenomic monitoring of spore-forming pathogens from clinical samples.

METHODS: We conducted a comparative analysis between a published spore enrichment protocol (Browne) and a novel method (Tanabe) developed as part of this study. The investigation employed a *Bacillus subtilis* spore suspension and stool samples from 8 children with inflammatory bowel disease. Both protocols utilized ethanol to remove vegetative cells. In the Browne protocol, spores were recovered using PBS, while the Tanabe protocol utilized a mixture of Tween-80 and glass beads. Isolated spores were quantified using microscopy and characterized using V6-16S rRNA gene and shotgun metagenomic sequencing.

RESULTS: The Tanabe protocol recovered significantly more spores from the control spore suspension than the Browne protocol. Although both protocols effectively enriched for spore-forming taxa in patient stools, distinct taxonomic profiles were observed in the spores isolated from each protocol. This difference is attributed to the enhanced spore recovery achieved by the Tanabe protocol. In particular, the Tanabe protocol led to an enrichment of pathogens, including species belonging to *Anaeromassilibacillus* and *Actinomyces*, as compared to the Browne protocol.

CONCLUSION: Our optimized protocol allows for improved spore detection from clinical samples, resulting in an enrichment in spores revealed in the sequencing data. Routine metagenomic characterization of spore populations from clinical samples have the potential to allow for early detection of emerging toxigenic strains of spore-forming pathogens that may exist as spores prior to the onset of clinical disease.

WP044

A non-human primate model of human coronavirus HCoV-22E recapitulates aspects of respiratory disease observed in humans

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OBJECTIVE: Seasonal human coronaviruses (HCoVs) account for 10–30% of respiratory tract infections. However, there are relatively few animal models that exist to study pathogenesis and interventions. Nonhuman primates have been shown to be good models of moderate disease for SARS-CoV-2, suggesting they may also be suitable models for seasonal coronavirus infections. In our study, we describe a nonhuman primate disease model of infection with the seasonal coronavirus HCoV-229E.

METHODS: Male Rhesus macaques were challenged intranasally with the dose of 1.78×10^6 TCID50 of the HCoV-229E virus. Infectious virus was detected throughout the course of infection. In total six animals were included in the study; three were vaccinated with a fowl adenovirus-based recombinant SARS-CoV-2 vaccine before challenge in order to evaluate cross-protection.

RESULTS: Animals developed characteristic signs of an upper respiratory tract infection, including elevated body temperature, mild nasal discharge, and tracheobronchial lymph node enlargement. Hematological and biochemical markers showed a decrease in white blood cell counts following infection. Four weeks after infection, the primates were euthanized, and histopathological analysis of the lungs was performed to evaluate the extent of pulmonary disease. Mild fibrosis and inflammation were observed.

Interestingly, a group of animals that received the adenoviral-based SARS-CoV-2 vaccine and subsequent challenge with HCoV-229E showed reduced viral shedding and reduced lung pathology, suggesting low-level cross protection.

CONCLUSION: Our study demonstrated that the non-human primate model of HCoV-229E infection mimics aspects of disease observed in humans. Additionally, low levels of cross-protection were conferred to animals that received the recombinant fowl-adenoviral SARS-CoV-2 vaccine. This animal model, therefore, has the potential to expedite the development of vaccines and therapeutics for HCoV-229E as a representative model for seasonal coronaviruses.

WP045 - WITHDRAWN

WP046

Four-week HCV prophylactic antiviral strategy for HCV-viremic donors to HCV-negative kidney transplant recipients

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OBJECTIVE: There remains a critical organ shortage for kidney transplantation in Canada. By using organs from hepatitis C virus (HCV) viremic donors, the donor pool can be expanded. Options for managing recipients in such cases include early perioperative initiation of direct-acting antivirals (DAAs). This strategy has the potential to allow for shorter treatment courses, thereby reducing drug-associated costs. We developed a quality improvement initiative to evaluate the feasibility and efficacy of providing perioperative DAA therapy for an abbreviated 4-week course in HCV-viremic to HCV-uninfected kidney transplant recipients.

METHODS: Eligible patients included adult patients from Nova Scotia, who were HCV-uninfected. Donors were excluded if they had received prior DAA therapy or had chronic HBV or HIV coinfection. Recipients were excluded if they had chronic HBV or HIV coinfection or had established chronic liver disease. Adult HCV-naïve recipients of HCV-viremic kidney received glecaprevir-pibrentasvir perioperatively (within 6 hours of surgery) and continued for a 4-week course. The primary outcome of interest was the proportion of patients achieving sustained virologic response 12 (SVR12).

RESULTS: Of the 6 recipients included, 4/6 had HCV levels below quantification/detection by week 1 post-transplant, and 6/6 had HCV levels below detection at the end of 4 weeks of therapy. No patient had relapsed HCV viremia post-treatment, and 4 have reached SVR 12 thus far. There were no episodes of rejection among any recipient, and the average creatinine at the end of 4 weeks of therapy was 109 μmol/L.

CONCLUSION: Our shortened treatment approach shows safety and efficacy in patients receiving kidneys from HCV viremic donors. Also, it reduced treatment costs which encouraged insurance agencies to engage in this prophylactic course before HCV viremia in those recipients.

WP047

The effect of antiplatelet agents on end-organ dysfunction and mortality in community acquired pneumonia: A systematic review and meta-analysis

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OBJECTIVE: Community-acquired pneumonia (CAP) is a significant cause of morbidity and mortality worldwide. The host response to infection leads to inflammation and activation of coagulation cascades (immunothrombosis), increasing thrombotic risk in CAP. Antiplatelet agents have pleotropic effects with antithrombotic and anti-inflammatory activity. We performed a systematic review and meta-analysis to evaluate the effect of antiplatelet agents on mortality, cardiovascular events, and organ failure in adults hospitalized with CAP.

METHODS: Medline, Embase, CENTRAL, clinicaltrials.gov, and ICTRP were searched to identify randomized clinical trials (RCT) and observational studies meeting predefined inclusion criteria. Following PRISMA guidelines, article screening, data extraction, and risk of bias

assessments were completed by two blinded independent reviewers. Data were analyzed using random effects models, with statistical significance defined using a two-sided α of 0.05. Heterogeneity was defined using the I^2 statistic.

RESULTS: Fourteen observational studies (n = 125,363) and one RCT (n = 185) were included. Among observational studies, there was no significant difference in the pooled risk ratio of all-cause mortality in adults hospitalized with CAP comparing those who received antiplatelets to those who did not, though heterogeneity between studies was high (I^2 0.93). In the one included RCT, development of acute coronary syndrome was significantly decreased among those who received antiplatelets with relative risk of 0.10 (95% CI 0.01 to 0.75).

CONCLUSION: The effect of antiplatelet agents in adults hospitalized with CAP remains uncertain. RCT data suggest potential benefit; however, only one small trial has been completed. Observational data are highly heterogeneous, yielding conflicting results. Further randomized data are needed to determine the efficacy of antiplatelet agents in CAP.

WP048

'It's welcoming there': A qualitative analysis evaluating a community-based skilled nursing facility that supports patients with substance use disorders complete antibiotic therapy for severe bacterial infections

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OBJECTIVE: To assess the preferences and experiences of patients with substance use disorders who are hospitalized with severe bacterial infections and referred to complete antibiotic therapy at a specialized short-stay, community-based nursing facility (CNF). This study will provide a qualitative component to enrich the conclusions of a concurrent quantitative study of this facility.

METHODS: Patients with substance use disorders, who were admitted to an acute care hospital with a severe bacterial infection, stabilized, and then referred to the CNF for completion of at least 2 weeks of intravenous antibiotic therapy, were recruited for the study. Semistructured interviews were conducted at two time points: 1) at the time of study enrollment, while still in hospital and 2) at the end of their antibiotic treatment. Interviews were transcribed verbatim and subjected to two rounds of inductive coding. A second researcher reviewed the codes, and disagreements were handled through discussion. Thematic analysis was used to identify themes to describe the participants' preferences and experiences.

RESULTS: Thirty-six patients hospitalized with severe bacterial infections were recruited over a 9-month period. Thirty-nine percent of patients had no fixed address. Interviews were available from 33 patients, only 24 of whom were ultimately transferred to the CNF. Most participants expressed a preference to complete their antibiotics at CNF, and the experiences of those that stayed at CNF were overwhelmingly positive. Preliminary thematic analyses identified four major themes: *previous treatment failures and the inadequacy of current living situations, escape from the hospital environment, value of nonjudgmental personalized care, and the CNF feeling like home.*

CONCLUSION: This qualitative study contributes to the existing literature by exploring the preferences and experiences of patients with substance use disorders with severe bacterial infections. These results provide a valuable addition to quantitative evaluations of effectiveness and cost considerations of specialized community-based models of care.

WP049

Donor diversity in fecal Microbiota transplantation: microbial composition differences in donor stool microbiomes

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OBJECTIVE: Fecal microbiota transplantation (FMT) is a treatment option for recurrent *Clostridioides difficile* infection and is being explored as a therapy for other indications. A FMT program based in an urban metropolitan region

performs rigorous clinical and microbiology laboratory-based screening tests on stool donors. Age, BMI, medication history, high-risk activity, and physical and mental health are assessed within eligibility criteria. The aim of this work was to determine the microbial diversity in donor stool from individuals who passed all screening tests to donate in a FMT program.

METHODS: Three stool donations from five stool donors (two female and three male) were collected ($n = 15$), each 2-4 months apart (average = 3 months (1st and 2nd donation) and 2.8 months (2nd-3rd donation) and processed for 16S rRNA gene sequencing (V4 region) using the Illumina MiSeq (Illumina, CA). Bacterial microbiome analysis was complete with the UNOISE pipeline (USEARCH v11.0.667 and VSEARCH v2.10.4), QIIME1 and FastTree. Relative abundance, alpha and beta diversity were determined.

RESULTS: Relative abundance, alpha and beta diversity of bacterial species in samples were consistent within donors but significantly different across donors. Genus level relative abundance profiles were similar between Donors 1 and 2, and Donors 3 and 4. Donor 5 had a dissimilar profile with a significantly higher abundance of *Prevotella* spp compared to all other donors. Samples from Donor 4 had the greatest species richness and evenness, whereas samples from Donor 5 had the lowest alpha diversity.

CONCLUSION: Although stool donors are subjected to the same eligibility criteria and screening tests to donate in a FMT program, the composition of stool microbiomes significantly differ across donors. These compositional differences may be attributed to early childhood exposures, epigenetics, donor diet, and lifestyle influences including exercise and personal stressors. FMT programs should consider incorporating these additional variables in their donor screening criteria.

WP050

Factors associated with a positive urine culture in paediatric patients with a diagnosis of urinary tract infections in the emergency department

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OBJECTIVE: Diagnosing pediatric urinary tract infections (UTIs) in the emergency department (ED) is challenging, given unclear infectious focus and imperfect urinalysis sensitivity and specificity. Accurate diagnosis is critical to avoid unnecessary treatment and oversight of alternative diagnoses. This study aims to identify factors associated with positive urine cultures in pediatric ED patients diagnosed with presumptive UTIs.

METHODS: This secondary analysis of a retrospective cohort study involved patient charts with presumptive UTI diagnoses in a tertiary paediatric ED from January to December 2022. The primary outcome was positive urine cultures ($\geq 50 \times 10^6$ CFU/L). Independent variables included demographic variables, medical history, clinical presentation, urine sampling methods, laboratory results, and bacterial strains. Ambiguous diagnoses were reviewed by an emergency pediatrician and a pediatric infectious diseases/medical microbiologist. Retrospectively, it was estimated that analyzing 350 charts would yield more than 100 negative and 200 positive urine cultures, allowing the evaluation of 10 independent variables with 10 outcomes for each. Univariate and multivariate logistic regression identified factors associated with positive urine cultures.

RESULTS: Of 449 charts reviewed, 358 met eligibility. Median age was 34 months, with 253 (70.7%) females, and 96 (26.8%) diagnosed with cystitis. Only 61% (219) of urinary cultures in patients with a presumptive UTI were positive. Significant predictors of a positive culture were positive nitrites (OR 10.7) and the presence of leukocyte esterase at 3+ (OR 31.7). Abdominal pain during examination reduced the odds of a positive culture (OR 0.26). Other parameters were not statistically significant in our multivariate logistic regression.

CONCLUSION: Over a third of diagnosed UTIs did not have a positive urine culture. Only positive nitrites and leukocyte esterase (3+) on urinalysis were significantly associated with positive urinary cultures ($p < 0.05$). Diagnosing paediatric UTIs presents ongoing challenges, risking overdiagnosis and overuse of unnecessary antimicrobials.

WP051

Factors affecting adverse events in immunocompromised patients with *Pneumocystis* pneumonia

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OBJECTIVE: There has been limited data about the risks of adverse outcomes and mortality in non-HIV immunocompromised patients with *Pneumocystis* pneumonia (PCP). We designed this retrospective study to determine and compare the PCP outcomes and risk factors among various groups of immunocompromised patients.

METHODS: We retrospectively collected clinical manifestations, laboratory data, imaging studies, and treatment outcomes of patients diagnosed with PCP at University Health Network from January 2011 to 2022. A composite of outcomes from 21-day ICU admission and 28-day mortality was developed. Multivariable logistic regression analysis and estimated adjusted odds ratio (aOR) were used to determine the concurrent effects of covariates.

RESULTS: A total of 182 PCP cases in immunocompromised patients including 19 (10.4%) HIV infection, 54 (29.7%) hematologic malignancies, 32 (17.6%) hematopoietic stem cell transplant (HSCT), 33 (18.1%) solid tumours, 26 (14.3%) solid organ transplantation (SOT), 12 (6.6%) autoimmune diseases, and 6 (3.3%) other immunosuppression were reviewed and analyzed (median age 59.5 [IQR 45.5–69.5] years, male: 112 [61.5%]). Prolonged (at least 4 weeks) lymphopenia and neutropenia were present in 115 (64.6%) and 27 (15.2%) patients, respectively. Overall, 44 of 182 patients (24.2%) developed composite outcomes with 39 ICU admissions (21.4%) and 17 (9.3%) deaths. Significant risk factors from univariate analysis were SOT (29.5% versus 9.4%; $p < 0.001$), chronic liver disease (34.1% versus 6.5%; $p < 0.001$), prolonged lymphopenia (84.1% versus 56.5%; $p < 0.001$), hypoxemia (54.5% versus 39.9%; $p = 0.037$), lung nodules (40.9% versus 68.8%; $p = 0.001$), and pleural effusion (31.8% versus 9.4%; $p < 0.001$). In multivariate analysis, SOT (aOR 3.8 [IQR 1.1–13.8]), prolonged lymphopenia (aOR 8.8 [IQR 2.1–37.4]), and chronic liver disease (aOR 6.3 [IQR 1.8–22.2]) were statistically significant variables.

CONCLUSION: SOT recipients had the highest risks of composite ICU admission and mortality outcomes. Prolonged lymphopenia and chronic liver disease were also correlated with worsening outcomes.

WP052

Treatment of drug resistant tuberculosis with bedaquiline, pretomanid, linezolid with or without moxifloxacin (BPaL/M): Feasibility and implementation challenges in Western Canada

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OBJECTIVE: Drug-resistant tuberculosis (DR-TB) previously required treatment with a protracted course of toxic second-line TB drugs with suboptimal efficacy. Novel 6-month oral regimens of BPaL/M are now recommended, but implementation of BPaL/M in Canada is not well described. We analyzed six TB people treated with BPaL/M in Western Canada to inform expanded use.

DISCUSSION: Six-month, all-oral BPaL/M regimens appeared effective in a small number of people with DR-TB or rifamycin intolerance. Treatment was complicated by delays with drug resistance testing, drug use approval, and delivery leading to prolonged hospital admissions and isolation. In order to fully realize patient and health system benefits of BPaL/M treatment in Canada, streamlining of laboratory testing and access to these medications must be prioritized.

WP053

Salmonella septic arthritis and osteomyelitis in patients receiving tumour necrosis factor-α inhibitors

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OBJECTIVE: Salmonellae are gram-negative bacteria that can cause a variety of diseases in humans, including gastroenteritis, bacteremia, and focal infections. Individuals who are immunosuppressed are at increased risk of *Salmonella* infections, and individuals receiving tumour necrosis factor-α (TNF-α) inhibitor therapies appear to be at especially increased risk. Over the last 15 years, there are emerging reports of *Salmonella* septic arthritis and osteomyelitis in patients receiving TNF-α inhibitor therapies. This review summarizes and critically appraises the

literature surrounding *Salmonella* musculoskeletal infections in patients receiving TNF-α inhibitor therapies. Potential pathophysiologic mechanisms are discussed.

METHODS: The MEDLINE, EMBASE, and Google Scholar Databases were searched for this review. Relevant key words and MeSH terms were incorporated in conjunction with Boolean operators to retrieve appropriate peer-reviewed articles. The reference lists of the most relevant articles were searched manually for additional articles of relevance.

RESULTS: Several reports of *Salmonella* septic arthritis and *Salmonella* osteomyelitis were discovered among patients on TNF-α inhibitors. There was considerable variation with respect to onset of infection after therapy initiation, underlying indication for TNF-α therapy, the type of TNF-α inhibitor used, and long-term outcome.

CONCLUSION: TNF-α inhibitors are used abundantly worldwide to treat a variety of autoimmune diseases. This review hopes to raise awareness of the increased risk of *Salmonella* musculoskeletal infections in patients receiving these therapies. This review will find broad applicability in immunology, infectious diseases, rheumatology, gastroenterology, and in other specialties where TNF-α alpha inhibitor therapies are used commonly.

WP054

Clinical characteristics and demographics of patients experiencing methicillin-sensitive *Staphylococcus aureus* bacteremia as a function of high inoculum cefazolin resistance: A population-based multi-year study

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OBJECTIVE: Cefazolin is a recommended therapy for methicillin-susceptible *Staphylococcus aureus* (MSSA) bloodstream infections (BSI). Some strains exhibit reduced susceptibility to cefazolin when present in high inoculum (HIE), with reports of worsened outcomes. We sought to investigate the incidence of MSSA, demonstrating HIE over time across a general population.

METHODS: All MSSA BSI (first isolates) were analyzed from 2012–2014 and 2019. Cefazolin minimum inhibitory concentration (MIC) was determined at standard (SI: 5×10^5 CFU/mL) and high inoculum (HI: 5×10^7 CFU/mL) by broth microdilution (CLSI). Isolates were defined as having the HIE if they had a $\geq$4-fold difference between MIC at SI and HI. *BlaZ* and *agr* allele types were determined by whole genome sequencing (WGS). Patient characteristics were collected from chart audits. Continuous variables are presented as medians evaluated using Mann-Whitney *U*-test. Binary variables were compared using a Fischer's exact test.

RESULTS: During the study period, 871 residents experienced at least one episode of MSSA BSI. With 836 MSSA isolates tested for HIE. Rates of HIE were highest in 2012 (38.9%) and decreased through subsequent years (29.7%, 26.5%, and 24.4%), $p = 0.019$. MSSA BSI with HIE isolates differed in median age (65 [IQR 48–76] versus 62 [IQR 55–78]; $p = 0.031$) but not sex or comorbidities ($p > 0.05$). Isolates with HIE were not more likely to be community-acquired, nor associated with a particular presentation ($p > 0.05$) other than septic arthritis (RR 1.30; $p = 0.02$). MSSA BSI with HIE were not more likely to present with elevated markers of inflammation such as C-reactive protein ($p > 0.05$). Isolates expressing HIE predominantly had *blaZ* A (RR 2.038, 45.3%; $p \leq 0.0001$) and *agr* 3 (RR 2.891, 42.9%; $P \leq 0.0001$).

CONCLUSION: MSSA BSI exhibiting the HIE against cefazolin was common in Calgary, Alberta decreasing yearly from 2012 to 2014 and in 2019. Clinical demographics and patient characteristics did not significantly differ between groups. HIE was strongly associated with *blaZ* A and *agr* 3.

WP055

Septic bursitis: Insights from a Canadian single-centre study

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OBJECTIVE: Septic bursitis, typically affecting superficial bursae in the olecranon and prepatellar regions, poses a challenge in terms of universally accepted management. While surgical debridement is advantageous for source control, its frequent association with potential risks for subsequent complications necessitates a closer examination.

METHODS: A retrospective analysis of individuals aged 18 and above who received a clinical diagnosis of septic bursitis at an infectious diseases run cellulitis clinic between July 1, 2015, and March 1, 2023.

RESULTS: 124 cases of septic bursitis were identified. 78.2% were male (97/124), with a mean age of 53.35 (range 19–100). *Staphylococcus aureus* 36/57 (63.1%) was the most common causative organism identified with methicillin-susceptible *S. aureus* (MSSA) in 28/57 (49.1%); MRSA 8/57 (14%); *Streptococcus* species 9/57 (15.8%) and gram-negative organisms 2/57 (3.6%). Among the cases, 45/124 (36.6%) had a history of previous trauma, and 54/124 (43.9%) had chronic health conditions. Diabetes mellitus was the most prevalent underlying disease, accounting for 25/54 (46.3%). Antibiotics were administered to 121/124 (97.6%) without the need for hospitalization. Follow-up clinic visits were attended by 113/124 (91.1%), averaging 2 visits, and 66/124 (53.2%) received empiric antibiotics alone, without requiring bursal aspiration or swab culture. Signs and symptoms of reinfection post-treatment termination occurred in only 4 cases (3.2%). The duration of treatment for those with MSSA did not differ significantly from those with MRSA in their fluid culture (21.22 [SD 8.87] versus 17.71 [SD 5.88]; $p = 0.332$). In 13 cases (10.6%) where invasive procedures were employed for bursal fluid drainage, 4 patients developed chronic draining wounds at the aspiration site.

CONCLUSION: Considerable variability persists in determining the most effective approach for managing septic bursitis. On the basis of this review, the predominant course of treatment involved nonoperative methods, primarily using empiric antibiotics. The need for further prospective studies is evident to establish the optimal management strategy for this specific patient population.

WP056

Long COVID and associated factors among Chinese immigrants in Canada

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OBJECTIVE: Long COVID, characterized by persistent COVID-19 symptoms, is an emerging public health concern. Despite population variations, research on this issue in Canada is limited. This study addressed this knowledge gap by investigating the prevalence of long COVID, key symptoms, and related factors among Chinese in Canada, one of the vulnerable immigrant populations during the pandemic.

METHODS: We conducted a cross-sectional online survey on 591 Chinese Canadians aged 16 and above with support from the Public Health Agency of Canada (PHAC) in late 2022. Long COVID was defined as symptoms persisting beyond 12 weeks postinfection. The questionnaire included sociodemographic, psychological resilience, clinical status, vaccination, and long COVID experiences. Binary logistic regression analysis in SAS software 9.4 was used to explore the factors affecting long COVID.

RESULTS: In this study of 488 eligible participants, 260 had previously contracted COVID-19, and around 24.2% of those infected reported long COVID symptoms. Common symptoms included memory problems (42.9%), fatigue (40.0%), and anxiety and depression (30.2%). 70% of respondents who endured long COVID exhibited at least one underlying disease, with allergies being the most common. The median (IQR) duration of long COVID was 5 (2–12) months. After confounders adjusting, the odds of long COVID in women was about 2.5 (95% CI 1.30 to 4.75) times that of men Also, as the health condition worsened, the odds of long COVID increased ($p < 0.05$). Participants with a history of vaccine side effects had higher odds of long COVID (OR 2.48 [95% CI 1.32 to 4.63]).

CONCLUSION: The findings suggest that certain populations are at higher risk of long COVID. Support for people with existing health problems, weaker immune systems, and women is important to manage long COVID in at-risk populations. This could involve strict infection control, protective measures, and comprehensive COVID-19 vaccination. Moreover, exploring the link between long COVID and prior vaccine complications is recommended.

WP057

Optimal specimens for SARS-CoV-2 testing appear to vary depending on the predominant variant of concern (VOC)

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OBJECTIVE: SARS-CoV-2 testing was initially approved for nasopharyngeal (NP) swabs, but saliva was accepted as an alternative with variable yield to NP swabs in different studies. Antigen kits were initially validated using nasal swabs but anecdotal reports with the onset of the

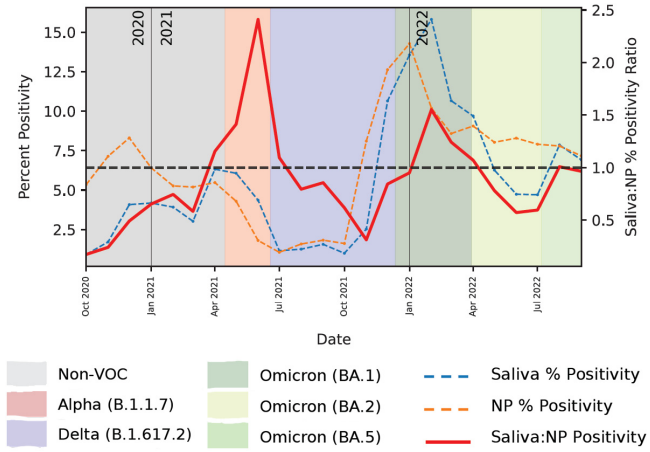

Figure WP057-1: Positivity of SARS-CoV-2 Tests from Saliva and NP Samples (2020-2022)

Omicron VOC suggested that buccal/oral/nasal combined swabs were more sensitive. This study analyzed COVID-19 percent positivity of saliva:NP samples over the span of the COVID-19 pandemic.

METHODS: Percent COVID-19 positivity of saliva and NP samples were collated at a tertiary care academic clinical microbiology laboratory serving a large Canadian urban area from October 2020 through November 2022. Results were graphed along with the ratio of saliva:NP positivity and the predominant VOC based on provincial data. Provincial indications for testing for NP and saliva samples were reviewed.

RESULTS: The positivity rate of saliva:NP specimens significantly varied over the study period correlating with different VOCs. There were significant rises in the saliva:NP positivity ratio to 2.4 and 1.6 when the alpha (B.1.1.7) VOC was predominant in May and June 2021 and when the Omicron BA.1 VOC was predominant in January and February 2022, respectively (Figure WP057-1). The positivity ratio was less than 1 prior to the emergence of VOCs (late 2020) and when the delta variant (B.1.617.2,) was abundant (July to November 2021) and with the onset of Omicron BA.2. Indications for testing were comparable for NP and saliva samples throughout the study period.

CONCLUSION: COVID-19 diagnostics are typically approved on the basis of validation data using specimen types collected at a set time. Our data suggest that the ideal specimen type for testing may change over the course of a pandemic varying on VOC. Diagnostic companies, regulatory and public health authorities, clinical laboratories, and clinicians should take this into account and revalidate assays as appropriate with the onset of new VOCs.

WP058

Clinical practice guideline-supported administration of monoclonal antibody therapy for high-risk patients with COVID-19: Experience of a quaternary care centre

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OBJECTIVE: While SARS-CoV-2 continues to circulate, severely immunocompromised patients remain at risk of severe COVID-19 disease. Treatment with anti-SARS-CoV-2 monoclonal antibodies (mAb) may benefit high-risk patients, although clinical outcome data in these patients are lacking.

METHODS: We conducted a prospective observational study of patients receiving mAb at a quaternary care centre (McGill University Health Centre) November 2021 to April 2022. Patient characteristics and clinical outcomes for 3 months for those receiving mAb for COVID-19 following institutional clinical practice guidelines (CPGs) were collected. We report factors associated with hospitalization and mortality.

RESULTS: 205 patients received mAb with median age 59 (IQR 45–71) years; 102 patients (50%) were female. Eighty-two (40%) were transplant recipients; 47 (23%) patients had a hematologic malignancy, 25 (12%) had a solid organ malignancy, and 51 (25%) had another indication for mAb. The majority (80%) had mild disease severity at presentation, 14% had moderate, and 6% had severe disease. Median time from symptom onset to mAb was 3.0 days (IQR 2.0–5.5 d). Among outpatients ($n = 97$), clinical outcomes were favourable (no COVID-19-related hospitalizations or death) in 90 (93%), while 93 (86%) of those who received mAb as inpatients ($n = 107$) were discharged without COVID-19-related readmission or death, 4% were readmitted, and 10% died. In logistic regression analysis, age <70 was associated with favourable outcomes (adjusted odds ratio [aOR] 0.36 [95% CI 0.13 to 0.99]; $p = 0.04$). Dis-

ease severity was associated with unfavourable outcomes (aOR 9.59 [95% CI 2.06 to 46.98]; $p = 0.004$ for severe versus mild). Outpatients versus inpatients had a significant difference in adherence to CPGs (85% versus 58%; $p < 0.001$); nonadherence occurred in inpatients given mAb for severe disease or slightly outside the recommended time (<7 days) from symptom onset.

CONCLUSION: Overall, CPG-supported mAb administration was associated with favourable clinical outcomes among high-risk patients. CPGs were generally followed, suggesting they may be a useful model to guide future therapies.

WP059

Assessing COVID-19 bivalent vaccine uptake and associated factors among Canadian Chinese

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OBJECTIVE: While COVID-19 vaccination is a significant public health success, addressing vaccine hesitancy remains critical for the ongoing pandemic control. Identifying the population's willingness toward COVID-19 vaccinations and their underlying reasons is crucial for successful Canada's vaccination program. Current research mainly targets general vaccine hesitancy, neglecting minorities. This study specifically explores the acceptance of new bivalent COVID-19 vaccines among the Canadian Chinese, one of the major ethnic minorities.

METHODS: With support from the Public Health Agency of Canada (PHAC), we conducted a cross-sectional online survey of 591 Chinese Canadians aged 16 and above in late 2022 when the bivalent vaccine was about to be introduced in Canada. The questionnaire included aspects of sociodemographic, psychological resilience, beliefs, experiences, and knowledge related to COVID-19 vaccine. To assess factors impacting willingness for new bivalent vaccines, we employed binary logistic regression in SAS software 9.4.

RESULTS: Among the 488 eligible respondents of this study, only ~25.5% expressed a willingness to receive the bivalent COVID-19 vaccine. Willingness was greater when the respondent received or intended to get the flu vaccine (OR 3.48 [95% CI 2.05 to 5.92]) and supported vaccination for pregnant women (OR 3.96 [95% CI 2.16 to 7.25]). Conversely, reluctance was greater with respondents who had never been vaccinated (OR 0.05 [95% CI 0.01 to 0.48]), were twice vaccinated (OR 0.08 [0.95% CI 0.03 to 0.19]), experienced vaccine side effects (OR 0.50 [95% CI 0.27 to 0.89]), believed there was insufficient information about COVID-19 vaccines (OR 0.52 [95% CI 0.28 to 0.95]), and favoured masks over vaccines (OR 0.34 [95% CI 0.16 to 0.70]).

CONCLUSION: Willingness for the new bivalent COVID-19 vaccine appears low among Chinese immigrants in Canada, mainly due to concerns about insufficient vaccine information and past vaccine-related side effects. Government, health authorities, and media must counter misinformation and enhance comprehension of the vaccine's benefits and possible side effects. This will aid in promoting vaccination within this community.

WP060

Evaluation of a protocol for managing the cyclosporine and nirmatrelvir/ritonavir drug-drug interaction in kidney transplant recipients

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OBJECTIVE: Nirmatrelvir/ritonavir (NRMr) interacts with calcineurin inhibitors (CNI). Limited evidence exists for reinitiating CNIs post-NRMr. This study aims to assess the application of a standardized protocol managing this interaction.

METHODS: This is a retrospective study between May 2022 and November 2023. As per protocol, cyclosporine (CsA) dose was reduced by 80% at NRMr start and up to 2 days post-NRMr. CsA levels were drawn 2 days post-NRMr. If the first level was subtherapeutic, CsA was resumed at 100%, and the level was repeated 1 week later. If supratherapeutic, the dose reduction was maintained for another 2 days, then reinitiated at 100% pre-NRMr dose. Acute kidney injury (AKI), hospitalization, and death were collected through 30 days post-NRMr therapy.

RESULTS: Of 42 kidney transplant recipients (KTR) identified, 35 met eligibility criteria and were analyzed. Nine KTR did not follow the protocol instructions. At baseline, 83% of patients were in therapeutic range. At the first follow-up (FU) 2 days post-NRMr, the average CsA level was higher by 23 µg/L ($P = 0.51$). There was a greater proportion of patients with subtherapeutic and supratherapeutic levels compared to baseline (20% versus 9% and 31% versus 9%). Nonadherence to the protocol was observed in 5/18 levels outside therapeutic range. At the second FU, there was a correction of subtherapeutic and supratherapeutic levels (14% and 14%). Of the 16 patients requiring additional monitoring, levels returned to baseline values within 30 days. Two KTR experienced AKI for unrelated reasons to COVID-19 treatment and one resolved with increased fluid intake. There were 4 hospitalizations, but none related to the initial COVID-19 treatment management. There was no graft rejection or death 30 days post-NRMr.

CONCLUSION: Although CsA levels outside therapeutic range were common immediately post-NRMr treatment, levels were restored rapidly. No clinically relevant safety events occurred within the 30 days. Adherence to the protocol is crucial.

WP061

Exploring the effects of vitamin D on COVID-19 infection, disease severity, and long COVID

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OBJECTIVE: This study aims to explore the effects of vitamin D on COVID-19 infection, disease severity, and long COVID among Chinese immigrants in Canada. Specifically, we will investigate whether vitamin D supplement intake is associated with a reduced risk of COVID-19 infection, disease severity, and long COVID. The findings from this study may contribute to the development of effective preventive and therapeutic strategies for COVID-19, particularly among vulnerable populations.

METHODS: Conducted from late 2022 to early 2023, our online survey engaged Chinese immigrants in Canada. Distributed via social media and community networks, participants aged 16 and above provided informed consent to answer questions on demographics, the impacts of COVID-19, and their vitamin D supplementation habits. Utilizing SAS for our statistical analysis, we investigated the association between vitamin D intake and COVID-19-related outcomes. This study accounted for potential confounding variables, such as age and health status. Statistical significance was established at a p value of less than 0.05.

RESULTS: Out of 492 eligible respondents, 237 (48.2%) reported regularly taking vitamin D supplements. Females were more likely to report taking vitamin D supplements than males (52.4% versus 42.7%), and the proportion of individuals taking vitamin D supplements significantly increased with age. Our results did not show a significant association between taking vitamin D supplements and reduced COVID-19 infection risk. However, among people with infection, multivariate logistic regression analysis showed that taking vitamin D supplements was associated with a reduced risk of developing severe infection (OR 0.55 [95% CI 0.31 to 0.99]).

CONCLUSION: Our study suggests that regularly taking vitamin D supplements may be associated with a reduced risk of developing severe COVID-19 infection. These findings are consistent with previous research and highlight the potential benefits of vitamin D supplementation for COVID-19 prevention and treatment, particularly among vulnerable populations.

WP062

Monitoring of SARS-CoV-2 variants in wastewater using whole-genome sequencing

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OBJECTIVE: Wastewater-based surveillance (WBS) provides valuable information on community prevalence of diseases including COVID-19. WBS is advantageous compared to clinical testing as each wastewater (WW) sample is representative of the whole community, detecting viruses shed from asymptomatic individuals, and those who do not seek medical attention. We aimed to estimate the cocirculation of SARS-CoV-2 lineages in WW across Alberta using

whole-genome sequencing (WGS), comparing results with clinical trends.

METHODS: WW samples were collected thrice weekly from 11 treatment plants, serving a combined population of 3 million Albertans from July 2022 to June 2023. After ultrafiltration and nucleic acid extraction, SARS-CoV-2 markers N1 and N2 were quantified using RT-qPCR. Each week, we prepared a WGS library with one sample per site, using the ARTIC amplicon panel and Illumina library prep workflow, followed by Illumina MiniSeq sequencing. The Freyja tool estimated lineage abundances. WW data were compared with patient-derived SARS-CoV-2 sequencing data from the provincial public health laboratory during the same period.

RESULTS: 518 sequenced WW samples met inclusion criteria, while sequencing data from 20,000 patient samples were available for comparison. Only Omicron lineages were identified in both data sets. We observed three lineage peaks in the WW data set: BA.5 (July 2022), BQ.1 (Dec 2023), and XBB.1.5 (March 2023). The dominant lineage composed 80%–90% of the total variants detected in the WW samples, with other variants detected at lower levels. The same dominant lineages and succession trends were observed in the clinical data.

CONCLUSION: WBS and clinical monitoring gave similar results, delivering insights into variant prevalence and changes over the study period. A single WW sample can provide a snapshot of the variants in the population; however, to gain comparable clinical data, thousands of individuals must be tested within the same time frame. With lower costs, long-term WBS offers insights into viral genetic drift.

WP063

Performance of IgA and IgG antibodies in the serological classification of recent SARS-CoV-2 infections among pregnant individuals

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OBJECTIVE: IgG antibodies against SARS-CoV-2 provide evidence of prior COVID-19 and/or vaccination; however, its utility in assessing SARS-CoV-2 infection timing remains unknown. We aimed to evaluate the performance of anti-SARS-CoV-2 IgA and/or IgG antibody markers in serologically classifying recent COVID-19 among vaccinated and unvaccinated pregnant individuals.

METHODS: We retrospectively selected pregnant individuals with confirmed SARS-CoV-2 who were either two-dose vaccinated ($n = 137$) or unvaccinated ($n = 171$) prior to PCR-confirmed COVID-19. All sera were collected either before ($n = 180$) or after 60 days ($n = 128$) following COVID-19 and were tested for IgA and IgG antibodies against SARS-CoV-2 spike (S), receptor binding domain (RBD), and nucleocapsid (N) using the Meso Scale Diagnostics platform. Antibody positivity was designated, according to previously validated assay cut-offs.

RESULTS: Seropositivity for anti-N IgG combined with anti-S (S+N+) or anti-RBD (RBD+N+) IgG yielded 78% sensitivity/23% specificity for S+N+, and 78% sensitivity/24% specificity for RBD+N+, in identifying COVID-19 in individuals within 60 days. In contrast to IgG, both S+N+ and RBD+N+ for IgA demonstrated lower sensitivity (S+N+: 47%; RBD+N+: 48%), but higher specificity (S+N+: 80%; RBD+N+: 77%). When stratifying by vaccination status, the same trends were observed among both unvaccinated and vaccinated individuals, with higher sensitivity and lower specificity for IgG compared with IgA (Unvaccinated — IgG: S+N+, 83% sensitivity/18% specificity; RBD+N+, 83% sensitivity/20% specificity; IgA: S+N+, 51% sensitivity/80% specificity; RBD+N+, 53% sensitivity/74% specificity; Vaccinated — IgG: S+N+ and RBD+N+, 73% sensitivity/33% specificity; IgA: S+N+, 43% sensitivity/80% specificity; RBD+N+, 44% sensitivity/80% specificity).

CONCLUSION: This preliminary work demonstrates that S+N+ or RBD+N+ yields higher sensitivity but lower specificity for IgG compared to IgA when classifying individuals within 60 days following COVID-19 diagnosis. Future work is needed to determine their suitability in an algorithm for serologically identifying recent COVID-19.

WP064

COVID-19 non-severe therapy consult service: Reflections on a hub and spoke model

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OBJECTIVE: COVID therapeutics are critical for SARS-CoV-2 pandemic management and protecting vulnerable patients from adverse COVID outcomes. The COVID-19 Non-Severe Therapy Consult Service screens, assesses and prescribes nonsevere COVID medications using centralized virtual health care in a hub-and-spoke model for all patients to ensure timely candidate identification, medication supply stewardship, equitable distribution, and quantifiable care.

METHODS: The COVID-19 Non-Severe Therapy Consult Service, comprising pharmacists and physicians with COVID expertise, was implemented on March 1, 2022. Public self-referral is promoted as the primary referral method, with health care professional referrals and automatic referrals triggered by positive COVID PCR tests as additional referral pathways. Vaccination history and risk-factor data are amalgamated and leveraged to streamline automated referral prioritization for COVID medication assessment. Data analytics monitor capacity, predict human resource requirements, and maximize patient throughput. Prescribing protocols task-shift prescribing from physicians to pharmacists.

RESULTS: From March 1, 2022, to December 31, 2023, 106,948 patients were screened, 17,791 patients were fully assessed, and 12,209 treatment courses were prescribed for nonsevere COVID. The service provided care to 12% of the population in XX and achieved a population-representative relative referral distribution across urban and rural settings. Automated referral prioritization enabled assessing individuals at highest risk for disease progression in a median of 1-day postpositive test report. Pharmacists prescribed 97.6% of all COVID nonsevere treatments following the adoption of designated pharmacist prescribing for all first-line therapies.

CONCLUSION: A technology-enabled, hub and spoke virtual care model effectively supports equitable nonsevere COVID therapeutic distribution. Automated referral prioritization intelligence enables efficient identification and assessment of high-risk treatment candidates, and a collaborative structure facilitates prescribing task-shifting to pharmacists. Similar models should be evaluated for screening, assessment, and treatment of other infectious diseases.

WP065

Public acceptability of rapid COVID self-testing: Insights from a community-embedded implementation project

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OBJECTIVE: Point-of-care testing technology represents a transformative health care tool that can enhance health promotion by enabling self-determination, access, and autonomy. This project explores the public acceptability of rapid COVID self-testing during a global health crisis through engagement strategies in demedicalized, community-led settings.

METHODS: We collected 2,392 survey responses between July 2021 and June 2022 through an online survey platform developed using REDCap. We evaluated the rapid COVID self-testing implementation project by measuring its impact across the dimensions of the RE-AIM Framework. At-home self-test kits were distributed at asymptomatic rapid testing sites in Halifax, NS. The test kit packages provided a link and QR code to the survey.

RESULTS: Survey respondents were, on average, 45.02 (SD 16.73) years old and predominantly from urban areas (87.6%). Most respondents obtained self-test kits directly at rapid testing sites (75.8%) or received them from family/friends (18.9%). The majority (94%) reported ease in test usage, instruction adherence, and result interpretation. Participants expressed a preference for acquiring test kits in easily accessible and commonly frequented public spaces, with pharmacies, grocery stores, malls, and transit hubs frequently suggested. Also, respondents advocated for increased access in rural areas. Nearly all participants (99.6%) expressed willingness to utilize self-test kits again, with 64.5% planning weekly testing.

CONCLUSION: Test kit users indicated a high level of satisfaction, ease of use, and a notable interest in self-determination, autonomy, and access to care with this convenient at-home testing tool. These findings suggest the potential for broader applicability beyond COVID, highlighting the prospect of self-testing as a versatile tool across various health diagnostic domains.

WP066

Care framework for individuals at risk of and experiencing persistent COVID-19

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OBJECTIVE: Profoundly immunocompromised individuals are at risk of protracted symptomatic viral infection. Standard antiviral treatment and duration may be inadequate to control symptoms and facilitate viral cure in the context of limited host immunity. The COVID-19 Therapy Consult Service, a centralized virtual care team, identified unique care needs of profoundly immunocompromised individuals, and implemented a care framework to identify, assess, treat, and monitor these patients.

METHODS: The existing automated COVID referral system was leveraged to enable prompt case detection starting February 19, 2023. The centralized model facilitated rapid and uniform model adoption on a provincial scale. As of April 5, 2023, individuals with persistent COVID were considered for treatment with both nirmatrelvir/ritonavir and remdesivir for a prolonged duration with or without tixagevimab/cilgavimab. As of May 1, 2023, patients identified at risk of persistent infection were considered for extended treatment with nirmatrelvir/ritonavir or remdesivir.

RESULTS: From February 19, 2023, to August 31, 2023, the team identified 14 patients experiencing persistent and 46 at risk of experiencing persistent COVID. All patients with persistent COVID were immunocompromised due to medications (e.g., B-cell-depleting therapy) with or without a hematological malignancy (71%). Most patients were at risk of persistent COVID due to a hematological malignancy (71%), medication (52%), or both (26%). Following implementation of the at-risk approach, 4 of the at-risk patients progressed to persistent COVID. The remaining 91% (42/46) at-risk patients did not progress to persistent infection and were not referred to the consult service within 30 days. During the persistent infection follow-up period, 57% had respiratory symptom resolution, 69% became COVID negative, and 77% survived.

CONCLUSION: Expedient care framework adoption at the provincial level identifies and uniformly responds to an unmet care need. Ideal management of those at risk of and with persistent COVID-19 is unknown, and emerging evidence will inform future management.

WP067

PLOVER: A novel data system for province-wide lab test aggregation, public health response, and outbreak investigations by whole genome sequencing

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OBJECTIVE: Public health laboratories require sophisticated laboratory information systems for high throughput testing and communication to stakeholders. However, enterprise applications tend to be inflexible and poorly interconnected due to requirements for robust operations on central IT infrastructure. To address the emerging COVID-19 pandemic, we transformed a small, internal project into a custom Web application, PLOVER, that served as the primary repository for COVID-19 test results and outbreak investigations requiring linked whole-genome sequencing results.

METHODS: PLOVER is built on the Django Framework, an enterprise web application (Python frontend, SQL backend). COVID-19 testing data from the provincial reference laboratory, front-line labs, private labs, border testing, and industry surveillance are integrated via APIs and SFTP connections. As pandemic needs changed, features were added using Django design patterns for data types, user roles (contact tracing), automatic case notifications, data dissemination, and extension to other pathogens.

RESULTS: PLOVER has supported over 700 users since January 2020 (peak 150 active per month) with over 6,600,000 COVID-19 results (43,000,000 raw records). Data schemas and algorithms were designed to allow data to be live for users within approximately one hour of receival. In addition, over 800 cluster investigations have been reported through PLOVER. Features have expanded beyond COVID-19, to human influenza, avian influenza, and health-care-associated infections to integrate detailed epidemiological information with laboratory testing and sequencing results for surveillance and outbreak analyses.

System design has allowed nearly continuous operation since January 2020 apart from one major upgrade; frequent minor releases require only momentary downtime.

CONCLUSION: Building on an advanced, open-source framework, we deployed a province-wide repository for laboratory testing and sequencing with support for outbreak investigations with HA staff. Embracing a rapid development framework has allowed us to deploy and evolve a custom secure enterprise application—and avoid pitfalls of workarounds such as spreadsheets—with minimal staff.

WP068

Global Clinical Phage Rounds (G-CPR): An international collaborative educational forum addressing patient cases treated with bacteriophage therapy

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OBJECTIVE: Antimicrobial resistance (AMR) is predicted to be a leading cause of death worldwide as we enter the postantibiotic crisis. Bacteriophages have been used for over a century and are promising for persistent infections when antibiotic options are limited due to resistance, toxicities, or ineffectiveness in biofilms. With limited clinical trial data or consensus guidelines on phage therapy, international collaboration and education are a pressing need, and examples are provided here.

METHODS: A group of infectious disease physicians, microbiologists, and phage scientists have established an international forum to discuss cases eligible for or under phage therapy. Advice is provided by clinical and laboratory experts. Cases are presented confidentially, in a grand rounds format with moderators and discussants.

RESULTS: The group was formed with representatives from Phage Australia, AMMI Canada, Mayo Clinic, and ESCMID. In 12 months, the group has grown to 300 members, mostly infectious disease specialists and clinical microbiologists, with laboratory phage scientists from all over the globe. There have been 9 sessions, with up to 80 joining each session online and more accessing recordings. Sessions are interactive with polls and opinions from the group providing valuable information for future directions. Cases have been from the United States, Israel, Belgium, Australia, France, Canada, and other countries. Cases represented are pretreatment, during treatment, or posttreatment, including critical discussion on reported cases. Topics have included bone and joint, urinary tract, pulmonary, and intra-abdominal infections. Evaluations have been highly positive (4.6/5.0 average score) both for structure and impact.

CONCLUSION: In just 12 months, a virtual network of 300 mostly physicians from over 35 countries have formed to discuss confidential cases on phage therapy. Experiences were shared, and impactful education was provided to improve clinical care. Moving forward, the patient experiences and sense of community provided by the network are expected to assist with challenges to phage therapy implementation in the future.

WP069 – WITHDRAWN

WP070

Genomic relationships between environmental and clinical *Vibrio parahaemolyticus* isolates in Canada

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OBJECTIVE: *Vibrio parahaemolyticus* (Vp) is a significant source of gastroenteritis, particularly in coastal regions via the consumption of raw shellfish. Core-genome multilocus sequence typing (cgMLST) and phylogenetic methods remain underutilized in Vp research, despite their promise to provide high-resolution insights via clustering and evolutionary relatedness. Our objective

was to use phylogenetic and cgMLST methods to characterize the genomic relationships in a collection of clinical and environmental Vp isolates spanning two decades.

METHODS: A total of 653 Vp isolates (310 clinical, 343 environmental) were collected between 1999 and 2022. After conducting DNA extraction, library prep, and whole genome analysis (WGS) analysis on all isolates, we developed a custom bioinformatics pipeline in Nextflow to perform quality control, de novo assembly, and single nucleotide polymorphism (SNP) calling and consensus generation. We ran cgMLST analysis using the Vp schema from pubMLST.org and clustered isolates based on alleles found at 2,254 unique loci. We also generated a whole-genome phylogenetic tree of all isolates using FastTree2, filtering for quality and recombination.

RESULTS: Using a threshold of 10 or fewer allelic differences, we identified 27 cgMLST complexes containing more than two isolates. While most complexes were either predominantly environmental or clinical (i.e., clinical/environmental, 146/3, 47/0, 18/0, 0/17, 0/8), some complexes contained a mix of sources. In our phylogenetic tree, we detected significant recombination, especially within 15% of branches where its influence was multiple times higher than the norm. After filtering for recombination, we used this tree to identify 38 instances of environmental and clinical isolates fewer than 50 SNPs apart ($<9.68 \times 10^{-6}$ SNP distance). Eleven of these pairs further had collection dates at most 1 year apart.

CONCLUSION: Whole-genome phylogenetic and cgMLST methods can provide detailed insights into Vp relationships and clustering trends. Future expansion of these methods holds great potential for outbreak detection and source attribution.

WP071

Pretreatment drug resistance of human immunodeficiency virus type 1 subtypes in HIV patients in Ghana: A cross-sectional study

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OBJECTIVE: The emergence of drug resistance during therapy and the transmission of resistant strains to antiretroviral therapy (ART)-naïve patients both contribute to treatment failure and compromise the gains made with ART. Genotypic drug resistance testing is, therefore, important to guide the selection of drugs for initiation of therapy or for a switch to new regimens. However, the contribution of pretreatment drug resistance to treatment failure in Ghana is not known. Therefore, we determined the presence of drug resistant HIV-1 strains in ART-naïve HIV patients.

METHODS: Sixty-nine (69) ART-naive HIV-1 infected persons were studied from three major ART clinics. Demographics and clinical data were documented, and blood samples were collected. HIV-1 protease and reverse transcriptase genes were amplified by conventional polymerase chain reaction (PCR) and directly sequenced. Sequences were assembled, edited, and submitted to the Stanford HIV Drug Resistance database (HIVdb) for subtype and drug resistance analyses.

RESULTS: The mean viral load and CD4+ lymphocyte counts were 1.38×10^5 copies/mL and 409 cells/μL, respectively. We found 64% participants with HIV-1 subtype CRF02_AG, 26% with subtype B, and the remaining with subtypes CRF06_cpx, A, C, and G. Seven different drug resistance mutations (K103N – 2.7%, V179I – 2.7%, A98G – 2.7%, E138A – 5.4%, V32L – 2.3%, V11L – 2.3%, L10LF – 2.3%) were present in nine participants. These were mutations against non-nucleoside reverse transcriptase inhibitors (NNRTI) or accessory mutations against protease inhibitors (PI). No nucleoside reverse transcriptase inhibitor (NRTI) mutation was found in this study.

CONCLUSION: CRF02_AG is the predominant HIV-1 subtype in Ghana with significant increase in the occurrence of HIV-1 subtype B, and low levels of pretreatment HIV-1 drug resistance were observed. Given that drug resistance is increasing in the sub-Saharan region, it is important to continue active surveillance to monitor the emergence of drug resistance strains to guide HIV ART.

WP072

Evaluation of dried blood spot testing among HIV-1 viral controllers with the Roche COBAS AmpliPrep/COBAS TaqMan HIV-1 Qualitative Test, version 2.0 (HI2QCAP)

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OBJECTIVE: Dried blood spots (DBS) have been increasingly adopted because of their ease of use and stability over fresh blood. The Roche HI2QCAP is a qualitative assay that detects HIV-1 total nucleic acid from DBS samples to assist with HIV diagnosis. However, the assay's performance among HIV viral controllers is unknown. We sought to evaluate the utility of DBS specimens tested with HI2QCAP among a cohort of individuals with HIV-1 viral control phenotypes.

METHODS: Patients actively followed at a tertiary hospital-based HIV clinic were reviewed. Adults aged 18 and older who were serologically diagnosed with HIV-1 and maintained viremic control without any anti-retroviral therapy were included. Viremic control was defined as plasma HIV-1 RNA viral loads of $\leq$400 copies/mL over the most recent 12-month period or for $\geq$90% of all viral load measurements. Samples were collected for parallel testing of DBS with the HI2QCAP assay and whole blood with a gold-standard HIV reference lab-developed proviral assay targeting HIV-1-*pol* and LTR-*gag* regions. Descriptive statistics were used, and results were compared for categorical agreement.

RESULTS: Seven individuals met the inclusion criteria and underwent parallel testing. Participants' median age was 48 years old, and 4 were female. DBS testing achieved categorical agreement with reference testing in all but one patient who resulted DBS negative, reference assay positive for *pol* and LTR-*gag* and had a plasma HIV-1 RNA viral load of 197 copies/mL. Additionally, DBS testing correctly identified a patient as positive who was *pol* positive but LTR-*gag* negative by the reference assay.

CONCLUSION: DBS-based testing demonstrated reliable and robust performance for the qualitative HIV-1 assay HI2QCAP among HIV viral controllers. These initial results support the current approach of orthogonal testing algorithms employed by HIV reference laboratories and encourage future studies with larger cohorts to validate DBS testing among unique HIV immuno-phenotypes.

WP073

A global perspective: The gene expression profile of tuberculosis disease among people living with HIV

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OBJECTIVE: In 2022, tuberculosis (TB) was the leading cause of death among people living with HIV (PLWH) worldwide. Currently, screening methods are symptom-driven, which makes detecting TB challenging, with up to 75% of TB going undetected among PLWH. This research aims to investigate the transcriptomic profile of TB in PLWH with hopes of delineating host and TB interaction and improving early TB diagnosis among PLWH.

METHODS: Participants were recruited from Medellin, Colombia, and additional datasets were retrieved from publicly available database from the United Kingdom, Uganda, and India (GSE107991, GSE107104, and GSE162164). Data were classified into four different groups confirmed by TB microbiology and HIV serology testing. Inclusion criteria included age $\geq$18 years old, and naive to HIV and TB treatment. RNA-sequencing analysis and pathway analysis were done.

RESULTS: A total of 96 participants were included in the study as follows: people diagnosed with TB ($n = 31$), HIV ($n = 23$), TB among PLWH cohort ($n = 29$), and non-HIV/non-TB cohort ($n = 13$). 11,618 differentially expressed genes were found between all four cohorts with 7,897 upregulated and 3,721 downregulated genes (adjusted

$p = 0.05$ and fold change $= \pm 1.5$). Upregulated genes unique to TB among PLWH include *DPP8*, *AK9*, *ATF2*, *KLH9*, *CREBRF*, *PAG1*, *TAB3*, *MR1*, *PDK3*, and *ABL2*. Downregulated genes unique to TB among PLWH include *NONO*, *LCK*, *ARF6*, *ILF3*, *NCL*, *SGK1*, *MADD*, *RCC2*, *BAP1*, and *CDK9*. A total of 1,415 genes were shared in all four cohorts.

CONCLUSION: A total of 2071 upregulated genes and 1143 downregulated are unique for TB among PLWH, which have the potential to serve as diagnostic biomarkers. Upregulated genes such as ATF2 and TAB3 have been implicated in IL-1 signaling and NF-κB signal transduction pathways. Downregulated genes such as *NONO*, *LCK*, *ARF6*, *ILF3*, *NCL*, *SGK1*, *MADD*, *RCC2*, *BAP1*, and *CDK9* have been correlated to the positive regulation of biological processes.

WP074

Switch to bictegravir/emtricitabine/tenofovir alafenamide (B/F/TAF) among vulnerable HIV-infected individuals: Evidence for long-term efficacy

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OBJECTIVE: Single-tablet regimens are associated with higher rates of sustained virological suppression and patient satisfaction. This is true of STRs, including unboosted integrase strand transfer inhibitors with an increased barrier to resistance, tolerability, and fewer drug interactions. We have previously demonstrated sustained virologic suppression over 18 months among 41/43 HIV-infected active injection drug users following a switch of prior ARV therapy to the STR B/F/TAF. The objective of this study is to evaluate whether this benefit would be maintained over an additional 24 months of follow-up.

METHODS: The cohort consisted of 43 individuals who were followed up after having received B/F/TAF for 18 months. They remained enrolled in a multidisciplinary program, with B/F/TAF provided with enhanced adherence support, allowing daily observed therapy. The end point of analysis was the rate of virologic suppression after an additional 24 months of follow-up, for a total of 42 months after initiating B/F/TAF therapy.

RESULTS: Forty-three subjects were included in this analysis: median age 54 (34-66) years, 11.1% female, 20% indigenous, 37.8% men who have sex with men, and all were active drug users, with 91.1% being fentanyl users. At 18 months of follow-up, we noted median CD4 count 612 cells/mm^3. All 43 remained on B/F/TAF for the 24 months of follow-up, with no long-term disengagement. 41/43 had maximal virologic suppression, including both participants with detectable HIV RNA at month 18. Two cases of detectable HIV RNA (1,520 and 3,000 copies/mL) were documented at month 42. In both cases, virologic suppression was achieved after resumption of B/F/TAF.

CONCLUSION: Among a group HIV-infected injection drug users experiencing transient viremia, switching to B/F/TAF remains effective in the long term. Its efficacy and tolerability make it a particularly useful therapeutic option in this vulnerable population.

WP075

Multiple antibiotic resistance tracing by plasmid profile analysis of bacteria isolates from medical dump bin

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OBJECTIVE: This study investigated the prevalence and diversity of antibiotic resistance genes in bacteria isolated from medical refuse and to trace the spread of resistance using plasmid profile analysis.

METHODS: The incidence, isolation, and characterization of bacterial isolates from medical dump bin, were investigated using pour plating and other standard microbiological techniques. Antibiotic susceptibility profiles of characterized bacterial isolates were determined using the disc diffusion method, while the presence of plasmids, extrachromosomal DNA elements known to carry antibiotic resistance genes, was confirmed through plasmid extraction and agarose gel electrophoresis.

RESULTS: Total bacterial count (TBC) for soil samples vary from 16.9 to 20.1 CFU/mL and from 200 to 210 CFU for bin swabs. The total number of twenty-seven (27) bacteria were isolated and six (6) strains were identified. *Bacillus* spp being the most numerous has a total of nine (9) strains, followed by *Corynebacterium* spp (8), while *Pseudomonas* spp and *Salmonella enterica* have a total of three (3) bacteria each, and *Neisseria* spp and *Staphylococcus* spp have total of two (2) bacteria each. Both gram-positive and gram-negative bacteria have shown different resistance to multiple antibiotics. The molecular weight of the plasmids

in the bacteria isolates were *S. enterica* having one plasmid (23.1 Kbp), *Corynebacterium* spp (BS4) having two plasmids (6.6-23.1 Kbp), *Pseudomonas* spp, *Corynebacterium* spp (BS2) having one plasmid with 23.1 Kbp each, and *Staphylococcus* spp was not possessed by any plasmid.

CONCLUSION: By evaluating the wide range and abundance of antibiotic-resistant bacteria and plasmids in dumpsites, this research highlights the importance of proper waste management practices to stop the spread of antibiotic resistance genes and protect the public's health.

WP076

Candida auris outbreak associated with patients with SARS-CoV-2 in the intensive care unit of a high-complex hospital in the city of Cúcuta, Colombia

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OBJECTIVE: The work presented aimed to identify *Candida auris* infection in critical patients with SARS-CoV-2 in an intensive care unit of a high-complex hospital in Colombia, as well as to describe the antifungal susceptibility of the isolates.

METHODS: A descriptive and retrospective study was performed in 14 patients with confirmed SARS-CoV-2 infections who had *C. auris* coinfection during their stay in an intensive care unit during the outbreak registered between November 2020 and April 2021. The diagnosis of fungal infection by *C. auris* was performed by following the guidelines of the Microbiology Laboratory of the National Institute of Health of Colombia, which indicates that any yeast sample from an ICU, identified by VITEK as *Candida* spp, or *C. haemolonii* and additionally shows resistance to at least one antifungal, had to be sent and notified to the National Institutes of Health through a local public health laboratory for subsequent molecular identification by MALDI-TOF.

RESULTS: An outbreak of COVID-19-associated *C. auris* infections was reported in 14 patients. All of the affected patients were under mechanical ventilation, had central venous catheters, steroid therapy, and prolonged antibiotic therapy. *C. auris* was isolated from blood in 11 patients (11/14) and from urine in 3 patients (3/14). The 64.2% had comorbidities, the most common being hypertension and diabetes mellitus (6/14). Mortality was 54.5% among the patients with candidemia. The 85.7% (6/7) of dead patients had bacterial coinfections, being the most common isolate *Pseudomonas aeruginosa*. Antifungal susceptibility testing showed that 64.2% (9/14) were resistant to fluconazole (MIC >32 mg/L), 71.4% (10/14) were resistant to AMB (MIC > 2 mg/dL), but all of them were susceptible to equinocandins.

CONCLUSION: *C. auris* is an emerging threat due to the rapid transmission in health care settings associated with the diagnostic difficulty by standard equipment. Also, multidrug resistance becomes a therapeutic challenge given the low availability of echinocandins in developing countries.

WP077

Burkholderia cepacia ST 767 causing a 3-year nosocomial outbreak in a hemodialysis unit

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OBJECTIVE: Kidney failure leads to reduced diuresis and the accumulation of nitrogenous substances in the body. Hemodialysis is employed as a partial substitute for renal function to enhance patient survival. The global concern arises from water contamination during hemodialysis, leading to patient bacteremia. The *Burkholderia cepacia* complex (Bcc) is frequently found in hemodialysis water, posing a threat to immunosuppressed patients due to its virulence factors and resistance to various antimicrobial agents, contributing to their persistence in hospital environments and host pathogenesis. This study aimed to characterize Bcc isolates collected from blood of patients, water, and dialysate at a Public Hospital in Brazil (2019–2021).

METHODS: Thirty-three isolates came from patients undergoing hemodialysis treatment, and 24 from water/dialysate. Sequencing the *recA* gene identified Bcc species, and virulence factor genes (*cblA*, *esmR*,

zmpA, *zmpB*) presence was assessed. Considering the outbreak's epidemiology, Bcc isolates were characterized using Multi Locus Sequence Type (MLST) and Pulsed Field Gel Electrophoresis (PFGE). Biofilm assays were conducted at 20°C and 35°C. Antibiograms were performed using disc diffusion on agar.

RESULTS: The gene *zmpB* was identified in all isolates, while *zmpA* was present in 96.5% of isolates, with none possessing *cblA/esmR* genes. All human isolates were resistant to gentamicin, colistin, ampicillin/sulbactam, and imipenem and 48.5% exhibited resistance to amikacin. All isolates from water produced biofilm at 20°C. Using PFGE, we noticed that all isolates (human and water) belonged to the same pulsotype, identified as *B. cepacia*, sequence type ST-767.

CONCLUSION: The persistence of this pulsotype over 3 years indicates its continuous presence in the pipeline, contaminating hemodialysis patients despite routine water disinfection with peracetic acid. This persistence is likely due to biofilm production. Moreover, several isolates exhibited multidrug resistance, complicating patient care.

WP078

Genetic epidemiology of invasive *Serratia* isolates in a tertiary hospital system: Insights from whole-genome sequencing

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OBJECTIVE: To describe the genomic epidemiology of *Serratia marcescens* isolates from patient specimens identified in a tertiary hospital system, and to determine any clustering indicative of possible in-hospital transmission.

METHODS: We prospectively identified consecutive patient specimens positive for *Serratia marcescens* by mass spectrometry at the Hamilton Regional Laboratory Medicine Program from January to November 2022. We used purified genomic DNA to create individually barcoded short-read libraries that were enriched for ~1000 bp insert sizes. We sequenced libraries on the Illumina NextSeq 2000 platform 2 × 150 bp. We used Trimmomatic (v.0.39) to remove Illumina adapters, followed by *de novo* genome assembly with Unicycler (v.0.5.0). We used Bakta (v.1.9.1) to annotate the genomes, and Bandage (v.0.8.1) to detect extrachromosomal genetic sequences. We assigned taxonomic classifications using the Genome Taxonomy Database toolkit, with iToL to ascribe phylogenetic relationships. We used the Comprehensive Antibiotic Resistance Database to identify resistance determinants.

RESULTS: We identified 72 *Serratia marcescens* isolates from 50 (68.4%) males and 22 (30.5%) females, with a median age of 66.5 years (IQR 58.75–76). We sequenced 10 (13.6%) blood, 21 (29.1%) respiratory, 26 (36.1%) urine, and 15 (20.8%) specimens from other sources. The median genome size was 5.1 Mb, with a median GC content of 59.81%. Genomes had a median of 36 contigs, with a median N50 statistic of 350 kb. Whole-genome sequencing identified 35 (48.6%) *Serratia marcescens*, 14 *S. ureilytica*, 12 *S. bockelmannii*, 9 *S. nevei*, and 2 *S. nematodiphila* isolates. Fifteen (20.8%) isolates had predicted plasmids, with the same number predicted to have conjugative transposons. Most isolates harboured resistance determinants: 71 (98.6%) had the *adeF* multi-drug efflux pump and an altered PBP3, and 70 (97.2%) with the aminoglycoside resistance marker *AAC(6')-Ic*. No spatiotemporal relationships were seen with phylogenetic clustering.

CONCLUSION: Additional granularity is gained by the use of whole-genome sequencing to identify *Serratia* spp. The prevalence of putative conjugative transposons in clinical isolates has not been widely described.

WP079

Carbapenamase-producing Enterobacterales in patient sink and shower drains

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OBJECTIVE: Carbapenamase-producing Enterobacterales (CPE) outbreaks have been linked to contaminated hospital plumbing. We evaluated the utility of a program to test and disinfect drains potentially exposed to CPE-colonized patients.

METHODS: Between 2018 and 2023, CPE-colonized patients at St. Michael's Hospital, Toronto, had their hand hygiene sink, bathroom sink, and in-room or communal shower drain tested for CPE and disinfected with accelerated hydrogen peroxide at discharge. Colonized drains underwent enhanced cleaning and disinfection, and retested. Cleared drains were periodically retested. Results were considered discordant if the CPE enzyme differed between patient and drain. Drains were considered "cleared" if two swabs were negative, and no additional positive tests occurred for 6 months.

RESULTS: Overall, 123 CPE colonized inpatients were associated with 760 sink drains. On the precleaning test, 5% (22/414) of swabs were positive for CPE. Positivity was highest for shower drains (9%, 7/80), and hand hygiene sinks (7%, 11/162), and lower for bathroom sinks (2%, 4/172). Excluding communal shower drains, 39% of positive sink specimens were discordant. KPC was the most common CPE enzyme identified from sinks/drains, while OXA-48 was the most common enzyme identified from patients. Most (95%) of drains were successfully decontaminated: 59% after initial disinfection, and 36% with extensive cleaning. One shower drain remained positive despite repeated cleaning and disinfection. No case clusters associated with the same room or drain were noted, and no nosocomial case was linked to a previously colonized drain.

CONCLUSION: Only 5% of drains in rooms housing CPE patients were positive, of which more than one-third were discordant and not associated with the CPE-positive patient that triggered the testing. Sink-drain testing of patient rooms housing CPE-positive patients may not be an efficient strategy to prevent drain contamination or CPE transmission.

WP080

Prevalence of intestinal parasites and associated risk factors among Debre Genet Primary School students, Naeder Adiet District, Tigray, Ethiopia

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OBJECTIVE: To assess the prevalence of intestinal parasites and associated determinant factors among Debregenet primary school students in Neadier Adiet district, Tigray, Ethiopia

METHODS: Cross-sectional study was conducted from February to April 2020 among 382 students. Stool sample was collected from each student and examined for intestinal parasite stages using direct wet-mount and formal-ether concentration techniques. Pretested and structured questionnaires were used to gather relevant information on socio-demographic and risk factors associated with intestinal parasitic infections. Data were analyzed using SPSS version 20, and binary logistic regression was used to assess the possible association between the independent and outcome variables. Descriptive statistics were used to provide a clear picture of the frequency distribution of both dependent and independent variables. Statistical significance was declared at $p < 0.05$ with 95% CI.

RESULTS: The overall prevalence of the intestinal parasites among the school children was 29.6%. The species of intestinal parasites identified were *Giardia lamblia* 53 (13.9%), *Hymenolopies nana* 23 (6.1%), *Schistosoma mansoni* 12 (3.1%), *Entamoeba histolytica* 8 (2.1%), hookworm 7 (1.8%), and *Enterobius vermicularies* 3 (0.8%) with 7 (1.8%) double infections. Factors like hand washing before a meal, frequency of trimming fingernails, presence of a latrine at home, clean latrine availability in school, cleanliness of living environments, and source of drinking water were significantly associated with intestinal parasitic infections ($p < 0.05$).

CONCLUSION: There is a need for health education on personal and environmental hygiene, and deworming so as to reduce the rate of intestinal parasitic infections in the study area.

WP081

Comparison of the efficacy of povidone-iodine solution with intranasal mupirocin ointment in decolonizing *Staphylococcus aureus* from the nasal cavity of health care workers: A single-blind randomized controlled trial

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OBJECTIVE: Nasal colonization of *Staphylococcus aureus* is a risk factor for nosocomial infections. Hence, the consumption of medications that decolonize this pathogen can serve as a pivotal approach to preventing such infections. Our study aimed to compare the efficacy of povidone-iodine solution with intranasal mupirocin ointment in the decolonizing *S. aureus* from the nasal cavity of health care workers.

METHODS: This single-blind randomized controlled trial was conducted on health care workers carrying *S. aureus* nasally. After proving nasal colonization by culture, participants were assigned to intervention groups A and B with an allocation ratio of 1:1. Group A received intranasal mupirocin ointment twice a day for 5 days. Group B received povidone-iodine solution twice a day for 5 days. After the completion of the decolonization period, sampling was conducted to re-evaluate the colonization of *S. aureus*.

RESULTS: In this study, 54 health care workers with a mean age of 39.37 [SD 7.80] years were included, 42.6% and 57.4% of whom were male and female, respectively. They were randomly assigned to each of the intervention groups. After the intervention, individuals who received povidone-iodine had significantly more positive cultures than those who received mupirocin (37.0% versus 11.1%; $p = 0.026$). Furthermore, age, gender, wards, and employment duration were potential factors affecting the efficacy of mupirocin and povidone-iodine in decolonizing *S. aureus* from the nasal cavity.

CONCLUSION: The study findings revealed that both mupirocin and povidone-iodine were effective in decolonizing *S. aureus* from nasal carriers. However, mupirocin was more effective compared with povidone-iodine.

WP082

Surveillance for health-care-associated infections and antimicrobial resistant organisms in Canadian long-term care homes: A cross-sectional survey

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OBJECTIVE: Our understanding of the burden of health-care-associated infections (HAIs) and antimicrobial resistant organisms (AROs) in Canadian long-term care homes (LTCHs) is limited, in part, because nationwide surveillance in this setting has yet to be established. A survey was administered to better understand local HAI and ARO surveillance activities across Canadian LTCHs.

METHODS: The Canadian Nosocomial Infection Surveillance Program administered a 12-item cross-sectional survey directly to LTCHs across all provinces and territories in English and French languages. We defined LTCHs as government-licensed homes for individuals with medical needs who require 24-hour onsite access to registered nurse care and/or treatment.

RESULTS: Between June 1 and November 28, 2023, 770 of an estimated 2,087 contacted LTCHs responded to the survey (37%). Of the respondents, 41% (318/770) were publicly funded, 67% (504/758) had between 51 and 200 long-term care beds, and 92% (694/758) reported having a designated person who leads infection prevention and control. The majority of LTCHs reported conducting outbreak surveillance (680/713, 95%) and surveillance for at least one type of HAI (672/740, 91%). The most common HAIs under surveillance were urinary tract infection (79%), gastroenteritis (75%), and *Clostridioides difficile* infection (75%). Half of LTCHs reported testing new residents for AROs via preadmission or admission cultures (368/713, 52%), of which, at least 90% tested new residents for methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *Enterococcus*, and 55% tested new residents for extended-spectrum β-lactamases. Almost two-thirds (63%) reported monitoring systemic antibiotic use.

CONCLUSION: The majority of LTCH respondents conducted surveillance for HAIs, and half of them tested for AROs in new residents; however, generalizability to all Canadian LTCHs is limited due to possible sampling, non-response, and social desirability biases. Despite differences in the scope of surveillance activities, mechanisms to measure the burden of HAIs and AROs in this setting exist and may provide the foundation for future national surveillance activities.

WP083

Seasonal trends in incidence and in-hospital mortality of hospitalization due to all-cause community acquired pneumonia (CAP) and

pneumococcal CAP (pCAP) in Canada, 2009–2019

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OBJECTIVE: Community-acquired pneumonia (CAP) varies seasonally, with increases in incidence typically occurring in winter months. Yet, there is limited comparative evidence across respiratory seasons regarding the incidence rate (IR) and mortality of pneumonia hospitalizations in Canada. This study describes IR and in-hospital mortality due to all-cause CAP and pneumococcal CAP (pCAP) hospitalizations in Canadian adults stratified by seasonality.

METHODS: This retrospective study used national administrative databases from the Canadian Institute of Health Information (CIHI) to identify patients hospitalized with CAP as the most responsible diagnosis (MRDx) or as a diagnosis other than MRDx (ODx) from 2009 to 2019. The IR and in-hospital mortality of hospitalizations due to all-cause CAP and pCAP were analyzed. The outcomes were stratified by age, year, summer (May–October), and winter (November–April).

RESULTS: Over the 10 years observed, the average IR of pneumonia hospitalizations (per 100,000 at risk) in those aged ≥18 years per year was 434.23 in CAP and 5.06 in pCAP. The average IR was higher in winter than that in summer (CAP: 243.75 versus 190.48; pCAP: 3.02 versus 2.04). The average in-hospital mortality (per 100 cases) per year was 12.36 in CAP and 7.87 in pCAP over 10 years. In CAP cases, the average in-hospital mortality was comparable between winter and summer (12.44 versus 12.25), whereas, in pCAP cases, it varied across years with winter in-hospital mortality, compared to summer, lower in 2014/2015, higher in 2016/2017, 2018/2019, and comparable in remaining years. Additionally, individuals aged ≥65 years for CAP and pCAP had higher IR and in-hospital mortality in both seasons each year compared to those aged <65 years.

CONCLUSION: A significant burden of disease persists throughout the year, particularly in those aged ≥65 years. Deseasonalization of preventive measures is of importance, and pneumococcal vaccination efforts must persist independent of season.

WP084

Evaluating copper-coated surfaces in a tertiary care paediatric hospital: Effects on microbial load and health-care-associated infections

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OBJECTIVE: Surfaces in hospital rooms are frequently contaminated with bacteria that can potentially cause health-care-associated infections (HAIs). The primary objective of this observational cohort study was to assess whether copper-coated surfaces would impact microbial burden on high-touch surfaces in a high-acuity paediatric setting, and the secondary outcome was rate of HAIs.

METHODS: Spray-coated copper surfaces (bed, overbed table, toilet seat, grab bar) were installed in 10 patient rooms in paediatric intensive care and oncology inpatient units; 10 similar rooms were chosen as controls. Patients were admitted to rooms based on convenience allocation during the 1-year study period. Environmental samples were collected on 28 occasions from high-touch surfaces, and overall bacterial colony counts were determined. HAI cases were identified through a surveillance database, and rates were calculated per 10,000 patient days. Poisson regression and negative binomial mixed-effects model were applied.

RESULTS: There were 71 patients admitted to intervention and control rooms during the study period. Patients admitted to intervention rooms were more likely to have an admitting diagnosis of infection (29.7% versus 2.9%). Overall, there was a trend toward lower colony counts in copper rooms over the 28 sampling episodes (relative risk [RR] 0.74 [95% CI 0.50–1.08]; $p = 0.11$), but there was variability depending on the type of surface. There was a trend toward higher HAI rates in intervention rooms (48.2 versus 30.5 cases per 10,000 patient days, rate ratio 1.58 [95% CI 0.78 to 3.20]; $p = 0.20$).

CONCLUSION: This study found no statistically significant reduction in colony counts or HAI rates associated with copper-coated surfaces. Influencing factors could include lower microbial loads due to the newness of the building, low baseline HAI rate, variations in the copper alloy's antimicrobial efficacy, and differences in patients admitted to intervention rooms compared to control rooms. The short study duration may obscure the intervention's full impact.

WP085

Estimation of the incidence of provincial health-care-acquired COVID-19 infection

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OBJECTIVE: To use administrative data to determine provincial incidence of health-care-associated COVID-19 infection (HAI COVID) rates in acute care settings across pandemic waves.

METHODS: Acute care admissions from March 1, 2020, to March 31, 2023, from the provincial Discharge Abstract Database were linked with polymerase chain reaction COVID-19 test results from the Province's Laboratory Information System. Admissions with COVID-19 were grouped into four categories of increasingly likely HAI COVID as follows: a positive COVID-19 test at ≥3 days, ≥5 days, ≥8 days, and ≥15 days after admission. Rates per 10,000 non-COVID inpatient days (days at risk, before COVID positive) were calculated for each category, overall, and by pandemic wave. Rate ratios for each wave relative to the fifth (Omicron) wave were calculated using Poisson regression.

RESULTS: Approximately 42,500 admissions were positive for COVID-19 during the study period. The Omicron wave had higher HAI COVID rates in each category than previous waves. Using our most conservative HAI definition of infection ≥15 days after admission, ~10 HAI COVID cases per 10,000 non-COVID inpatient days occurred during the Omicron wave and the rate ratio [95% C.I.] of HAI cases in waves 1 (Alpha), 2 (Beta), 3 (Gamma), and 4 (Delta) to wave 5 (Omicron) were 0.03 [0.02, 0.04], 0.03 [0.02, 0.04], 0.16 [0.14, 0.18], and 0.12 [0.11, 0.14], respectively.

CONCLUSION: HAI COVID rates varied by pandemic wave, with highest rates occurring in the Omicron wave. This may reflect increased transmissibility of the Omicron variant compared to other variants, increased community prevalence, as well as potentially lower vaccine effectiveness against the Omicron variant. These features will continue to impact current and future HAI rates, as Omicron subvariants remain prevalent.

Disclaimer: All inferences, opinions, and conclusions drawn in this abstract are those of the authors, and do not reflect the opinions or policies of the data steward(s).

WP086

Navigating the threat of carbapenemase-producing organisms: Time-series analysis of a public health surveillance initiative from 2014 to 2023

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OBJECTIVE: Carbapenemase-producing organisms (CPO) can cause life-threatening infections and spread antimicrobial-resistant genes between bacterial species posing a significant threat to public health. The threat of CPO necessitates vigilant surveillance programs to monitor their incidence and understand factors that drive their spread. We describe trends in provincial CPO case detection from August 25, 2014, to May 30, 2023.

METHODS: Provincial CPO surveillance captures all persons admitted to an acute care facility or who receive intensive care at an outpatient setting. Molecular genotyping of CPO-positive specimens is performed at the British Columbia Centre for Disease Control Public Health Laboratory using a custom multiplex qPCR assay. Clinical indicators were gathered using a survey instrument. Surveillance data were restricted to complete case information and time series analysis used X11 decomposition to inform modelling of CPO case counts by month with an autoregressive integrated moving average model (ARIMA).

RESULTS: The analytic data set included 1,036 CPO cases over the surveillance period. An ARIMA (1,1,1) model best fit the CPO time series using the criteria of AIC (662) and accuracy (0.794). An ARIMA (1,0,0) model was used to estimate the average number of CPO cases per month. On average, 11.45 (95% CI 3.56 to 19.35) CPO cases are detected, and the number of cases increases by 0.310 (95% CI

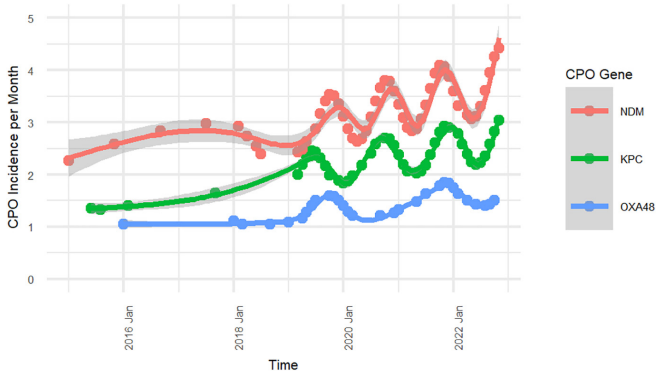

Figure WP086-1: Time-series analysis of provincial CPO cases with no recent travel history

0.0245 to 0.596) to 0.925 (95% CI 0.785 to 1.06) cases per month.

CONCLUSION: The number of observed CPO cases has increased over time between 2014 and 2023, in British Columbia (Figure WP086-1). Additional studies on the risk factors associated with CPO case incidence are needed.

WP087

Launching a provincial acute care respiratory illness surveillance system

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OBJECTIVE: The purpose of launching the respiratory illness (RI) surveillance system is to address the need for a provincial, standardized, early detection, and monitoring system for RI activity in acute care and to inform infection prevention and control (IPC) practices. Our goal is to employ an ongoing, collaborative, partnership-focused approach that offers accessible and relevant RI surveillance products to health authority IPC partners.

METHODS: The surveillance system uses administrative health data to develop indicators in collaboration with IPC, public health, and data and analytics colleagues. Populations under surveillance include patients presenting to an emergency department (ED) and the acute care inpatient population. Pediatric and adult syndromic indicators were developed for daily ED visits based on presenting complaints (CEDIS codes) for cough and fever and cough, fever, and shortness of breath, respectively. Data are updated weekly and shared with IPC partners in an interactive, internally accessible dashboard. Indicators are presented at the provincial level and stratified by, age, health authority, and facility.

RESULTS: The implemented syndromic surveillance system provides access to indicators for counts and proportions of ED visits for RI symptoms for both adults and pediatric patients. By providing timely awareness of RI burden at the provincial, health authority, and facility levels, this system informs strategy and operational decisions, allocation of resources, and IPC measures. Feedback from users indicates that they find the dashboard to be an excellent resource.

CONCLUSION: We have learned from the system launch that continued collaboration with end-users, public health officials, and data and analytics colleagues is crucial to the creation of practical, standardized surveillance products. Established partnerships will be leveraged to build future indicators for symptomatic patients visiting EDs, being hospitalized, and being admitted to critical care with a positive test for respiratory syncytial virus, COVID-19, or influenza A and B.

WP088

Pneumocystis pneumonia outcomes in patients with immunocompromising conditions: A population-based study over 20 years (2002–2022) in one Canadian province

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OBJECTIVE: While it is well established that HIV-positive and non-HIV immunocompromised patients are susceptible to *Pneumocystis* pneumonia (PCP), comparing PCP outcomes between patients with different underlying immunocompromising conditions is critically important to optimize chemoprophylaxis strategies.

METHODS: In this population-based cohort, we compared 30- and 90-day all-cause mortality following PCP diagnosis

among hospitalized immunocompromised patients in one Canadian province between April 1, 2002, to December 31, 2022. We linked several provincial health administrative databases using unique encoded identifiers and included all adult patients hospitalized with PCP based on diagnostic codes recorded in hospital discharge abstracts. We used unadjusted and adjusted logistic regression models to estimate unadjusted and adjusted odds ratios (uOR and aOR) and 95% CIs for the associations between underlying immunocompromising conditions and PCP outcomes.

RESULTS: A total of 1,327 patients were hospitalized with PCP, including 123 (9.3%) SOT recipients, 515 (38.8%) patients with active cancer, and 761 (57.4%) HIV-positive patients. 30-day and 90-day mortality rates were 10.6% and 19.5% in SOT recipients; 25.2% and 43.9% in patients with active cancer; and 8.0% and 13.3% in HIV-positive individuals. In the unadjusted model, organ transplantation was not associated with increased risk of 30-day or 90-day mortality ($uOR_{30\text{-day}}$ 0.66 [95% CI 0.36 to 1.20]; $uOR_{90\text{-day}}$ 0.71 [95% CI 0.44 to 1.13]), whereas solid tumour ($uOR_{30\text{-day}}$ 5.43 [95% CI 3.38 to 8.74]; $uOR_{90\text{-day}}$ 6.61 [95% CI 4.31 to 10.14]) and hematologic malignancy ($uOR_{30\text{-day}}$ 2.43 [95% CI 1.59 to 3.70]; $uOR_{90\text{-day}}$ 4.03 [95% CI 2.88 to 5.63]) were associated with increased risk. However, in the multivariable model, organ transplantation increased the risk of 30-day or 90-day mortality ($aOR_{30\text{-day}}$ 3.30 [95% CI 1.71 to 6.37]; $aOR_{90\text{-day}}$ 3.43 [95% CI 2.01 to 5.86]) compared to active cancer ($aOR_{30\text{-day}}$ 1.01 [95% CI 0.73 to 1.41]; $aOR_{90\text{-day}}$ 0.65 [95% CI 0.49 to 0.87]). The association between mortality and underlying HIV was negative in the unadjusted model ($uOR_{30\text{-day}}$ 0.28 [95% CI 0.20 to 0.39]; $uOR_{90\text{-day}}$ 0.22 [95% CI 0.17 to 0.29]), and positive in the adjusted model ($aOR_{30\text{-day}}$ 1.71 [95% CI 1.19 to 2.47]; $aOR_{90\text{-day}}$ 1.79 [95% CI 1.33 to 2.41]).

CONCLUSION: SOT recipients, followed by HIV-positive patients, have the strongest associations with PCP-associated mortality. We did not observe a significant association between other immunocompromising conditions and PCP-associated mortality.

WP089

Role of high-efficiency particulate air purifier in improvement of air quality and effective removal of indoor air contaminants at long-term health care facilities

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OBJECTIVE: Aerosol-generating medical procedures (AGMPs), such as airway suctioning and mechanical ventilation, can be carried out in certain long-term health care facilities (LTC) that have an established medically enhanced care unit (MECU). These procedures can potentially generate infectious aerosols in high concentrations and increase the risk of airborne transmission of pathogens. Particulate matter can further increase risk, as these particles tend to alter the behaviour of bioaerosols in the air. HEPA purifiers can eliminate 99.97% of dust, bacteria, and any airborne particles measuring 0.3 µm in size in controlled settings. The objective of this study was to assess the *in situ* effectiveness of HEPA purifiers in reducing particulate matter (PM 2.5) and potential bioaerosol concentrations during AGMPs within a MECU of a LTC facility.

METHODS: Airborne particulate matter concentrations were measured in a MECU and non-MECU before and during use of a HEPA purifier. HEPA purifier was turned off in the morning and activated at noon, running at the highest speed, continuously for 3 hours on each sampling day. Particulate matter sampling was conducted at ~1 m from resident's head. Outdoor particulate matter concentration was gathered from the Government of BC website. Sampling was conducted for 3 days. The statistical analysis was conducted using RStudio Version 2023.03.0.

RESULTS: The HEPA purifier demonstrated the ability to provide a marked percentage reduction of PM 2.5 in both MECU and non-MECU. Equivalent air changes per hour was effectively enhanced, thus reflecting an improvement in the ventilation and the overall indoor air quality.

CONCLUSION: Our study demonstrates that HEPA purifiers are effective in reducing airborne particulate matter, which can potentially lead to lower bioaerosol concentrations and dispersion in LTC facilities. During viral respiratory infection season, the use of HEPA purifiers may help reduce droplet and airborne transmission risk, and their use should be considered alongside other infection control measures.

WP090

Whole genome sequencing of 10 *Enterobacter hormaechei* revealed widespread transmission of *bla*$_{KPC-3}$ through two modes of transmission

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OBJECTIVE: An unusual cluster of nine *Enterobacter hormaechei*-KPC positive cases were found following routine screening of hospitalized patients within a window of 48 hours and identified through eight distinct units at a tertiary-care hospital in Quebec. This unusual situation led the hospital to investigate their putative relatedness and mode of transmission.

METHODS: Ten clinical isolates of *E. hormaechei* harboring the *bla*$_{KPC}$ carbapenemase gene detected by an in-house modified multiplex real-time PCR protocol were sent to the Reference Laboratory of Quebec in order to investigate their putative relatedness using pulsed-field gel electrophoresis (PFGE) analysis. A 10th specimen, collected and characterized 1 month prior the 9 cases collected between July 24 and July 25, was also analyzed for comparison. To better characterize the molecular epidemiology of the isolates, whole genome sequencing analysis was also performed by the National Microbiology Laboratory.

RESULTS: The PFGE analysis revealed the presence of two related clusters ($n = 7$ and $n = 2$) in addition to one distinct pulsotype. Multi-locus sequence typing (MLST) showed ST uniformity within all 9 isolates (ST43) while the 10th isolate was ST29. Short- and long-read sequencing delivered 10 complete and circular identical IncN plasmids habouring *bla*$_{KPC-3}$ gene within the Tn*4401*b-3 transposon. Two distinct patterns of carbapenemase mobilization (clonal, $n = 9$; ST43) and horizontal ($n = 1$; ST29), apparently not related to the health care environment or catheters and drains, may have contributed to the spread of *bla*$_{KPC-3}$.

CONCLUSION: We characterized the genome of 2 distinct *E. hormaechei* strains carrying the same IncN plasmid that spread through clonal ($n = 9$) and transposon-mediated horizontal gene transfer ($n = 1$). This concerning widespread of multidrug resistant isolates, as evidenced by genomic prediction of a resistance phenotype, may direct our efforts toward investigating other underestimated common source, which may explain such a number of affected patients, from different hospital units.

WP091

Shining a light on surgical site prevention: Nasal photodisinfection to prevent SSI in cardiac surgery

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OBJECTIVE: Nasal decolonization prior to cardiothoracic and orthopedic surgery has been shown to reduce surgical site infections (SSI) due to *Staphylococcus aureus*. This is now included as an essential practice in updated SSI guidelines. This study was conducted to assess the efficacy of nasal photo disinfection (a novel type of decolonization) for prevention of deep and organ space surgical site infections after cardiac surgery.

METHODS: This quality improvement study was conducted at the Mazankowski Heart Institute in Edmonton, AB. Nasal photodisinfection was performed on all patients presenting for cardiac surgery from June 1, 2023 to the present. The data presented are from June 1 to November 30, 2023. This procedure was done immediately prior to surgery. A combination of methylene blue and CHG was applied to the anterior nares followed by application of a nonthermal non UV light for a total of 2 minutes. This procedure was completed twice. Surgeries performed after hours or on weekends were excluded. The primary outcome was the development of deep and organ space surgical site infections. This was done using existing surgical site infection surveillance conducted by the infection prevention and control department at the Mazankowski Heart Institute. Secondary outcomes were in compliance with photodisinfection.

RESULTS: A total of 654 patients were eligible for photodecolonization. Forty-five patients (6.8%) did not receive treatment for reasons that included allergy to CHG, ongoing nasal oxygen therapy, patient refusal, and lack of supplies (one day). During this 6-month period, there were 2 deep or organ space infections. The average number of infections per 6-month period over the last 3 years is 8.

CONCLUSION: Nasal photodisinfection is a well-tolerated and easy to implement procedure that resulted in a significant decrease in surgical site infections resulting in cost savings.

WP092

Characterizing the gap in vaccination status in older adults residing in complex continuing care in an urban hospital

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OBJECTIVE: As recommended by the National Advisory Committee on Immunizations (NACI), adult vaccinations are a cornerstone of preventative care, especially for older and medically complex patients in complex continuing care (CCC) hospitals. Yet, there is no framework to ensure up-to-date routine adult vaccinations, including those against pneumococcal disease, herpes zoster, and tetanus. This study aimed to characterize the vaccination status of patients in a CCC and identify barriers to vaccination.

METHODS: A 10-year retrospective review of vaccinations was conducted of patients aged 50 years and older admitted to a 170-bed CCC program in an urban hospital. This included pneumococcal 23-valent polysaccharide, pneumococcal 13-valent, 15-valent, or 20-valent conjugate, Zostavax, Shingrix, and tetanus toxoid-containing vaccines. Institution and provincial electronic medical records (EMRs) were reviewed, and patients were interviewed. A cause-and-effect analysis was performed to identify barriers to vaccination and inform a pareto analysis.

RESULTS: All 143 patients admitted to CCC were included, and all met NACI criteria for vaccination against the three diseases. Average length of stay was 594 days (range 65 to 6931 days). 99.3% (142/143) were unvaccinated against herpes zoster, 98.6% (141/143) against pneumococcal disease, and 98.6% (141/143) were overdue for tetanus vaccination. Both patients who received pneumococcal vaccination were part of a previous vaccine campaign. The province publicly funded none for pneumococcal vaccination and only 12.1% (17/142) for Shingrix. Most frequent barriers to vaccination were the lack of a vaccine record and related EMR constraints, cost, and lack of a standardized hospital vaccine assessment.

CONCLUSION: These results highlight critical gaps in routine adult vaccinations in chronic care settings and has inspired next steps, including a formulary review for the addition of vaccines not funded publicly and EMR support for immunization records. However, this also calls for a broader framework to support adult vaccination assessments in chronic care settings.

WP093

Verification, analytical sensitivity, cost-effectiveness, and comparison of four *Candida auris* screening methods

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OBJECTIVE: Our primary objective was verifying chromogenic media culture (CC), broth enrichment followed by CC (BE-CC), PCR, and broth enrichment followed by PCR (BE-PCR) for *Candida auris* identification in screening specimens. Secondary objectives included test characteristic and cost-effectiveness determination.

METHODS: We prospectively evaluated CC, BE-CC, PCR, and BE-PCR in simulated bilateral axillary-groin specimens spiked with *C. auris* and/or non-*C. auris* yeast. We incubated CHROMagar Colorex Candida Plus agar aerobically on the Kiestra system at 37°C for 120 hours. We used a modified CDC protocol for PCR. For broth enrichment, we incubated Oxoid salt/dulcitol broth at 37°C for 48 hours at 250 rpm. We calculated test characteristics using CLSI methods. Cost-effectiveness analysis assumed a 5% positivity rate. We analyzed data using R v.4.3.0, with two-sided statistical tests and $p < 0.05$.

RESULTS: We tested 188 CC, 222 PCR, 63 BE-CC, and 64 BE-PCR specimens at varying dilutions, of which 342 (63.6%) were *C. auris*. At a 100 CFU/mL threshold, CC had a diagnostic sensitivity of 96.7% (95% CI 82.8% to 99.9%), and specificity of 94.7% (95% CI 74.0% to 99.0%), with a 5-day turnaround time (TAT). The analytical sensitivity of CC was 256.34 CFU/mL (95% CI 81.02 to 811.02). At a 100 CFU/mL threshold, PCR had a diagnostic sensitivity of 100% (95% CI 90.7% to 100%), and specificity of 100% (95% CI 80.5% to 100%), with a one-day TAT. The analytical sensitivity of PCR was 27.11 CFU/mL (95% CI 11.34 to 64.76). The analytical sensitivity of BE-CC and BE-PCR was 16.32 CFU/mL (95% CI 2.36 to 112.82) and 2.75 CFU/mL (95% CI 0.63 to 12.06), respectively. At a 5% positivity rate, the cost per case detected was $257 for CC, $307 for PCR, $809 for BE-CC, and $860 for BE-PCR.

CONCLUSION: CC provides the best balance of performance, cost, and TAT. In a high-prevalence setting, PCR's decreased TAT may offset its cost. BE offers marginal improvements, given its cost and TAT.

WP094

Impacts of COVID-19 on invasive fungal infections in Canadian ICU populations

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OBJECTIVE: Epidemiological studies characterizing invasive fungal infections (IFIs) in Canadian intensive care unit (ICU) settings have been sparse, in particular, with emergent concerns surrounding COVID-associated Pulmonary Aspergillosis (CAPA). Hence, this study investigates changes in IFI incidences, fungal species distribution, demographic factors associated with infection, and mortality in ICU patients before and during the SARS-CoV-2 pandemic.

METHODS: This retrospective chart review looked at all patients admitted to a tertiary care hospital ICU from 2019 to 2021 with a positive fungal culture (n = 362). The patients were separated into two periods, before and during the SARS-CoV-2 pandemic, with a subgroup analysis of COVID patients. IFI was diagnosed as originating from a sterile site, in accordance with the EORTC/MSGERC guidelines. The extracted data included demographic, microbiological, and clinical findings. A series of unadjusted and adjusted regression analyses were performed to identify predictors of IFI incidence and related association with in-hospital mortality during both periods.

RESULTS: IFI incidence (n = 76) increased by 8% (OR 1.60; p value = 0.080) from the prepandemic to pandemic period, which was significant when adjusted for confounders (adjusted odds ratio [aOR] 1.92; p = 0.028). The mean age and LOS for IFI patients was 60.63 years and 41.96 days, respectively. Adjusted ORs showed significantly increased subspecies distribution between periods in invasive candidiasis (n = 59, aOR range: 2.58 to 8.2; p < 0.05)—particularly with *C. albicans* (n = 36, aOR 2.58; p = 0.010)—and invasive aspergillosis (n = 5, OR 4.91; p = 0.015), with only two cases of CAPA detected. Two cases of invasive mucormycosis were noted. Demographic and immunosuppressive factors, in addition to period-related changes in mortality and COVID-19 status were not found to be associated with IFIs.

CONCLUSION: Overall, there was a significant increase in the presence of IFIs in ICU populations during the pandemic. Thus, this study emphasized the need for additional epidemiological investigations into IFI risk, with respect to SARS-CoV-2 impacting critically ill patients.

WP095

Prevalence of laboratory confirmed Creutzfeldt-Jakob Disease from three Ontario tertiary care centres between 2012 and 2022

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OBJECTIVE: Globally, Creutzfeldt-Jakob Disease (CJD) affects 1 in a million people annually, but there is a paucity of recent Canadian data. This study evaluates all laboratory-confirmed CJD cases in three tertiary Ontario hospitals over the last 10 years.

METHODS: Using laboratory information systems, all patients with a laboratory confirmed CJD between 2012 and 2022 were identified at three tertiary hospitals in Ontario. Retrospective chart reviews were completed with qualitative analysis to identify trends in descriptive epidemiology.

RESULTS: Thirty patients were identified across all three sites, with a mean age of 67.4 years at presentation. Patients had a mean of 2.2 visits (range 1–5) to the centre prior to admission and CJD testing. The most common symptoms included: loss of coordination and balance (63.33%; 19), changes in behaviour (60%; 18), progressive mobility loss (53.4%; 16), memory loss (50.0%; 15), and involuntary movements (50.0%; 15). Magnetic resonance imaging findings revealed potential indicators of CJD with 76.7% displaying diffuse restriction, and 50.0% showing asymmetrical hyperintensities. The mean duration from symptom onset to CJD testing was 91 days. Positive results for EP-QuIC were observed in 90.0% of patients, whereas 83.3% were positive for 14-3-3 ELISA. Sporadic CJD was identified in 93.3% of the cases (28). In terms of postdiagnosis care, 46.7% were discharged home, while 36.7% were transferred directly to palliative care. The average duration from symptom onset to death was 121 days, and from CJD diagnosis to death was 35 days. Notably, more cases of CJD were diagnosed postpandemic, with 12 cases occurring in 2022 alone.

CONCLUSION: This study emphasizes the importance of considering CJD as a differential diagnosis and subsequent laboratory testing in the context of appropriate neurologic symptoms that overlap with many noninfectious diseases. This is especially important as most cases were sporadic CJD, and thus, patients lacked risk factors and obvious indications for testing.

WP096

Ancient cesspit contents reveal evidence for human parasite infections in 15th–16th century Bruges, Belgium

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OBJECTIVE: Paleoparasitology, the study of human and animal parasites recovered from archeological sites, is providing important insight into parasite epidemiology throughout human history in varying geographical contexts. This study aimed to understand the species of parasites that infected merchants living in medieval Bruges, Belgium.

METHODS: Three sediment samples from different layers of a cesspit excavated from an elite estate in the international quarter of the city were studied. Following standard methods in paleoparasitology, samples were rehydrated and disaggregated in trisodium phosphate, sieved, and analyzed using microscopy to visualize preserved helminth eggs.

RESULTS: Eggs from parasites spread by the fecal-oral route including *Ascaris* and *Trichuris trichiura* were found in high concentrations. Zoonotic taxa including *Dicrocoelium*, *Fasciola*, and *Taenia* were also recovered. These parasites are consistent with those found in other archeological sites in Belgium. Additionally, an egg of *Schistosoma mansoni* was recovered, a parasite that is not transmitted within Belgium.

CONCLUSION: The presence of *Schistosoma mansoni* in the cesspit provides evidence for long-distance travel of an individual from endemic regions in Africa. *Schistosoma mansoni* has been found at one other archaeological site in Europe, a 15th century latrine in Montbéliard, France. Bruges was a major trading centre in Medieval Europe and housed numerous foreign merchants. Archeological materials originating from Italy and Spain were recovered from the cesspit attesting to the inhabitant's connections to the Mediterranean region. The parasites recovered from the cesspit show that those living in the elite estate were affected by common parasites found in the region, especially those transmitted by the fecal-oral route. However, individuals who used the cesspit were also infected with parasites transmitted in Africa attesting to long-distance travel of individuals in the community.

CASE REPORT SYMPOSIUM
Friday, April 12

CR01
Powassan virus encephalitis after tick bite in rural Manitoba

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OBJECTIVES:

1. Increase awareness of Powassan virus infection and encephalitis
2. Understand expanding range of black-legged ticks in Canada
3. Recognize the importance of further research into Powassan virus

DISCUSSION: This was the first case of Powassan virus (PV) encephalitis identified in Manitoba. PV is an emerging infection carried by black-legged ticks (BLT) that serve as both vector and host. BLT range is expanding through Canada, so encounters are likely to increase. Currently, there are a lot of gaps in our knowledge of PV in Canada; it is not a reportable illness in Canada, so cases are likely underdiagnosed. Transmission of PV can occur within 15 minutes in animal studies, and 3 h in human reports, which is faster than transmission of other tick-borne pathogens. On the basis of CDC data, infection carries high rates of morbidity and mortality. It most often presents with encephalitis. There are no specific treatments for patients that are infected, which means awareness of it and preventative measures to prevent infection are essential. PV encephalitis should be on the differential for patients presenting with encephalitis after a tick bite.

CR02
Neck mass misdiagnosed as a possible malignancy: Tularemia, the ancient disease that remains unknown to the medical community and a high risk to laboratory personnel

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OBJECTIVE: Increasing awareness and education about tularemia to avoid delay in treatment and improving communication with the laboratory personnel to ensure safety while handling suspect high-risk pathogens.

DISCUSSION: *Francisella tularensis* is a risk group 3 pathogen and presents a risk for laboratory personnel due to its aerosolization potential, low infectious dose, and fatality rate ranging from 2% to 60%. Our case demonstrates the lack of awareness in the medical community to recognize tularemia infections and the need for safer referral practices and improved communications with the laboratory to ensure personnel are taking the appropriate measures while handling patient samples to avoid potentially serious consequences. Luckily, in our case, the disease was detected and with a double coverage of antibiotics, the patient was able to improve drastically.

CR03
Topical, oral, and bladder-instilled phage therapy treats *E. coli* cystitis: An open-label single patient Canadian clinical trial

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OBJECTIVE: Urinary tract infections (UTIs) are a common problem worldwide. Increasing antibiotic resistance has led to the consideration of alternative therapies for UTIs, including bacteriophage (phage) therapy (PT). The objectives of this report are to explain the 34 steps involved in providing phage therapy in Canada through an Open Label Individual Patient (OLIP) clinical trial, appreciate how chronic suffering from urinary tract infections is a serious condition, and explain how phage therapy is increasingly considered a tool at the global level to address difficult-to-treat infections.

DISCUSSION: There are three take-home messages for this case. First phage therapy in Canada requires a clinical trial (NCT04437519 for our case) and is a detailed process. Second, phage therapy is essentially safe and seemingly effective (also supported by a recently published systematic review). Third, the demand for phage therapy is growing daily due to our antibiotic resistance crisis and increasingly complex medical care.

CR04

Balamuthia mandrillaris: A locally acquired fatal case, possibly a first for Canada

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OBJECTIVE: We present a case a fatal case in an 83-year-old male of *Balamuthia* encephalitis preceded by long-standing buttock lesions.

DISCUSSION: *Balamuthia mandrillaris* is a free-living amoeba and a rare pathogen, which causes granulomatous amoebic encephalitis, often associated with a preceding dermatologic lesion. Commonly associated with soil in temperate areas, its true distribution is not well described and is likely underdiagnosed. There are about 200 cases reported globally, predominantly from southwestern United States. This is likely the first locally acquired case in Canada (not travel associated), indicating the need to consider *Balamuthia* in the differential diagnosis of locally acquired encephalitis. Significant delay in acquiring the diagnosis and accessing testing raises the consideration for a locally accessible test for clinical relevance.

CR05

Mediastinal necrotizing lymphadenitis histoplasmosis in a 16-year-old patient with Crohn's disease

Adiel Marom, Christos Karatzios, Fransico Noya, Marina Salvadori

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OBJECTIVE: Report a case of histoplasmosis in an immunocompromised paediatric patient (treated by anti-TNF-α). This is the first case reported in our centre in over two decades.

DISCUSSION: While *Histoplasma capsulatum* is a rare pathogen in the paediatric population, especially in our region, it is an important cause of prolonged fever with granulomatous mediastinitis, especially in patients treated with anti-TNF-α.

CASE REPORT POSTER PRESENTATIONS

Friday, April 12

FP001

A case of severe native valve infective endocarditis (IE) caused by *Streptobacillus moniliformis* (rat-bite fever)

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OBJECTIVE: Outline the presentation and microbiologic diagnostic challenges of infective endocarditis secondary to *Streptobacillus moniliformis*.

DISCUSSION: *S. moniliformis* is a fastidious facultative anaerobic gram-negative bacillus that causes rat-bite fever (RBF) in North America; it is a part of nasopharyngeal/oropharyngeal flora in rats. Human transmission occurs through contact with rodents. Most commonly, infectious with RBF has clinical manifestations of fevers, arthralgias, and rash. Infective endocarditis secondary to *S. moniliformis* is a rare complication of this infection with high rates of morbidity and mortality. This, along with its difficulty to culture in the microbiology laboratory, warrants clinicians to maintain clinical suspicion in patients with pertinent exposures. Multidisciplinary care can improve outcomes.

FP002

Polymicrobial *Streptococcus mitis* and *Vagococcus fluvialis* infective endocarditis

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OBJECTIVE: *Vagococcus fluvialis* bacteremia has thus far been highly associated with infective endocarditis (IE); patients with this organism isolated in the bloodstream should be considered for echocardiography and monitored for acute clinical decompensation. Clinicians should periodically reference the International Society for Cardiovascular Infectious Diseases (ISCVID) website's "living document" for updates concerning high-risk causative pathogens of infective endocarditis. Clinicians are reminded to maintain a high level of suspicion for IE when a patient presents with a fever and a new murmur, especially in the context of intravenous drug use or poor dentition.

DISCUSSION: *Vagococcus fluvialis* has emerged as a pathogen of interest and should raise suspicion for IE in cases of monomicrobial or polymicrobial bloodstream infections; however, it is notably absent from microbiologic IE criteria and laboratory guidelines. When isolated in the bloodstream, *Vagococcus fluvialis* is highly associated with IE; moreover, there exists a potential association with fulminant clinical courses and destructive valvular lesions; as such, we propose *Vagococcus fluvialis* be considered for inclusion in the list of "typical" IE pathogens in the Duke-ISCVID IE criteria, and we recommend continued clinical surveillance of *Vagococcus fluvialis* infective endocarditis cases.

FP003

Partially treated *Actinomyces oris* native mitral valve endocarditis masquerading as subacute, relapsing fevers over a 6-month period

Jason Zou[1], Melanie Murray[1,2]

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OBJECTIVE: Reports of endocarditis secondary to *Actinomyces* are rare, and there are no consensus guidelines on optimal treatment regimens. Herein, we describe an unusual case of *Actinomyces* endocarditis, highlight challenges encountered in diagnosis, and discuss current dilemmas in treatment.

DISCUSSION: Clinicians should retain an index of suspicion for *Actinomyces* endocarditis when encountering subacute systemic symptoms with a history of dental disease. *Actinomyces* species are broadly β-lactam susceptible, which can lead to delayed diagnosis from partially effective treatment. Optimal treatment regimens are not well characterized, but case series suggest prolonged courses of β-lactams are required.

FP004

Bacteremia secondary to a phenotypically susceptible *bla*$_{\text{CTX-M-27}}$ positive *Escherichia coli*

Geneviève M Amaral[1], Gordon Ritchie[1,2], Samuel D Chorlton[1,3], Calvin KF Lo[1], Aleksandra Stefanovic[1,2], Nancy Matic[1,2], Michael Payne[1,2], Marc G Romney[1,2], Christopher F Lowe[1,2]

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OBJECTIVE: Tracking the spread of multidrug-resistant gram-negative bacteria is a global health priority. Molecular assays can rapidly identify resistance genes to support early antimicrobial stewardship. However, these assays are limited by their targets, and genotype may not always reflect phenotypic resistance. We describe a case of *bla*$_{\text{CTX-M}}$ detection by BioFire BCID2 FilmArray (bioMérieux, Marcy-l'Étoile, France) in a phenotypically susceptible *Escherichia coli*.

DISCUSSION: Our case highlights a key limitation of molecular (PCR-based) methods for antimicrobial resistance detection, whereby a genetic target did not accurately predict phenotype. Molecular assays remain an important rapid diagnostic tool supplementing conventional phenotypic susceptibility testing. Whole-genome sequencing can provide discordance resolution, and future work should focus on refining bioinformatic analyses to optimize genomic predictors of resistance.

FP005

Presumed travel-related pulmonary cystic echinococcosis in a child: Case report

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OBJECTIVE: To highlight:

1. The possibility of travel-related cystic echinococcosis.
2. Differences in the presentation of cystic echinococcosis between children and adults.
3. The differential diagnosis of a paediatric cystic lung lesion.

DISCUSSION: This case of pulmonary cystic echinococcosis was instructive given atypical epidemiology. In North America, most *Echinococcus granulosus* disease occurs in migrants from endemic areas or is locally acquired in the context of specific risk factors. Travel-related cystic echinococcosis is rarely reported and may be underestimated. This patient presumably acquired infection during prolonged travel to India. Children are more likely than adults to have pulmonary cystic echinococcosis; the differential diagnosis includes congenital lung cysts. Developmental factors may affect reporting of classic symptoms (e.g., expectoration of salty membranes with pulmonary cyst rupture). Travel-related cystic echinococcosis should be considered when exposure history and radiologic findings are potentially consistent.

FP006

Cutaneous alternariosis in acute lymphocytic leukemia

Reza Rahimi Shahmirzadi, Danielle Ouellette, Abeer Albaadani, Sarah Shalhoub, Huma Saeed, Michael Silverman Silverman, Lili Ataie

Western University, London, ON, Canada

OBJECTIVE: To discuss the importance of considering cutaneous fungal infections when examining immunocompromised patients with an unusual skin lesion

DISCUSSION: Neutropenia in hematological malignancies heightens the risk of severe cutaneous fungal infections. Cutaneous alternariosis, an emerging concern in immunocompromised patients, manifests with diverse clinical features. A heightened level of suspicion is crucial when evaluating immunocompromised patients with unusual skin lesions.

FP007

Snowshoe hare virus meningoencephalitis in a child

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OBJECTIVE: To present a rare cause of meningoencephalitis in a child.

DISCUSSION: California serogroup viruses (CSGV) causing meningoencephalitis are likely under-diagnosed and under-recognized in Canada.

FP008

Malaria in Canada? A case of *Babesia microti* infection in a returning traveler from Nova Scotia

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OBJECTIVE: We report a case of babesiosis masking as malaria in a traveler from the Yucatan Peninsula in Mexico and Nova Scotia, Canada – two different geographical locations where *Babesia microti* has been reported.

DISCUSSION: A 64-year-old male born in Yarmouth, Nova Scotia, currently living in Alberta, presented to the Emergency Department with fever, myalgias, malaise, and constitutional symptoms that began 5 weeks after travel to Nova Scotia, Canada. 3.5 months prior, he had traveled to Yucatan, Mexico. Routine testing revealed small ring trophozoite forms with normal sized erythrocytes lacking Schuffner's dots suggestive of *Plasmodium falciparum* (0.7% parasitemia) on blood smear. Given travel to Mexico, it was felt that this may be more consistent with *P. vivax* infection despite morphologic ambiguity. Follow-up malaria confirmation using RT-PCR was positive for the pan-*Plasmodium* target, but negative for speciation on two separate occasions. He was treated with atovaquone/proguanil and discharged. One-week post-discharge, he continued to have fevers, rigors, and lethargy (repeat smears demonstrated 0.9% parasitemia, which could not be speciated

on RT-PCR). Given travel to Nova Scotia and inconsistent ring-form morphologies, testing for Babesiosis was conducted—with positive *Babesia* spp serology and PCR testing (presumptive *B. microti*). When these results became available, the patient had completed a terminal primaquine course with resolution of symptoms.

FP009

Bedaquiline, pretomanid, linezolid, and moxifloxacin (BPaLM) treatment for multidrug-resistant extrapulmonary tuberculosis (MDR-EPTB) in Canada: A case report

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OBJECTIVE: Updated global TB guidelines recommend the novel oral 6-month BPaLM regimen for MDR-TB based on superior efficacy, and reduced toxicity demonstrated in clinical trials that were dominated by isolated pulmonary TB. Data for its effectiveness for EPTB remain limited. Herein, we present the first reported case of EPTB treated with BPaLM in Canada and review available evidence.

DISCUSSION: This case highlights the first report in Canada of the safe and effective use of BPaLM for TB involving an extrapulmonary site. Shorter duration, improved effectiveness, and reduced toxicity suggest that BPaLM should be considered when determining the ideal treatment regimen for MDR-TB, including nonsevere EPTB. Further research is needed to clarify longer-term outcomes and optimal dosing of BPaLM for EPTB, especially in more severe forms of disease or with malabsorption concerns.

FP010

First case report of disseminated gonococcal arthritis in a Canadian province

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OBJECTIVE: Disseminated gonococcal infections (DGIs) are a rare, but often debilitating, complication of *N. gonorrhoeae* infections. Often presenting as arthritis-dermatitis syndrome, true suppurative joint infections are an even more rare form of DGI. Here, we present the first known case of DGI in a Canadian province in more than 10 years.

DISCUSSION: DGIs, while rare, need to remain on any clinician's differential for septic arthritis given the increasing prevalence of gonorrheal infections in Canada. Epidemiology of *N. gonorrhoeae* infections, and their increasing prevalence, is discussed. In addition, patients who are at risk of delaying access to care, such as people who inject drugs and unhoused individuals, are at higher risk of complicated hospital stays. This report reinforces the need for adequate postoperative pain control for patients who inject drugs.

FP011

Navigating the challenges: Managing mold, mycobacterial, and viral infections in a hematopoietic stem cell transplant recipient

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OBJECTIVE: To discuss the challenges in concurrently managing mold, mycobacterial, and viral infections in a hematopoietic stem cell transplant recipient.

DISCUSSION: Concurrent treatment of mold, mycobacterial, and viral infections in a patient with history of hematopoietic stem cell transplant is difficult due to drug interactions and potential adverse events.

FP012

Candida blankii: The difficult capture of a fungus with pathogenic potential

Arjun Sharma, Ana Cabrera, Fatimah AlMutawa

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OBJECTIVE: Over the past decade, there have been increasing reports of infections due to the yeast *Candida blankii* (*C. blankii*). Here, we describe two cases in adults—the first reported human cases in Canada—more than 50 years after its isolation by Canadian scientists in minks.

DISCUSSION: These cases highlight the pathogenic potential for *C. blankii*, along with the challenges associated with identifying the organism and determining its susceptibility patterns. Improving existing assays would aid in more timely identification and initiation of therapies.

FP013

Unmasking complexity: Navigating the diagnostic challenge of a false-positive cryptococcal antigen in chronic meningitis with suspected indolent CNS B-cell lymphoproliferative neoplasm

Melissa Fowler, Lise Bondy, Seth Climans, Jonathan Lau, Eric To, Yiannis Iordanous, Marilyn Phung, Jeffrey Fuller, Michael Silverman, Reza Rahimi Shahmirzadi

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OBJECTIVE: Chronic meningitis is a diagnostic challenge with a broad infectious and noninfectious differential diagnosis. Herein, we describe a patient with chronic meningitis and an initial positive cerebrospinal fluid (CSF) cryptococcal antigen (CrAg), who was later found to have a possible central nervous system B-cell lymphoproliferative neoplasm. Causes of false-positive CrAg results were also reviewed.

DISCUSSION: This case explores additional causes of false-positive CrAg and emphasizes the importance of interpreting test results in the complete clinical context, especially with a challenging diagnosis, such as chronic meningitis.

FP014

Less is more? Two cases of cryptococcosis treated using single-dose liposomal amphotericin B as part of induction therapy in solid organ transplant recipients

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OBJECTIVE:

1. Recognize unique manifestations of cryptococcosis in solid organ transplant (SOT) population.
2. Exemplify challenges of managing cryptococcosis in SOT.
3. Demonstrate a potential alternative regimen for cryptococcosis in SOT using single-dose liposomal amphotericin as part of induction therapy.

DISCUSSION: Cryptococcosis management in SOT is complicated by drug interactions (triazoles, antirejection medications) and amphotericin B-induced nephrotoxicity. To our knowledge, these are the first reported cases of cryptococcosis in SOT successfully treated using single-dose LAmB as part of induction therapy. Further data supported by randomized trials or observational studies may help evaluate the efficacy of this regimen in SOT and identify appropriate treatment candidates.

FP015

A palatable diagnosis: Disseminated blastomycosis with mucocutaneous involvement

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OBJECTIVE: Illustrate a case of disseminated blastomycosis in an immunocompetent host with diffuse nodular skin lesions and hard palate involvement. This case highlights the unique mucocutaneous manifestation of blastomycosis.

DISCUSSION: *Blastomyces dermatitidis*, a thermally dimorphic fungus, is typically found in soil enriched with decaying vegetation and thrives in humid conditions across North America. Blastomycosis most commonly manifests as pulmonary disease but can disseminate to the skin, bone, and genitourinary system. Cutaneous lesions typically appear as ulcerated or verrucous plaques, occasionally adorned with pustules. Involvement of the palate, gingiva, and tongue is uncommon, and similar to cutaneous lesions, can have varied appearances. The diagnosis of blastomycosis is established through demonstration of characteristic braid-based budding organisms on histopathologic examination and fungal culture. Because of the diverse presentations of blastomycosis, it may not

be initially considered in the clinical differential diagnosis of mucocutaneous lesions, and, thus, diagnosis may be delayed.

FP016

Bilateral thigh abscesses caused by *Mycobacterium chelonae* in the context of patient-administered testosterone injections

Lili Ataie[1], Esraa Babaeer[1,2], Sameer Elsayed[1], Lise Bondy[1], Megan Devlin[1], Huma Saeed[1], Mahshid Mohammadi[1], Sarah Shalhoub[1], Michael Silverman[1], Reza Rahimi Shahmirzadi[1]

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OBJECTIVE: To underscore the significance of considering cutaneous mycobacterial infections in the assessment of patients experiencing skin and soft tissue infections, particularly those with penetrating injuries and inadequate responses to conventional antibacterial therapies.

DISCUSSION: Rapidly growing nontuberculous mycobacterial infections should be considered in the differential diagnoses of persistent and treatment-resistant skin lesions or ulcerations, particularly following trauma and surgery, Therefore, a meticulous history-taking, physical examination, and collection of tissue biopsies for histopathological and microbiological investigations are essential for accurate diagnosis of this condition. Prompt empiric and culture-directed treatment is imperative for effective management.

FP017

Delayed presentation of rhinoscleroma with laryngeal involvement in a patient who immigrated to Canada from El Salvador 25 years prior to diagnosis

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OBJECTIVE: As immigration increases in Canada, neglected tropical diseases need to be considered in the differential diagnosis of commonly encountered clinical problems. Here, we describe a case of rhinoscleroma in a patient who immigrated to Canada 25 years prior to diagnosis.

DISCUSSION: This case highlights the importance of considering rhinoscleroma as a cause of sinonasal symptoms in patients who originate from endemic areas, even if they have been residing in Canada for several years. Despite its name, rhinoscleroma can involve the entire upper airway, including the larynx.

FP018

Invasive pulmonary *Irpex lacteus* infection in an immunocompromised patient with myelodysplastic syndrome

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OBJECTIVE: To discuss a case of *Irpex lacteus* invasive pulmonary infection in an immunocompromised patient and review the limited literature regarding this fungus as an uncommon agent of human disease.

DISCUSSION: We describe a case of fatal pulmonary *Irpex lacteus* infection in the context of MDS with prolonged neutropenia. Invasive molds are a significant cause of fungal disease in immunocompromised patients, with the bulk of infections caused by *Aspergillus, Fusarium, Mucorales*, and *Scedosporium* species. *Irpex lacteus* is a common environmental wood rot fungus, but an unusual human pathogen, with only a few cases of disease reported in the literature. There are no published antimicrobial breakpoints for this organism and no defined therapeutic regimens, making treatment decisions challenging. Along with other basidiomycetes, *Irpex lacteus* may represent an emerging cause of invasive mold infection in immunosuppressed individuals.

FP019

Prosthetic joint infection with carbapenem-resistant *Acinetobacter baumannii* treated with colistin and sulbactam-durlobactam: A case report and review of the literature

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OBJECTIVE: Describe a case of a carbapenem-resistant *Acinetobacter baumannii* infection of a prosthetic joint treated with colistin and sulbactam-durlobactam. Review the literature around *A. baumannii* bone and joint infections and the mechanism of action of sulbactam-durlobactam.

DISCUSSION: There is limited evidence to guide antimicrobial therapy of carbapenem-resistant *Acinetobacter baumannii* infections, and no evidence in the setting of prosthetic joint infections. For pulmonary and bloodstream infections caused by this organism, colistin is often used despite inadequate drug exposure at the tissue level, nephrotoxicity, and high mortality when used as monotherapy. Cefiderocol has shown limited effectiveness in both observational and randomized studies of these infections despite in vitro susceptibility. Sulbactam is a β-lactamase inhibitor that, at high doses, inhibits penicillin-binding proteins and has antibacterial activity itself. Durlobactam is a β-lactamase inhibitor with activity against OXA-type carbapenemases expressed by *A. baumannii* and protects the β-lactam activity of sulbactam in vitro. To our knowledge, this is the first described case of *A. baumanni* prosthetic joint infection.

FP020

A case report of long-standing profound neutropenia with uncertain etiology and concomitant cutaneous fungal infection

Esraa Ali Babaeer[1,2], Lili Ataie[1], Danielle Ouellette[1], Sameer Elsayed[1], Lise Bondy[1], Megan Devlin[1], Huma Saeed[1], Mahshid Mohammadi[1], Sarah Shalhoub[1], Michael Silverman[1], Lalit Saini[1], Reza Rahimi Shahmirzadi[1]

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OBJECTIVE: To discuss a significance of considering cutaneous fungal infections in assessing patients with chronic cutaneous ulcers unresponsive to antibacterial therapy and long-standing neutropenia.

DISCUSSION: Manifestation of fusariosis in clinical practice is heavily influenced by the immune status of the host and the entry point of the infection. Localized cutaneous Fusariosis should be considered in chronic unresponsive ulcers and associated profound neutropenia in patients with possible autoimmune processes.

FP021

Leveraging additive antibiotic effects: Management of an extensively drug-resistant *Pseudomonas aeruginosa* bloodstream infection

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OBJECTIVE:

1. Recognize that importation of resistant isolates arises from travel to regions of multidrug-resistant (MDR) pathogens.
2. Exemplify challenges of managing difficult-to-treat *Pseudomonas aeruginosa* infections.
3. Demonstrate how combinations of antibiotics may be used as salvage therapy.

DISCUSSION: Despite growing concerns of MDR pathogens, reliance on conventional phenotypic antimicrobial susceptibility testing constrains the initiation of effective treatment. Undertaking earlier, simultaneous susceptibility testing of conventional and nonconventional antimicrobials when suspecting MDR pathogens may streamline this process and reduce turnaround time. Our case also illustrates the ongoing challenges of managing MDR bacterial infections with limited available effective therapies. Clinicians may consider nonconventional antibiotic combination therapy to treat MDR infections by leveraging their potential additive effects.

FP022

Rituximab friend or foe? PML in a non-HIV patient with non-Hodgkin lymphoma post-rituximab and autologous stem cell transplant treatment

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OBJECTIVE: Progressive multifocal leukoencephalopathy (PML) is a devastating neurological disease caused by the JC virus and is traditionally linked to immunocompromised patients with untreated HIV. However, it is now emerging in non-HIV patients due to novel immunotherapies, such as rituximab. We present a case of a 69-year-old non-HIV patient with non-Hodgkin lymphoma (NHL) treated with rituximab and autologous stem cell transplantation.

DISCUSSION: This case underscores the need to consider PML in immunocompromised patients with subacute onset of focal neurological symptoms and rituximab exposure. While natalizumab is classically linked to PML, rituximab should also be recognized as a potential culprit. This is important to ponder as rituximab is a biologic treatment for many conditions ranging from NHL to autoimmune conditions, but one should be cautious of the potential devastating adverse events of this drug. Furthermore, exploring pembrolizumab's potential as a therapeutic option for PML in rituximab-exposed patients is crucial. In conclusion, the evolving landscape of PML demands heightened awareness in non-HIV patient populations, prompting careful evaluation of rituximab's role in precipitating this neurological condition and considering innovative treatments like pembrolizumab.

FP023

Chronic schistosomiasis in a paediatric patient following allogeneic haematopoietic stem cell transplantation: A case report and review of the literature

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OBJECTIVE:

1. To describe the first reported paediatric case of chronic schistosomiasis presentation following haematopoietic stem cell transplantation (HSCT)
2. To emphasize the importance of detailed pretransplant parasitic disease assessments
3. To highlight potential for serologic cross-reactivity of helminth antigens

DISCUSSION: This case underscores the challenges of undiagnosed chronic schistosomiasis post-HSCT. Our patient's history raised concerns regarding possible exposure to freshwater and poor sanitation in a country in eastern Africa highly endemic of *Schistosoma*. Chronic schistosomiasis results from immunopathological reactions to schistosome eggs, leading to inflammatory and obstructive disease in affected organs. *S. mansoni* specifically causes hepatosplenic inflammation and liver fibrosis. Diagnosis involves stool and urine examination, with sensitivity approaching 100% for four stool samples. Serology is less sensitive and specific due to cross-reactivity from other helminth antigens. We hypothesize that our patient's HSCT and engraftment facilitated a marked immune response to the schistosome eggs of chronic schistosomiasis. This case stresses the importance of pretransplant parasitic disease evaluations. Screening for schistosomiasis should be considered in patients from endemic regions. Treatment prior to transplant may prevent morbidity and mortality post-transplant in infected individuals.

FP024

Two simultaneous carbapenemase-producing Enterobacterales outbreaks in a Canadian tertiary care centre: Highlighting gaps in CPE screening and outbreak management

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OBJECTIVE: Targeted screening strategies used in our institution to prevent carbapenemase-producing Enterobacterales (CPE) outbreaks may be inadequate to address the increasing national prevalence of CPE. Our experience

illustrates certain gaps in existing practices and laboratory methods used for CPE screening and for the investigation of CPE outbreaks.

DISCUSSION: Our outbreak highlights two main points. The transmission of multiple CPE isolates from patients without any identified risk factors (e.g., foreign hospitalization) suggests that patients with CPE colonization are missed by our risk-based targeted screening; expanded admission screening criteria may be warranted. Second, the prolongation of the outbreak demonstrates the need to improve screening specificity, while maintaining sensitivity of CPE testing, and to improve the availability and rapidity of confirmatory testing and typing. Lastly, better evidence is needed to optimize management of CPE outbreaks.

FP025

Blastomyces dermatitidis mastoiditis and venous sinus thrombosis in an adolescent: An uncommon pairing of common diseases

Matthew Kochan, Sergio Fanella

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OBJECTIVE:

1. To present a case of *Blastomyces dermatitidis* otomycosis, mastoiditis, osteomyelitis, and soft tissue infection in a 14-year-old adolescent
2. To review the incidence and presentation of *Blastomyces* head and neck infections

DISCUSSION: Acute otitis media is common in children and complications such as labyrinthitis, mastoiditis, meningitis, and venous sinus thrombosis are well described complications of AOM. *B. dermatitidis* is endemic parts of Canada. However, head and neck infections caused by *Blastomyces are* relatively uncommon, and in our literature search we did not come across any cases of *Blastomyces* mastoiditis or venous sinus thrombosis in children. This case highlights the importance of considering unusual etiologies of relatively common presentations in paediatric infectious disease.

FP026

When malaria gets mixed: Complications in plasmodium species detection with multiplexed PCR

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OBJECTIVE: This case study aims to increase awareness and investigate the performance limitations of multiplex malaria polymerase chain reaction (PCR) testing, particularly the detection of mixed infections.

DISCUSSION: This case study highlights the need for awareness around detection challenges of low-level malarial infection with multiplex PCR. This is especially important in potential cases of mixed *Plasmodium vivax* or *P. ovale* infection given the therapeutic management implications. Findings in our setting suggest singleplex PCR testing may enhance sensitivity over the used multiplex design, especially in cases with a history of antimalarial treatment and/or suspected mixed infection. Nonetheless, the high observed overall qualitative concordance between microscopy, multiplex and singleplex PCR results was reassuring. Further efforts on optimizing assay design to limit target competition and broader applicability to other multiplex assays should be considered.

RAPID FIRE PRESENTATIONS

Session A
Oral Presentations: Wednesday, April 10
Poster Presentations: Friday, April 12

RFA01

Increased rates of laboratory confirmed cases of syphilis in western Canadian versus eastern Canadian blood donors: 2022–2023

Steven J Drews[1,2], Carmen L Charlton[1,2], Vanessa Tran[3,4], Hong Yuan Zhou[5,6], Gordon Hawes[7], Ilona Resz[8], Sheila F O'Brien[9,10]

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OBJECTIVE: Currently, there is a growing infectious syphilis outbreak in western Canada. Prior to donation, blood donors are screened for syphilis risks (e.g., sexual history, past diagnosis/treatment). Despite that screening, some blood donors will still be confirmed test-positive for syphilis during the blood donation process, and those donations will be discarded. This study compares the characteristics of confirmed test-positive syphilis donations in both western Canada (Manitoba West) and Eastern (East of Manitoba) for November 2022 to August 2023.

METHODS: Donors were defined as Western or Eastern. Following pretest screening, all blood donations were tested for syphilis (PK-TP assay, Beckman Coulter, USA). Confirmatory testing at one of two reference laboratories used the *Treponema pallidum* particle agglutination (TPPA) and the rapid plasma regain (RPR) assays. An RPR titer was of $\geq$1:8 was a proxy for possible infectious syphilis (primary, secondary, early latent). Data were collated using Excel (Microsoft, USA). Data analysis utilized GraphPad Prism (GraphPad Software, USA).

RESULTS: Total specimens tested for syphilis were western (n = 328,753) and eastern (n = 395,300). Rates of laboratory confirmed syphilis were higher in western (n = 44, 13.4/100,000 donations) versus eastern (n = 19; 4.8/100,000 donations, Fisher exact test, two-sided; p = 0.0001) donors. Most syphilis confirmations were in first-time donors (western Canada n = 31/44, 70%, eastern Canada 13/19, 68%). There was no difference in rates of possible infectious syphilis in western (n = 8, 2.4/100,000 donations) versus eastern Canada (n = 11, 2.8/100,000 donations, Fisher exact test, two-sided; p = 0.82).

CONCLUSION: Although rates of laboratory confirmed syphilis were higher in western versus eastern donors, Western donors did not have higher rates of infectious syphilis. We speculate that predonation screening may reduce the risks of collecting blood from a donor with infectious syphilis. Further studies might assess whether donors with laboratory-confirmed syphilis understood predonation screening questions or were completely unaware of a past infection.

RFA02

Sample processing methodology alters observed diversity in metagenomic and metatranscriptomic microbiome profiles from human stool

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OBJECTIVE: Owing to the high degree of variability inherent in microbiome profiling, establishing a consensus for microbial signatures or biomarkers of disease across studies is difficult. Differences in study methodology can further complicate comparisons since the laboratory protocols for sequence-based data capture and analysis are varied. The objectives of this research are to evaluate several methods for fecal sample storage and processing and to describe the impact of these methods on resulting taxonomic and functional gastrointestinal (GI) microbiome profiles.

METHODS: Briefly, healthy fecal samples are used to test the effect of different storage and extraction conditions on metagenomic and metatranscriptomic profiles. The comparative effect of both the preservant and the extraction kit on the metagenomic and metatranscriptomic profile of the sample was observed from DNA and RNA sequence data. Shotgun sequencing of nucleic acid libraries was performed using Illumina short-read sequencing technology, producing high-coverage sequence data containing millions of reads. Sequence data were analyzed using bioinformatic tools MetaPhlAn and HUMAnN for taxonomic and functional profiling, respectively.

RESULTS: In both metagenomic and metatranscriptomic analyses, the combined effect of nucleic acid storage and extraction was shown to produce significant differences in taxonomic profiles at the phylum and species level. The Firmicutes:Bacteroidetes ratio, species richness, Shannon Index, and beta diversity of microbiome profiles were all affected by methodology.

CONCLUSION: Our findings demonstrate that the experimental methodology used to stabilize and isolate nucleic acids from human stool samples can significantly impact the ability to capture GI microbiome diversity

from metagenomic and metatranscriptomic data. Notably, GI microbiome characteristics commonly used as health markers in disease research are differentially impacted by the specific combination of preservative reagent and nucleic acid extraction kit. This study describes important considerations for future metaomic microbiome research, including the choice of bacterial lysis approach and potentially detrimental mismatching of commercial reagents.

RFA03

Optimizing methods for the genomic surveillance of viral pathogens in wastewater

Ian Restall, Amjad Arrabi, Sarah Marttala, Andrew Bulir, Doris Williams, Jodi Gilchrist, David Bulir

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OBJECTIVE: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has underscored the epidemiological and public health benefits of wastewater surveillance of pathogenic viruses. Here, our goal is to develop and improve methods for the genomic surveillance of SARS-CoV-2 and a panel of viruses in wastewater that are of high risk to public health.

METHODS: SARS-CoV-2 amplicon sequencing methods were developed and optimized using Oxford Nanopore Technologies (ONT) kits and instruments. We used the 1,200 base pair (bp) Midnight (ver. 3) primer pools to amplify two amplicon pools and the ONT rapid barcoding kit for library preparation. For the surveillance of a broader panel of 66 viruses, we used Illumina's Viral Surveillance Panel kit and the MiSeq sequencing instrument. Library preparation was performed, according to the manufacturer's recommendations with critical modifications to the probe hybridization steps.

RESULTS: Sequencing SARS-CoV-2 genomes from wastewater has been optimized to reduce hands-on time, cost, and time to results. This was accomplished by switching to one-step PCR reactions, sample, and pool normalization, and generating 1,200 bp amplicons that enable the use of the ONT rapid barcoding kit. Initial attempts to validate Illumina's Viral Surveillance Panel enrichment of a panel of viruses in wastewater samples were ineffective. Following multiple rounds of testing and optimization, changes were made to the probe hybridization steps, and successful enrichment and sequencing of viral genomes in wastewater were successful.

CONCLUSION: Here, we have optimized sequencing methods for the surveillance of genomic variation in SARS-CoV-2 to decrease library preparation time and greatly reduce costs. In addition, we describe critical improvements to Illumina's Viral Surveillance Panel methods that allow for the successful sequencing of multiple viral genomes and the genomic surveillance of 66 viruses in wastewater that are of high risk to public health.

RFA04

Molecular epidemiology of rotavirus strains in Quebec from January to June 2023

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OBJECTIVE: Rotavirus vaccine is part of Quebec's public immunization program since 2011. In 2018, the province implemented an off-label, two-dose schedule of the RotaTeq vaccine. In 2022–2023, an increase in rotavirus positivity rate was noted. Genotyping of strains was performed to describe the molecular epidemiology of rotavirus during this period of increased incidence.

METHODS: All stool samples, from the province of Quebec, that tested positive for rotavirus by the in-house LSPQ RT-PCR multiplex viral panel between January 1st and June 30th, 2023, were included. A subgroup of samples tested with the Biofire gastrointestinal panel was also included. Strains genotype was determined by Sanger sequencing of VP4 (for genotype P) and VP7 (for genotype G) genes.

RESULTS: We genotyped 52 rotavirus positive samples from patients, with a median age of 4.9 years old (range 0.4 to 100 years old). Specimens were mainly submitted by laboratories from the Greater Montreal Area ($n = 45$, 86.5%) and included samples from 2 distinct outbreaks (11 samples from a day care and 5 samples from a long-term care facility). Sequencing of both genes was successful in 48 samples among which, genotype G3P[8] was largely predominant ($n = 43$, 89.6%). Genotypes G12P[8] ($n = 3$, 6.3%), G9P[8] ($n = 1$, 2.1%), and G2P[4] ($n = 1$, 2.1%) were also identified. Strains from the 2 outbreaks were from different clades of G3P[8].

CONCLUSION: G3P[8] was the predominant rotavirus genotype in stools submitted for viral testing at the LSPQ during the surveillance period. Our findings suggest that genotype G3 is still circulating widely and remains a cause of outbreak in Quebec, despite good immunization coverage. Although a switch toward G3P[8] genotype has been observed in other jurisdictions following RotaTeq® implementation, the potential impact of Quebec two-dose schedule on circulating strains should be explored.

RFA05

Prevalence of antibodies to human T-cell lymphotropic virus-1/2 in Canada over 33 years of monitoring in blood donors

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OBJECTIVE: Estimate the prevalence of anti-HTLV-1/2 in Canadian blood donors and assess the association with demographic variables and risk factors.

METHODS: First-time blood donors in all Canadian provinces except Quebec from 1990 to 2022 were included. Blood samples were tested for HTLV-1/2 by EIA, confirmed by Western blot analysis. Data were analyzed by logistic regression with year, age group, sex, region, neighbourhood material deprivation, and ethnocultural composition indices. Since 2005, all confirmed anti-HTLV-1/2-positive donors (cases) were invited to participate in a risk factor interview, and 4 nonpositive donors (controls per case) were matched for age, sex, and region. Case-control predictors of anti-HTLV-1/2 were analyzed using logistic regression.

RESULTS: There were 3,085,554 first-time donors from 1990–2022. Anti-HTLV-1/2 prevalence remained low (12.2 per 100,000 in 2022 (95% CI 6.4 to 23.5). The odds ratio was higher in females (2.0 [1.5 to 2.6]), older age groups (50+ 6.3 [4.3 to 9.2]), in BC and Ontario, in materially deprived (1.9 [1.2 to 2.9]) and ethnocultural neighbourhoods (7.5 [3.2 to 17.3]). Most anti-HTLV-1/2 in Ontario was HTLV-1, whereas in BC, half were anti-HTLV-2. There were 43 of 149 (28.8%) cases who completed an interview, 172 of 413 (41.6%) of controls. The strongest predictor of anti-HTLV-1/2 in case-control analysis was birth in a high prevalence country (OR 39.8, 7.8–204.3) but about 50% of anti-HTLV-1 and 90% of anti-HTLV-2 were Canadian-born.

CONCLUSION: Anti-HTLV-1/2 prevalence is low in Canada. While association with ethnocultural neighbourhoods is strong, high-prevalence country of birth accounts for about half of anti-HTLV-1; anti-HTLV-2 positives are usually Canadian-born. Anti-HTLV-1/2 transmission likely occurs overseas and within Canada.

RFA06

Assessing the potential for specimen pooling to streamline nosocomial surveillance of methicillin-resistant *Staphylococcus aureus*

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OBJECTIVE: In hospitals, identification of methicillin-resistant *Staphylococcus aureus* (MRSA) is important to reduce possible transmissions and serious outcomes. Traditional culture and susceptibility testing requires 48–72 hours, whereas Xpert polymerase chain reaction (PCR) can provide accurate MRSA detection in <1 hours. Unfortunately, the high cost of such commercial PCRs precludes their use in many laboratories. Using MRSA as a model, this study hypothesized that specimen pooling in a setting of low prevalence could reduce PCR costs and provide rapid results.

METHODS: 424 sequential nasal/groin specimens submitted for MRSA detection were subjected to routine culture-based detection using chromogenic media, and suspect colonies were confirmed using mass spectrometry and cefoxitin disk diffusion testing. These specimens were also pooled 1:8 or processed individually by Xpert MRSA PCR. Analytical sensitivity of PCR with and without pooling was compared to culture using triplicate 10-fold serial dilutions of a MRSA reference strain.

RESULTS: The analytical sensitivity and clinical performance of specimen pooling paired with Xpert MRSA PCR were equivalent to traditional culture-based detection. Of specimen pools, 66.0% (35/53) were MRSA-negative and

34.0% (18/53) were MRSA-positive. Pool resolution by PCR showed similar results as culture, identifying 116 MRSA-negative and 28 MRSA specimens.

CONCLUSION: At a prevalence of 6.6% (28/424), 1:8 specimen pooling with Xpert PCR provided equivalent results to culture-based methods and reduced the overall number of PCR reactions by 53.5%. Compared with individual PCR testing, specimen pooling would lower overall PCR costs, but the feasibility of this approach and extent of benefits afforded would depend on MRSA prevalence.

RFA07

Applying whole genome approaches to identify and resolve influenza A outbreaks in humans and animals

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OBJECTIVE: Traditionally, influenza A virus (IAV) sequencing focused primarily on hemagglutinin (HA) given its immunological significance and variability. However, HA alone may not provide sufficient resolution when analyzing transmission dynamics or viral evolution because variations in the other gene segments, including reassortments, are not tracked. Here, we compare HA-specific and whole genome-based phylogenies constructed from human and animal outbreak specimens to investigate the added value of whole genome sequencing (WGS)-based approaches.

METHODS: WGS libraries were generated and sequenced using Illumina-based technology. WGS analysis was performed using FluViewer_nf v0.2.0 (https://github.com/BCCDC-PHL/FluViewer_nf). Sequences with a minimum of 90% coverage across each segment were included in the analysis. Two data sets were analyzed: 1) human seasonal IAVs from the 22/23 season (n = 655), including 12 long-term care outbreaks, and 2) animal IAVs from 22/23 representing the ongoing highly pathogenic avian influenza outbreak (n = 169). We constructed HA-specific phylogeny, as well as whole-genome phylogeny obtained by concatenating all 8 IAV gene segments together (HA, M, NA, NP, NS, PA, PB1, PB2) prior to analysis. Contextual metadata (e.g., time, geography, source) was overlaid onto phylogenetic trees to assess whether genetic relationships aligned with epidemiological data.

RESULTS: Compared to HA-specific phylogeny, whole-genome phylogeny resulted in the identification of mutations and/or reassortments in other gene segments, both of which were important for understanding the ecology and epidemiology of these viruses, parsing out potential clusters of transmission, and identifying the emergence of variants with implications for virulence, transmissibility, and immunity in humans and animals. Furthermore, whole-genome phylogeny enabled identification of novel viruses with segments originating from different species.

CONCLUSION: While HA sequencing is crucial for genetic and antigenic characterization of IAVs, focusing exclusively on HA can overlook important genetic variability, including reassortment. As such, whole-genome approaches are essential to fully understand IAV evolution, pathogenicity, and transmission dynamics, especially during outbreaks.

RFA08

Epidemiology and clinical characteristics of severe malaria in Canada, 2014–2022

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OBJECTIVE: Malaria is a preventable and life-threatening infectious disease of significant global burden. Canadian

travellers remain at high risk of acquiring malaria during travel to endemic areas. The overall incidence of imported malaria in Canada is poorly understood due to variable provincial reporting processes. Severe malaria cases are systematically reported via parenteral malaria therapy requests to the Canadian Malaria Network (CMN), which facilitates access to this treatment. The purpose of this study is to describe the epidemiology and clinical characteristics of travel-related severe malaria in Canada.

METHODS: Data collected by the CMN were used to describe patient characteristics and clinical outcomes of severe malaria diagnosed in Canada from January 2014 to December 2022.

RESULTS: A total of 595 cases of severe malaria received parenteral therapy; patients received artesunate, quinine, or both (97.5%, 1.8%, and 0.7%, respectively). In 2022, the number of severe malaria cases ($n = 83$) was comparable to 2019 prepandemic levels ($n = 82$). Adults (20 to 44 years) comprised the predominant age group affected (231, 39%). Among the 169 children aged 0 to 19 years, the highest proportion of cases was reported in those less than 10 years (107, 63%). Of those who acquired malaria during travel in Africa (560), most were from West Africa (43.9%), followed by Central Africa (28.6%), and East Africa (21.3%); South Asia was the most common region in Asia (14/15, 93%). The majority of severe malaria was due to *P. falciparum* infection (519/595, 87%). The predominant reason for travel was visiting friends and relatives (321, 54%). Common complications included hyperparasitemia (150), jaundice (72), prostration (49), and impaired consciousness (46).

CONCLUSION: Malaria continues to pose a significant risk to Canadian travellers. More robust surveillance of imported malaria is needed to better understand those at the highest risk of infection and severe outcomes.

RFA09

Emergence of a novel FRI-type carbapenemase (*bla*$_{\text{FRI-12}}$) in *Enterobacter cloacae* complex located on a novel IncR plasmid isolated in Canada

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OBJECTIVE: Carbapenem-resistance in *Enterobacter* (CRE) species is often due to derepression of its intrinsic ampC in conjunction with mutations in outer membrane porins; however, increasing reports of CRE due to acquisition of mobile carbapenemases is of concern. Since 2015, increasing reports of a novel class A carbapenemase termed French imipenemase (FRI) have been described in Europe, Japan, and now Canada.

METHODS: *Enterobacter* spp were suspected to harbour a carbapenemase by growth on ChromID CARBA medium and positive phenotypic detection by modified carbapenem inactivation method (mCIM). Conventional PCR containing FRI-specific primers was conducted on suspect CRE. Additional phenotypic methods (Rosco Neo-Rapid Carb Kit, β CARBA) and antimicrobials (micro broth dilution and Etest) was conducted. Whole-genome sequencing (WGS) using both Illumina and Oxford Nanopore technologies was conducted. Genotypic data were analyzed to detect plasmid type, resistance genes, and sequence types.

RESULTS: Since 2018, we have collected 1 *Enterobacter* spp (ST1108) and 2 *E. asburiae* (ST1639, ST-novel) harbouring blaFRI-6, blaFRI-8, and the novel blaFRI-12, respectively. Detection of *E. asburiae* harbouring blaFRI-12 was confirmed by WGS. Susceptibility testing showed resistance to aztreonam and reduced susceptibility to imipenem. Rosco Neo-Rapid was positive but was negative for β CARBA. Genotypic resistance genes were detected: oqxA/B, fosA, qnrE1, blaACT-6-like, and blaFRI-12. All FRI types reported are associated with IncFII-type plasmids. blaFRI-12 gene was found on a 110 Kb IncR plasmid that showed only 44% coverage to known publicly available plasmids. blaFRI-12 is closest in sequence to blaFRI-5 (95.6% identity and 99% coverage) and differs by 13 amino acids. No additional resistance genes were found on the plasmid.

CONCLUSION: FRI carbapenemases are rare but emerging globally. Canada has identified two novel variants (blaFRI-6 and blaFRI-12). Given the intrinsic nature of *Enterobacter* spp to be carbapenem nonsusceptible, emerging *Enterobacter* spp-producing carbapenemases like blaFRI-types may be under-reported globally.

RFA10

Association between the use of a voluntary isolation centre and transmission of SARS-CoV-2: A matched cohort study of households

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OBJECTIVE: The risk of COVID-19 transmission is high in household settings. The ability to self-isolate can be particularly complicated for multigenerational and crowded households. We aimed to evaluate the effectiveness of a voluntary isolation centre (VIC), opened in a large, urban centre of Canada in September 2020, in reducing household transmission of SARS-CoV-2.

METHODS: We conducted a propensity score matched cohort study of the association between VIC use and household transmission. Households with VIC use were matched with up to 10 households without VIC use. Household outbreaks with a start date between September 12, 2020, and March 15, 2021, were included. Covariates in the propensity score included first case, age, gender, and specimen collection delay, household size, and neighbourhood factors based on the 2021 census. The outcome was household secondary attack rate, the number of at-risk household members with infection 1 to 28 days after the index date. Index date was defined as the number of days from outbreak start to VIC use for the VIC user household within matched groups.

RESULTS: 304 VIC user households and 30,246 non-VIC user households were identified. Of these, 303 VIC households were matched with 2,943 non-VIC households. After matching, VIC and non-VIC households were comparable on all covariates (standardized mean differences <0.1). Household secondary attack rates were 5.2% (53/1,015) for VIC households and 8.4% (787/9,408) for non-VIC households (HR 0.50, 95% CI 0.28 to 0.90). Stratified analyses suggested stronger associations when index cases were admitted within 2 days of symptom onset, and among households in neighbourhoods with high household crowding, and high percent visible minority.

CONCLUSION: Results of this study can be used by public health leaders to inform future use of voluntary isolation centres for the control of communicable diseases and the reduction disparities due to the inequitable distribution of infections.

RFA11

A comprehensive risk assessment algorithm-guided SARS-CoV-2 vaccine composition strategy

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OBJECTIVE: New SARS-CoV-2 variants have emerged, characterized by antigenic evolution, immune escape to vaccines and prior immune response, and/or increased growth dynamics versus prior variants. A real-time analysis of viral molecular evolution where antigenic changes are evaluated against risk of immune escape would inform on risk for immune escape from seasonally approved COVID vaccines and on future selection of seasonally updated variant vaccine candidates to maintain protection against severe clinical disease.

METHODS: Moderna performs continuous epidemiological monitoring and risk assessment of variants. This process groups antigenically similar sublineages that have consistent predicted/measured immune escape. Assessment of risk posed by new variants is performed through a proprietary risk assessment toolkit built upon published spike-antigenic sites and in-house neutralization results from preclinical and clinical sera. The resulting score has demonstrated correlation with measured neutralization activity from approved vaccines against key variants.

RESULTS: All variants of interest/concern have been grouped on the basis of molecular mutations and antigenic similarity. Our risk assessment score is used to predict the risk of immune escape from approved SARS-CoV-2 vaccines (Table 1).

CONCLUSION: Moderna's risk assessment algorithm represents a combination of active genomic surveillance with artificial intelligence-enhanced analysis of clinical, preclinical, and molecular evidence to deliver optimal strain selection in a condensed time frame.

Risk Assessment Score Predicted immune escape (fold-drop)					
Vaccine composition		Wuhan-Hu-1	BA.2.86	JN.1	JN.1.1.1
	mRNA-1273	1.0	128.37	139.1	139.1
	mRNA-1273.222	1.0	35.64	43.43	43.43
	mRNA-1273.815	1.0	1.0	5.0	5.0

This risk assessment scoring was used in the selection of new variant vaccines over the 2022 and 2023 seasons and is being used in anticipation of potential variant strain updates for the 2024 season. Clinical evaluations of the Spikevax 2023/2024 vaccine (mRNA-1273.815, monovalent XBB.1.5, [50 mcg]) demonstrated that the vaccine elicited substantial increases in neutralizing Ab titers (7.7–16-fold rise over preboost) against XBB sublineages, BA.2.86, and JN.1.

RFA12

FluViewer: An automated bioinformatic pipeline for generating influenza A virus consensus genomes regardless of viral subtype or host

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OBJECTIVE: Generating genome sequences from raw sequencing data is a bioinformatic bottleneck for high-throughput influenza A virus (IAV) genomic programs. To address this bottleneck, we created an automated pipeline called FluViewer. It generates consensus sequences for each segment of the IAV genome from any specimen, regardless of host and viral subtype.

METHODS: We used a collection of clinical and avian IAV specimens to assess the completeness of sequences produced by FluViewer over a range of quantitative polymerase chain reaction (qPCR) Ct values. We also used this collection to assess subtyping concordance between FluViewer and typing qPCR. To assess the genotype-level accuracy of the sequences produced by FluViewer, we generated 200 sets of simulated sequencing reads from reference sequences (modeling normal error rates), input them into FluViewer, and compared the output to the known sequence. We also assessed accuracy by comparing output from FluViewer and an alternate pipeline from another institution on 166 clinical specimens.

RESULTS: Sequences for the most relevant segments of the IAV genome (HA, NA, and M) were ≥95% complete for all specimens with qPCR Ct values ≤ 28 ($n = 215$, including 171 seasonal H1/H3s and 68 avian H5s). FluViewer subtyping was concordant with laboratory qPCR typing results for 57/57 (100%), 144/146 (98.6%), and 81/82 (98.8%) of H1, H3, and H5 sequences generated. FluViewer generated the expected genome consensus sequence for 100% of the sets of simulated sequencing reads. Output from FluViewer and the alternate pipeline also agreed closely; 1,304 genome segments were successfully generated by both pipelines and 1,288 (98.8%) of them had two or fewer mismatches between pipelines. FluViewer completed significantly faster and with fewer crashes than the other pipeline, however.

CONCLUSION: FluViewer automatically generates accurate and complete IAV consensus genomes for diverse IAV specimens and can improve bioinformatic throughput for clinical IAV genomic programs.

RAPID FIRE PRESENTATIONS

Session B
Oral Presentations: Thursday, April 11
Poster Presentations: Friday, April 12

RFB01

Use of Dalbavancin in treatment of acute bacterial skin and skin structure infections: Prospective case series from a Canadian perspective

Wayne Fung Leung, Janhavi Malhotra, Lili Ataie, Sameer Elsayed, Lise Bondy, Megan Devlin, Sarah Shalhoub, Huma Saeed, Mahshid Mohammadi, Michael Silverman, Reza Rahimi Shahmirzadi

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OBJECTIVE: Treatment of acute bacterial skin and skin structure infections (ABSSSIs) with parenteral antibiotics is difficult in marginalized populations, including people who inject drugs, due to challenges with homelessness necessitating prolonged hospitalization for IV therapy, and frequent accessing of IV lines for drug use. Dalbavancin, which is a novel lipoglycopeptide antibiotic with activity against gram-positive organisms, with a duration of action of 7–14 days may be an ideal antibiotic in patients in whom administering parenteral antibiotics may be difficult.

METHODS: Prospective cohort study consisting of 19 patients who were referred to the Cellulitis Clinic at London,

ON, Canada who were referred for ABSSSI between February 1 and July 30, 2023. Patients were treated as outpatients with one dose of IV dalbavancin. Patients had social factors, which precluded administration of outpatient parenteral antibiotics in a traditional setting, such as injection drug use, severe psychiatric comorbidities, or unstable housing.

RESULTS: The median age of patients enrolled was 43 (range 36 to 56) years, were predominantly male (74%), unemployed (90%), and with unstable housing (58%). Treatment with dalbavancin was successful in 13/19 (68%), indeterminate (presumed success as could not be reached for follow-up but were not admitted to any institution within our catchment area) in 3/19 (16%), and failure (needed further antibiotics following dalbavancin) 3/19 (16%).

CONCLUSION: Administering dalbavancin through a single IV infusion eliminates the need for indwelling IV access and may enhance treatment of ABSSSI without the need for hospital admission, in those with challenging socioeconomic factors who may have difficulty with adherence to outpatient antibiotic therapy.

RFB02

Verification of the Aptima bacterial vaginosis and candida/trichomonas assays on the Hologic Panther

Emily J MacAdam[1], Ross Davidson[2], Jolin Head[2], Colleen Jackson[2], Jason J LeBlanc[2], Greg McCracken[2], Glenn Patriquin[2], Audra Russell-Tattrie[2], Darren Sarty[2], Todd F Hatchette[2]

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OBJECTIVE: Microscopic methods for detecting bacterial vaginosis (BV) and candida/trichomonas (CV/TV) infections have been part of routine testing in microbiology laboratories, but molecular methods for BV and CV/TV detection are now available. This study aimed to verify the performance of the Hologic Aptima BV and CV/TV assay.

METHODS: Prospectively collected vaginal swabs for *Chlamydia trachomatis* (CT) collected in Aptima specimen transport media were retrieved that also had vaginal smears for BV testing. Vaginal smears were tested by conventional microscopic methods following Gram staining. BV was categorized by Nugent scoring and TV and CV by identification of yeast or trichomonas on the slide. The Aptima swabs were tested using the Aptima BV and Aptima CV/TV assays on the Hologic Panther system. Discrepant results between microscopy and the Aptima BV assay were resolved using the Seegene Allplex vaginitis panel. Reference standard positives or negatives would be concordance with two of the three tests.

RESULTS: Of the 103 positive BV specimens were tested using the Panther, 102 (99%) correlated with positive reference standard. Of the 76 negative BV specimens tested using the Panther, 74 (97%) correlated with the negative refence standard. There was 100% correlation of positive (25/25) and negative specimens (162/162) for TV and a 100% positive correlation (45/45) for CV. Of the 141 negative smears, 127 were negative for CV for a 90% negative correlation. Although potential false positives, these likely reflect increased detection rates with better sensitivity with the Aptima assay.

CONCLUSION: Overall, the high positive and negative agreement observed between the Aptima BV; CV/TV assays compared with traditional microscopic methods, suggests the assays are acceptable for testing. Following full-scale implementation of the Aptima BV and CT/TV assays, turnaround time was reduced from on average 13 days to 48–72 hours.

RFB03

Clinical validation of an optimized and automated agnostic diagnostic assay for detection of respiratory viruses

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OBJECTIVE: Current reference-standard molecular diagnostics, while cost-effective and clinically actionable, are limited in that they can only detect a select panel of pathogens. Metagenomic sequencing (mNGS) can enable agnostic pathogen detection. Previous research has

demonstrated the feasibility of mNGS for respiratory viral diagnostics. However, translational barriers exist to the widespread adoption of this technology. Here, we report the diagnostic performance of an optimized and automated mNGS assay for respiratory viral diagnostics that addresses many translational barriers.

METHODS: Our assay is a modified version of a previously published technique called Rapid-SMART9N. We optimized this protocol for sensitivity, throughput, and turnaround time. Our assay was automated using a Hamilton NIMBUS96 liquid handling robot. Clinical validation of the assay was performed using residual nasopharyngeal swabs submitted for routine diagnostic testing at Vancouver General Hospital and the BC Centre for Disease Control. Specimens were sequenced on a Nanopore GridION device for 3 hours, with subsequent data analysis on the cloud-based, user-friendly, BugSeq platform. Diagnostic performance metrics were estimated.

RESULTS: Assay optimizations resulted in an assay turnaround time of <12 hours. Significant differences in viral read counts across different days, operators, and reagent lots were not observed (Kruskal-Wallis: $p = 0.66$). Analytical limits of detection were estimated to be between 10^3 and 10^5 copies/mL for SARS-CoV-2, RSV, influenza A, and influenza B. Our assay is highly specific (100%; 192/192) and sensitive for specimens with an RT-PCR C_t value <30 (86.8%; 92/106). We reported incidental detection of viral pathogens not tested for in initial diagnostic screening in 14/347 (4.0%) of specimens. Strain typing was assigned for 79.6% of mNGS positive specimens.

CONCLUSION: We report the diagnostic performance of a rapid, sensitive, and high throughput mNGS assay with automated data analysis for respiratory virus detection. This assay addresses translational barriers and represents an important step toward widespread adoption of mNGS for diagnostic, infection control, and public health surveillance uses.

RFB04

Multivariate analysis of risk factors predicting 28-day mortality among adult patients presenting with bacteremia in the emergency department

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OBJECTIVE: To identify clinical mortality predictors among adult patients diagnosed with bacteremia in the emergency department (ED).

METHODS: This retrospective chart review included adults with bacteremia in a tertiary-care ED in 2019 and 2022. We excluded patients with blood contaminants and those discharged on palliative care. The primary outcome was 28-day mortality. Descriptive analyses evaluated demographics, comorbidities and clinical characteristics. Both univariate analysis and multivariate logistic regression identified mortality predictors at a significance level of 0.05.

RESULTS: Overall, 433 patients were included: 216 females (49.9%) and 217 males (50.1%) (mean age 74.1 [SD 15.2] years). The 28-day mortality rate was 15.2% (n = 66). In the univariate analysis, age ≥70 years (19.5% versus 6.4%), arrythmia (25.0% versus 12.3%), congestive heart failure (27.8% versus 13.5%), recent steroid use (24.3% versus 13.4%), hypotension (32.8% versus 12.4%), cardiac arrest (75.0% versus 12.4%), intensive care unit (ICU) admission (43.1% versus 10.3%), and mechanical ventilation (24.2% versus 11.5%) were significantly associated with mortality as was the absence of an infectious disease (ID) consultation (20.9% versus 10.5%). Rapid 1st dose antibiotic administration at arrival (<4 hours versus more), inappropriate initial antibiotic regimen and gram-negative versus gram-positive bacteremia were found to be nonsignificant. Multivariate analysis identified ICU admission (OR [95% CI] 6.0 [3.08–11.8]), pneumonia as the source of bacteremia (4.9 [2.62–9.32]), age ≥70 (3.2 [1.39–7.17]), hypotension at admission (2.1 [1.02–4.40]), and absence of ID consultation (2.0 [1.08–3.78]) as key determinants of 28-day mortality.

CONCLUSION: This retrospective study identified significant mortality predictors among ED patients presenting with bacteremia. Although past data showed that speed of first antibiotic dose and inadequate initial antibiotic selection increase mortality, our evaluation did not identify these as mortality predictors. However, consultation with an ID physician was seen as a significant element to decrease mortality in this high-risk population.

RFB05

Infectious diseases consultation is associated with reduced mortality in hospitalized patients with gram-negative bloodstream infection: A population-wide cohort study

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OBJECTIVE: Bloodstream infections (BSI) are common and associated with high mortality. Infectious diseases consultation (IDC) has been associated with reduction in mortality in *Staphylococcus aureus* and *Candida* spp BSI, but data are limited for GN-BSI. We evaluated the association between IDC and mortality in patients with GN-BSI in a retrospective population-wide cohort study in Ontario using linked health administrative databases.

METHODS: Hospitalized adult patients with GN-BSI between April 2017 and December 2021 were included. Hospitals with <25 cases of GN-BSI or <5 IDC in total were excluded. The primary outcome was time to all-cause mortality censored at 30 days, analyzed using a mixed-effects Cox proportional hazard model with hospital as a random effect. IDC 1–10 days after the index-positive blood culture, based on time of billing code, was treated as a time-varying exposure.

RESULTS: Of 30,159 patients treated across 53 hospitals, 11,013 (36.5%) received IDC. Median prevalence of IDC for patients with GN-BSI across hospitals was 35.0% with wide variability (range 2.7%–76.1%, interquartile range 19.6%–41.1%). 1,041 (9.5%) patients who received IDC died within 30 days, compared to 1,797 (9.4%) patients without IDC. In the fully adjusted multivariable model, including potential confounders, we observed a mortality benefit with IDC (hazard ratio 0.82 [95% CI 0.77 to 0.88]; $p < 0.0001$). This finding was consistent across multiple sensitivity analyses, including prolonging follow-up to 90 days, shortening the IDC window to 1–5 days, increasing the minimum number of IDC and/or patients required for hospital inclusion, and excluding potential outlier sites. Subgroup analyses showed that IDC could have greater benefit in patients with more complicated disease (nosocomial infection, polymicrobial or non-Enterobacterales infection, antimicrobial resistance, or non-urinary tract source).

CONCLUSION: IDC was associated with reduced mortality in patients with GN-BSI. If resources permit, routine IDC for this patient population should be considered to improve patient outcomes.

RFB06

HCV reinfection among people who use drugs treated for HCV infection: A long-term view

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OBJECTIVE: Comprehensive programs of care for priority populations, such as people who use drugs (PWUD), are needed to eliminate hepatititis C virus (HCV) infection as a public health concern by 2030. A primary challenge associated with such initiatives is the need for effective strategies to mitigate the risk of reinfection. Meta-analyses suggest a reinfection rate of ~5 per 100 person-years among key populations. The objective of this study is to assess reinfection rates among populations of PWUD successfully treated for HCV infection and maintained in long-term follow-up within a multidisciplinary program of care.

METHODS: In our program, we provide HCV therapy to PWUD within the context of a comprehensive, multidisciplinary program addressing all medical, social, psychologic, and addiction-related needs in the context of HCV therapy with strategies designed to maximize adherence. Once HCV cure has been documented, patients continue to be integrated in care. HCV RNA testing is repeated annually, or more frequently if clinically indicated. We conducted an ongoing, prospective evaluation of the last 308 successful courses of HCV therapy administered to PWUD in our centre to determine the rate of HCV reinfection and its correlates.

RESULTS: All participants were cured of HCV infection between March 19th and August 23rd. We document a median age of 47 (22–83) years, 28.2% female, 19.3% identifying as indigenous, 53.9% unstably housed, and 92.2% continuing active drug use (mostly fentanyl). Since 2019, we documented 8 cases of reinfection at a rate of 0.88 cases per 100 person-years. Of these 8 reinfected patients, 2 were female, 2 identified as indigenous, and all were experiencing unstable housing and ongoing drug use.

CONCLUSION: Our data suggest that a comprehensive and multidisciplinary approach to HCV therapy with long-term maintenance in follow-up after cure is achieved.

Strategies to educate participants on safer drug use practices and provision of safe supply to favour retention in care are associated with rates of reinfection below 1/100 patient-years.

RFB07

Impact of antimicrobial copper surfaces on microbial load and health-care-acquired infection rates in long-term care settings: A comparative study in Canada

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OBJECTIVE: Health-care-acquired infections (HAIs) are a significant cause of morbidity and mortality in long-term care (LTC) settings. Antimicrobial copper surfaces have been demonstrated to reduce microbial contamination in various health and public settings, but their effectiveness in LTC settings is underexplored. The objective of our study was to assess the impact of antimicrobial copper surfaces on microbial load and HAI rates compared to existing surfaces in LTC settings.

METHODS: A prospective, comparative study was conducted across units of three LTC facilities over a 6-month period. In each facility, antimicrobial copper was installed on designated common surfaces within the intervention units, while the control units maintained existing surfaces. Microbial load was measured through once weekly sampling of 30 cm^2 areas using Hygiena SuperSnap ATP bioluminescence assay and 3M Petrifilm aerobic count plates. HAI rates were monitored over the same period in two facilities. Staff sick days, relief leave, and overtime work hours were tracked, and costs associated with this were calculated.

RESULTS: There was a 79.3% and 34.1% ($p < 0.001$) reduction in microbial load on antimicrobial copper surfaces compared to existing surfaces using the ATP bioluminescence and aerobic plate count methods, respectively. Overall, HAI rates did not differ significantly between intervention and control units. There were 30 cases of HAI during the study period; 21 (70%), of which occurred during respiratory infection outbreaks in the intervention and control units (12 and 9, respectively). There was a net reduction of $21,048.90 in costs related to staff sickness, relief, and overtime pay in the intervention group compared with the control group.

CONCLUSION: This study demonstrates reduced microbial contamination of antimicrobial copper surfaces in LTC settings, as well as cost savings associated with fewer staff sick and relief days, and overtime work. Further studies are needed to accurately assess the impact of antimicrobial copper surfaces on HAI rates in LTC settings.

RFB08

MRSA isolates resistant to trimethoprim-sulfamethoxazole by VITEK 2 and BD Phoenix antibiotic susceptibility testing systems but susceptible by Etest and disk diffusion harbour a resistant subpopulation

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OBJECTIVE: Trimethoprim-sulfamethoxazole (TMP-SMX) is a common oral antibiotic used for the treatment of methicillin-resistant *Staphylococcus aureus* (MRSA) infections. Hemin-dependent heteroresistance has been identified previously in Europe and could explain the discrepancy in susceptibility results. This study aims to confirm the discrepancy in susceptibility testing and identify the presence of a TMP-SMX-resistant subpopulation in Canada.

METHODS: In this multi-centre study, 54 *S. aureus* clinical isolates resistant to TMP-SMX by VITEK 2 collected in 2 Canadian provinces were tested by disk diffusion and Etest using standard Clinical & Laboratory Standards Institute methods. Of the 54 isolates tested, 46 were MRSA. To determine whether the BD Phoenix system produced similar results to the VITEK 2, 15 TMP-SMX resistant by VITEK 2 isolates were tested on the BD Phoenix. Thirty-seven MRSA isolates were grown on Mueller Hinton (MHA) + 5% horse blood in the presence of TMP-SMX to identify the presence of a resistant subpopulation.

RESULTS: Of the 54 *S. aureus* isolates resistant to TMP-SMX by VITEK 2, 53 (98%) were found to be sensitive by disk diffusion and Etest. Of the 15 isolates resistant to TMP-SMX by VITEK 2 tested on BD Phoenix, 13 (87%) were found to be also resistant to TMP-SMX and sensitive by disk diffusion and Etest. TMP-SMX-resistant MRSA demonstrated small colonies in the zone of inhibition when grown on MHA + 5% horse blood.

CONCLUSION: This study identifies discordance in *S. aureus* susceptibility results for TMP-SMX by the VITEK 2 and BD Phoenix compared to disk diffusion and Etest. A TMP-SMX-resistant subpopulation was identified, which may have implications for how laboratories report susceptibility results. Further investigation is required to determine the clinical significance of these findings.

RFB09

Validation of Python scripts versus Excel for cleaning, analysis, and visualization of surveillance and methods evaluation data

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OBJECTIVE: Real-time surveillance of antimicrobial resistance data are optimal but many clinical laboratories examine resistance rates only annually, as analysis is often conducted manually via Excel and is time-consuming. Similarly, verification studies of susceptibility testing methods are often completed manually at a single moment in time, preventing robust ongoing analysis of parallel testing. Coded scripts, such as those from Python, offer a rapid, streamlined approach to data cleaning and analysis. In this study, we compare Python scripts against manual Excel methods for accuracy and time required for 1) the creation of the template/script; and 2) data analysis using AMR surveillance and antimicrobial susceptibility testing (AST) methods evaluation convenience data sets.

METHODS: The amount of time taken to create the template/scripts using Excel versus Python and the amount of time to use the template/scripts to clean, analyze, and visualize results starting with a raw data file was recorded. Accuracy of the data was compared. Raw data files were taken from: 1) a 2013-2022 AST *Klebsiella pneumoniae* data set; and 2) verification data set comparing VITEK 2 AST-N391 to disc diffusion for SPICE organisms, *Escherichia coli*, *K. pneumoniae*, *K. oxytoca*, *Pseudomonas aeruginosa*, and *Acinetobacter* spp. Python scripts were coded by an individual with an introductory computer science background.

Table RFB09-1: Results for time taken to create and analyze antimicrobial resistance data.

		Excel	Python
***K. pneumoniae* susceptibility testing dataset**	Time taken to create initial template/script for data cleaning, analysis, and visualization	10 hrs	12 hrs
	Time taken to clean raw data	35 min	11.58 secs (averaged over 10 runs)
	Time taken to transfer cleaned data into template	35 min	
	Time taken to calculate confidence interval	20 min	
VITEK®2 AST-N391 vs. disk diffusion performance verification dataset	Time taken to create initial template/script for data cleaning and analysis	12 hrs	2 hrs
	Time taken to clean raw data	40 min	2.04 secs (averaged over 10 runs)
	Time taken to transfer cleaned data into template	20 min	
	Time taken to calculate confidence interval	35 min	

RESULTS: Accuracy for both methods were comparable. Results for time taken to create and analyze data are shown in Table RFB09-1.

CONCLUSION: Python scripts offer a faster and more efficient method of data handling. Although Python requires a greater initial time investment in code generation, it can subsequently analyze data within seconds and decrease human error, time, and resources, which is particularly helpful for recurrent surveillance and method evaluation of projects and real-time data analysis. For optimization of the use of coded scripts, clinical laboratories should recognize the value of hiring a data scientist as part of laboratory personnel.

RFB10

Impacts of the SARS-CoV-2 pandemic on the seasonal incidence of hospitalizations for acute respiratory diseases among children

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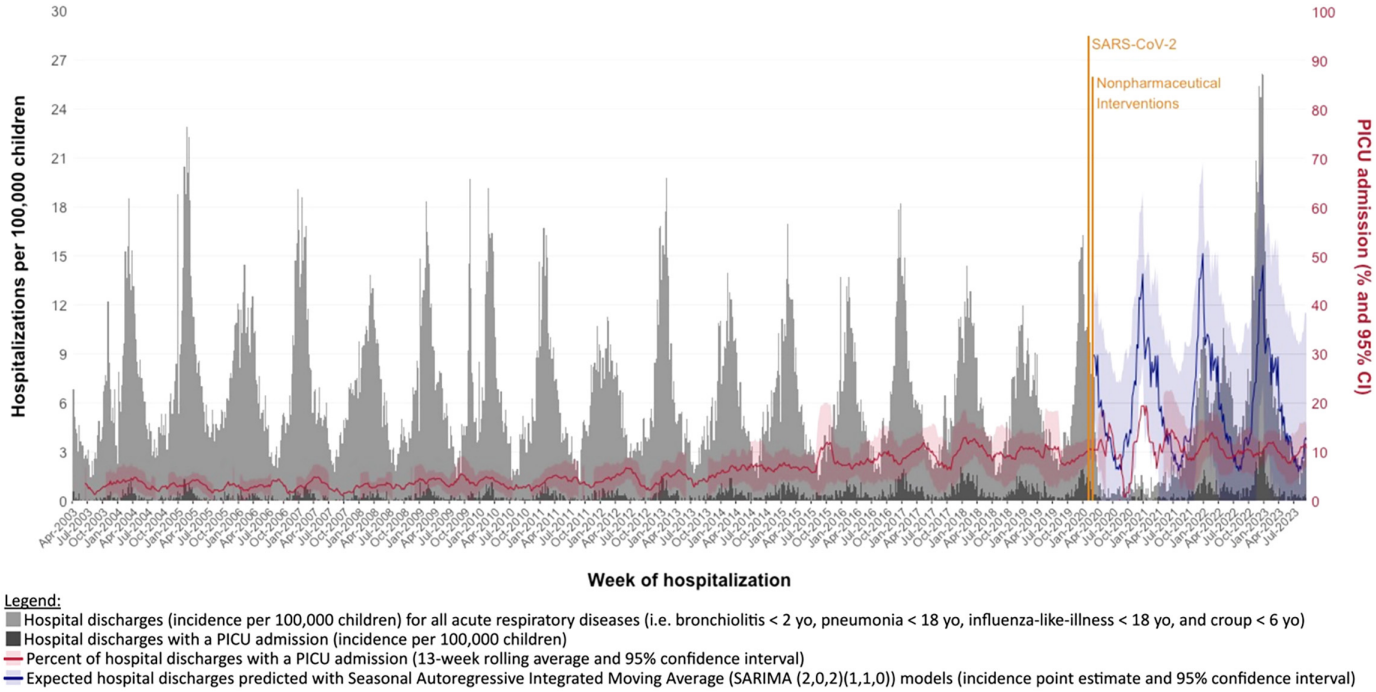

Figure RFB10-1: Weekly hospitalizations and PICU admissions for acute respiratory diseases among children from April 2003 to September 2003, and time series analysis of expected hospitalizations between April 2020 and September 2023. Data source: provincial hospital Discharge Abstract Data.

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OBJECTIVE: Acute infectious respiratory diseases (ARD) among children have a biennial; peak incidence is highest every other winter. This seasonal pattern of ARD was interrupted in 2020 by SARS-CoV-2 and nonpharmaceutical interventions (NPI). We measured the impact on the weekly incidence of hospitalizations and paediatric intensive care unit (PICU) admissions for ARD to quantify health care burden. We also measured the impact on the weekly percent of PICU admissions to monitor disease severity.

METHODS: From April 2003 to Dec 2023, all hospital discharges and PICU admissions for ARD (i.e., bronchiolitis, pneumonia, influenza-like-illness, and croup) among children aged 0-17 were identified in the provincial hospital Discharge Database. Weekly incidence was calculated using population denominators. Seasonal autoregressive-integrated-moving-average (SARIMA) models predicted the expected weekly hospitalizations from April 2020 onward. Incidence ratios compared observed versus expected incidence.

RESULTS: There were 63,776 hospitalizations for ARD among children from April 2003 to December 2023, of which 4,167 (6.53%) included a PICU admission (Figure RFB10-1). The average weekly incidence of hospitalization for ARD per 100,000 children decreased 12.71-fold during December 2020 to February 2021 (0.82 observed versus 10.42 [95% CI 5.11 to 15.73] expected), and increased 1.51-fold during December 2022 to February 2023 (16.28 observed versus 10.77 [95% CI 4.71 to 16.83] expected). The average percentage of PICU admissions steadily increased from 4.07% (95% CI 1.22% to 6.91%) in December 2003 to February 2004 10.48% (95% CI 8.36% to 12.60%) in December 2019 to February 2020. There was no significant change in the percentage of PICU admissions in December 2020 to February 2021 and in December 2022 to February 2023, 11.17% (95% CI 0.00% to 26.32%) and 11.86% (95% CI 9.33% to 14.39%), respectively.

CONCLUSION: SARS-CoV-2 and NPI had significant impacts on provincial health care burden of ARD among children. Initially hospitalizations for ARD decreased 12.50-fold during December 2020 to February 2021. With SARS-CoV-2 vaccine availability, increased population immunity, and relaxation of NPI, hospitalizations for ARD increased 1.53-fold during December 2022 to February 2023. However, there was no change in clinical severity based on the percentage of PICU admissions.

RFB11

Clinical and public health management of bacterial gastroenteritis in the world of culture-independent diagnostic testing (CIDT): A pilot study to evaluate kinetics of bacterial shedding by culture and CIDT

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OBJECTIVE: Bacterial gastroenteritis is a common infection worldwide with significant morbidity and mortality. Reliable microbiological diagnosis is important for patient and public health management. Many laboratories are replacing slow and insensitive culture-based methods with culture-independent diagnostic testing (CIDT), including nucleic acid detection. Microbial DNA may shed for many weeks after infection; however, there are limited data demonstrating this. We studied kinetics of bacterial shedding by both CIDT and culture following acute gastroenteritis with three prevalent pathogens. Primary outcome was to determine whether the positivity of CIDT differed compared to culture at defined intervals postinfection.

METHODS: This longitudinal observational study was conducted in Alberta between 2019 and 2022. Adult patients (≥18 years old) with culture-positive diagnostic stool specimens for Campylobacter, Salmonella, and Shiga toxin-producing *Escherichia coli* (STEC) were eligible. Participants gave their consent and were enrolled after routine public health assessment. Participants were requested to submit weekly stool specimens for weeks 2, 3, 4, 5, and 6 after diagnosis. Stools were tested by both BD MAX Enteric Bacterial Panel (PCR) and routine culture methods. Bacterial load was determined by quantitative PCR.

RESULTS: Thirty-seven of 83 enrolled (45%) submitted at least one additional stool. Diagnostic specimens were positive for Campylobacter ($n = 19$), Salmonella ($n = 8$), and STEC ($n = 10$). Median duration of CIDT positivity was 42, 29, and 22 days for Campylobacter, Salmonella, and STEC, respectively. Median duration of culture positivity was 29, 29, and 19.5 days. Overall agreement between methods was 88% (129/146). Negative CIDT testing had a negative predictive value of 100% for all pathogens compared to culture. Cycle threshold (CT) value concordance between BD MAX and quantitative PCR was poor ($R^2 = 0.45$).

CONCLUSION: Our study demonstrates the relationship between duration of positivity by CIDT and culture is similar based on our limited sample size. Campylobacter had the longest duration of shedding by CIDT compared to other pathogens. Negative CIDT ruled out positive culture in all cases. CT values from BD MAX did not correlate with qPCR and cannot be used for quantitation in our study. This justifies further larger studies to elucidate the clinical implications of CIDT positivity, as these tests are more widely implemented.

RFB12

SARS-CoV-2 seropositivity in Alberta: The Omicron era

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OBJECTIVE: We systematically evaluated SARS-CoV-2 seropositivity in Alberta before and after the arrival of the Omicron variant (first detected in Alberta on November 25, 2021) to better understand local COVID-19 epidemiology and support evidence-based public health decision making.

METHODS: Residual blood samples province-wide underwent SARS-CoV-2 antibody testing during 1-week periods every 3 months from September 28, 2021, to October 14, 2022. Anti-nucleocapsid-IgG was carried out on all samples while anti-receptor binding domain (RBD)-IgG was also done on specimens from unvaccinated individuals. The seropositivity for each sampling period was calculated.

Results were linked to provincial administrative, laboratory, and vaccine databases.

RESULTS: In total, 50,187 samples representing 47,282 individuals were surveyed during six survey periods (56.2% female; median age 55.6 [IQR 37–70] years). 6,637 (14.0%) were unvaccinated (57.2% female, median age 44 [IQR 27–63] years). Among unvaccinated Albertans, RBD-IgG seropositivity was 37.5% (95% CI 34.5% to 40.5%) in October 2021 with a rise to 74.8% (95% CI 72.5% to 77.1%) in October 2022. Anti-nucleocapsid IgG in all patients increased from 6.8% (95% CI 6.3% to 7.4%) to 27.3% (95% CI 26.2% to 28.3%) during January to October 2022. From January to March 2022, the largest increase in antinucleocapsid seropositivity was seen in those aged 0-9 years (+42.9%) followed by those 10–19 years (+34.9%). During July to October 2022, the change in seropositivity of anti-RBD was significant (5.6%; $p = 0.002$), whereas the rise in anti-N was not (0.1%; $p = 0.17$). For each sampling period, antinucleocapsid seropositivity was significantly higher among the unvaccinated group compared to those who were immunized (2 doses) or boosted (3+ doses) (all comparisons $p < 0.05$).

CONCLUSION: Despite large numbers of infections observed with the Omicron variant, vaccination likely contributed to a reduced risk of infection. The initial surge of Omicron infections was observed in younger age groups. By July 2022, the population infection rate seemed to be more constant. Longitudinal SARS-CoV-2 serosurveillance with data linkage provides valuable information for public-health policy decision-making.

POSTER PRESENTATIONS
Thursday, April 11

TP001
Culture-independent detection of *Helicobacter pylori* antimicrobial resistance markers in stool by metagenomic sequencing

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OBJECTIVE: *Helicobacter pylori*, the main cause of peptic ulcer disease, is a major risk factor for gastric cancer. Although antimicrobial resistance (AMR) in *H. pylori* contributes to treatment failure, Canadian laboratories rarely perform antimicrobial susceptibility testing for this fastidious organism. Metagenomic sequencing offers a way to inform clinical treatment and monitor AMR trends without culture. As part of a project to develop and implement an omics assay for the diagnosis and treatment of *H. pylori*, we sought to detect genetic markers associated with resistance to antibiotics used in *H. pylori* treatment by targeted amplicon sequencing (TAS) of stool specimens.

METHODS: Total DNA was extracted from stool spiked with serial dilutions of *H. pylori* lab strain ATCC43504. Genes associated with *H. pylori* resistance to clarithromycin, amoxicillin, rifamycin, and levofloxacin were amplified by PCR and sequenced via Illumina technology. Reads were screened for AMR genes using the Comprehensive Antibiotic Resistance Database (CARD) and Resistance Gene Identifier (RGI).

RESULTS: Genes associated with resistance to clarithromycin, amoxicillin, rifamycin, and levofloxacin were successfully amplified by PCR at spiked concentrations of 104, 106, 108, and 108 CFU/mL, respectively. Sequence comparison to CARD confirmed specific detection of the target genes. RGI detected mutations in pbp2 associated with amoxicillin resistance, but no markers for resistance to clarithromycin, rifamycin, or levofloxacin. On its own, pbp2 alone is not believed to confer phenotypic resistance. Consistent with the susceptible phenotype of *H. pylori* ATCC43504, no mutations were found in other genes associated with amoxicillin resistance.

CONCLUSION: Metagenomic sequencing of stool provides a culture-independent approach for detecting *H. pylori* AMR markers, offering potential advancements in noninvasive diagnosis and treatment. Further experiments in our development of an omics assay for *H. pylori* and its resistance profile will refine sensitivity and validate the

method using Canadian isolates and specimens, paving the way for clinical application.

TP002

Validation of Copan Amies gel swabs for the detection of *Streptococcus pyogenes* in throats on GeneXpert Xpress Group A Strep assay

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OBJECTIVE: Only Copan Eswabs are Health Canada-approved for use on the Xpert Group Strep A assay. Since many sites in our laboratory system use Copan Amies gel swab, this study evaluates the performance of this specimen type on the Xpress Group Strep A assay.

METHODS: The gel swab was eluted into 1 mL of sterile saline solution (0.9%) by vigorous rubbing for 15 s; then 300 µL of saline solution was loaded into the Xpert assay. The clinical performance of the Xpert assay was compared to culture. Discordant results were tested on Abbott ID NOW STREP A2 assay. Consensus results were determined by concordance of 2 out of 3 testing method. A limit of detection experiment was performed. Saline solutions of ~0.5 McFarland were prepared from 16- to 24-hour growth of *Streptococcus pyogenes*. Gel swabs were placed in the solution for 15 s and then inserted into the gel tube and stored at 4°C for 90 min. Gel swabs were eluted into a saline solution, as described above. Ten-fold serial dilution were prepared, and dilutions 10^{-5} and 10^{-6} were tested. Quantitation of colony forming unit (CFU) was performed. This experiment was performed on 9 independent swabs.

RESULTS: Of 106 clinical throat specimens, 69 were found positive by molecular assay and culture, 1 was found false positive on Xpert Group A Strep, and 36 were found negative by consensus method. The positive and negative percent agreement were 100.0% and 97.3%, based on consensus results. The limit of detection study demonstrated that an average of ~8 CFU/mL can be detected 100% of the time, similar to what the manufacturer reports for ESwabs (9 to 18 CFU/mL).

CONCLUSION: Elution of Copan Amies gel swabs into saline solution is suitable for the detection of *S. pyogenes* in throat by the Xpert Group A Strep assay.

TP003

Determining the limit of detection of antibiotic broth-enrichment, culture-based, and PCR-based methods for the detection of vancomycin-resistant enterococci and carbapenemase-producing Enterobacterales

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OBJECTIVE: Vancomycin-resistant Enterococcus (VRE) and carbapenemase-producing Enterobacterales (CPE) are antimicrobial-resistant organisms targeted for hospital screening program. Limit of detection (LOD) studies assessing different screening methods are limited. This study compared the LOD for VRE and CPE using culture-based or PCR-based methods direct-from-specimen or broth-enriched cultures.

METHODS: Ten mock specimens were created using negative fresh pooled residual nasal-rectal Eswab liquid transport media (Copan) spiked with clinical VRE ($n = 5$) or CPE ($n = 5$); 5 five-fold dilutions were prepared. The LOD to detect VRE and CPE was determined for three PCR methods (Cepheid GeneXpert and the Allplex Entero-DR Assay using the STARlet and STARlet-AIOS systems) and ThermoFisher selective agars (Brilliance VRE agar and Cefpodoxime MacConkey agar) tested directly from mock specimens and from enriched cultures using 30 µL and 300 µL of specimen inoculated into antibiotic-enriched brain-heart-infusion broth, incubated for 20 hours. The LOD for each method was calculated using the Public Health Ontario online Probit Analysis Tool and Analyse-It for Microsoft Excel V5.90 and compared against cost per screen, turnaround-time, and workload.

RESULTS: Broth-enriched methods using 300 µL inoculum had the lowest mean LOD in CFU/mL (341 for VRE and 281 for CPE), followed by broth-enriched methods using 30 µL inoculum (606 for VRE and 769 for CPE), and then direct specimen testing (1807 for VRE and 1511 for CPR). LOD for agar-based methods were not significantly different than those for polymerase chain reaction (PCR)-based agars.

CONCLUSION: There was not a dramatic difference in LOD by screening method. Taking into consideration costs per screen, turnaround-time, workload, and LOD, direct-from-specimen selective agar-based methods for VRE and CPE detection provide the optimal routine screening method. If deemed necessary in specific situations, direct PCR screening may be preferred for its lowest turnaround time, and broth-enriched PCR may be preferred for its lowest LOD.

TP004

Evaluation of TB Xpert MTB/Rif Ultra assay on formalin-fixed, paraffin-embedded tissues for *Mycobacterium tuberculosis* diagnosis

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OBJECTIVE: Xpert MTB/Rif Ultra assay is a real-time PCR assay detecting *Mycobacterium tuberculosis* (MTB) in sputum specimens. We evaluated Xpert MTB/Rif Ultra assay performance for MTB detection in formalin-fixed paraffin-embedded tissue (FFPET) compared with mycobacterial culture or reference laboratory laboratory-developed MTB PCR test (LDT).

METHODS: Archived FFPET samples with histological features of tuberculosis (i.e., granulomatous inflammation, with or without acid-fast bacilli) were selected and depending on tissue size, 2-4 20-µm thick scrolls were obtained. Five-hundred microliters of ATL Buffer (Qiagen, Hilden, Germany) was added to FFPET scroll and incubated for 5 min at 75°C to melt paraffin. After centrifugation, 50 µL proteinase K 600 mAU/mL (Qiagen) was added. The FFPET were incubated overnight at 56°C, and sample aliquots were processed according to manufacturer's instructions. MTB culture or reference laboratory MTB LDT was used as comparator for sensitivity and specificity calculations.

RESULTS: Out of 39 eligible FFPET samples, 22 were positive for MTB either by culture of concurrently collected fresh tissue specimen or reference laboratory MTB LDT on FFPET. Xpert MTB/Rif Ultra detected MTB in 15/22 positive specimens (68.2%). The 7 discordant positives included 3 lymph nodes, 2 spinal collection aspirates, and 1 lung tissue. Five false negatives had positive MTB culture from an accompanying specimen; the remaining two did not have specimens submitted for culture but MTB were detected by reference laboratory LDT MTB PCR. Of 17 negative samples (negative by reference laboratory LDT), all tested negative by Xpert MTB/Rif Ultra assay. Assay specificity was 100%.

CONCLUSION: Xpert MTB/Rif Ultra assay demonstrated 68.2% sensitivity relative to culture and/or reference laboratory LDT MTB PCR, with seven false negatives noted when compared. Sampling variability, exhaustion of tissue, DNA degradation during storage, and extraction variability may explain the false negative results. Specificity was found to be 100%.

TP005

Validation of a two commercial serology assays for the detection of antibodies against mpox virus

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OBJECTIVE: The sudden global surge in mpox cases in 2022 has brought attention to the need of a suitable serological test for the detection of antibodies specific against mpox virus (MPXV). In an effort to gain a deeper understanding of antibody dynamics and to establish a protocol for future serosurveys, we conducted a validation on both an electrochemiluminescent multiplex assay from Meso Scale Discovery (MSD) and an ELISA assay (Abbexa) for the detection of antibodies against MPXV.

METHODS: For this validation, we used residual serum samples collected between December 2021 and November 2022 from both uninfected individuals and those with confirmed MPXV infections (through PCR detection). These samples had undergone testing at the BC Centre for Disease Control Public Health Laboratory. For most of these samples, we obtained information on their mpox vaccination status, day of symptom onset, and number of lesions for infected cases.

RESULTS: On the MSD assay, results from samples collected more than 7 days after the onset of symptoms revealed elevated levels of antibodies against four out of five MPXV antigens tested. Particularly, A35R, B6R, and E8L displayed the best sensitivity and specificity for detecting antibodies in infected individuals. Notably, E8L exhibited

superior performance overall, with a sensitivity and specificity exceeding 95%. On the basis of these results, we tested an ELISA kit designed to detect antibodies against E8L with concentrations ranging from 15.6-1,000 ng/mL. Although it presented some cost advantages, we observed that its dynamic range was narrower compared to the MSD kit.

CONCLUSION: In conclusion, while the MSD kit has a higher sensitivity than the Abbexa kit, both platforms are suitable for detecting anti-E8L antibodies in individuals infected with MPXV.

TP006

Development of an amplicon-based whole genome sequencing assay for respiratory syncytial virus

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OBJECTIVE: To develop a WGS workflow for the surveillance of respiratory syncytial virus

METHODS: Representative respiratory syncytial virus-A (RSV-A) and RSV-B sequences from National Center for Biotechnology Information were aligned using Clustal Omega to generate consensus genomes for both RSV subtypes. PrimalScheme v1.4.1 designed multiplex primers to generate overlapping amplicons against each consensus genome. Amplicons were sequenced on a GridION Mk1 sequencer (Oxford Nanopore Technologies). Base calling and demultiplexing were performed using the native MinKNOW v22.10.7 software. A custom analytical pipeline included the removal of human and low-quality reads, competitive mapping against an RSV-A/RSV-B composite genome to determine viral type, minimap2 to align reads, iVar to remove primer sequences, medaka consensus, medaka variants, and bcf-tools to construct a consensus genome, and NextClade to determine viral clade and G-clade.

RESULTS: 135 RSV-A and 121 RSV-B near full-length (>15 kb) genomes were aligned to generate consensus genomes. Twenty-seven and twenty-six amplicons (750 bp) were designed to tile the RSV-A and RSV-B genomes, respectively. We sequenced the first 204 and 159 RSV from 2022 and 2023, respectively. The proportion of RSV-A increased from 56% in 2022 to 82% in 2023. RSV-A isolates comprising multiple A.D. genomic clades (or G-clade: GA2.3.5), while a single B.D.E.1 genomic clade (or G-clade: GB5.0.5a) predominated among RSV-B isolates.

CONCLUSION: We have designed a 2-pool multiplex PCR to coamplify RSV-A and RSV-B genomes for WGS on the ONT platform. Up to 96 genomes can be batched and sequenced on a GridION flow cell. RSV isolates collected from the beginning of the 2022 and 2023 respiratory seasons revealed multiple genomic clades of RSV-A, but only one RSV-B genomic clade. Ongoing surveillance of RSV is required to track RSV subtypes and monitor clade changes, especially in light of the recent approval of the RSV vaccine in children and the elderlies.

TP007

Evaluation of the QIAstat-Dx Respiratory SARS-CoV-2 Panel for the detection of viral and bacterial pathogens in nasopharyngeal swab specimens

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OBJECTIVE: This study evaluates the performance of the QIAstat-Dx Respiratory SARS-CoV-2 Panel (RS2P) for the detection of respiratory pathogens from nasopharyngeal swabs (NPS).

METHODS: NPS specimens were initially tested for respiratory pathogens by standard laboratory workflow. Three-hundred and fifty-five NPS, including 51 clinical negative specimens were tested on the RS2P. Among the 304 positive specimens tested, 289 were clinical specimens, and 15 were contrived specimens. Initial discordant results were retested on a platform different from the original one, and consensus result was obtained based on agreement of at least 2 of 3 assays. Percent positive and negative agreement (PPA, PNA) was calculated on a per target basis. Concordance by number of positive targets was calculated.

RESULTS: Compared with original testing results, the PPA and PNA were 83.6% and 98.0%. Out of 355 specimens, 50 positives on original testing were not fully concordant for all targets, and one negative was not concordant. On the basis of original test results, 98.0% concordance was obtained for negative specimens, 92.3% for specimens positive for 1 target, 68.8% for 2 targets, 50% for 3 targets, and 0% for 4

targets. After resolution of discrepancies, the PPA and PNA were 91.6% and 98.3%. All targets except for Coronavirus 229E, Coronavirus OC43, Influenza A subtype H1N1 and H3, and Respiratory Syncytial Virus had PPA and PNA >90%. When only targets with comparator assay Ct values <35 were considered, PPA and NPA were 96.7% and 99.9%, and only Coronavirus OC43 had a PPA <90%. RS2P was discordant from consensus results in 26 cases. Of 22 false negatives on RS2P, 19 (86.3%) had a comparator assay Ct value >30.

CONCLUSION: Overall, the QIAstat-DX RS2P performed well in detection of bacterial and viral targets from NPS specimens.

TP008

Detection of bacteria directly from synovial fluid using digital PCR: A proof-of-concept study

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OBJECTIVE: Diagnosis of joint infections is challenging due to the low sensitivity of direct Gram stains and the long turnaround time of culture. Digital PCR (dPCR) can detect nucleic acid targets with high sensitivity and resistance to inhibition. We examined the utility of dPCR to directly screen for bacteria in synovial fluids without prior nucleic acid extraction.

METHODS: The ThermoFisher Absolute Q and QIAGEN QIAcuity dPCR systems were compared to Gram stain, culture, and real-time PCR. The dPCR amplified 500 base pairs of the 16S rRNA gene, based on a real-time PCR, using EVA green dye. The limit of detection of each dPCR instrument was determined using purified bacterial DNA. The sensitivity and specificity of each dPCR instrument were assessed using culture-positive or contrived and culture-negative synovial fluids.

RESULTS: dPCR was able to detect the 16S gene in extracts as low as 10 copies/µL. In 30 culture-positive neat synovial fluids, both dPCR instruments detected 20 (67%) as positive, 9 (29%) as indeterminate, and 1 (3%) as negative. Indeterminate dPCR results direct from specimens correlated with higher CT values on 16S real-time PCR performed on extracted nucleic acids. A total of 49 culture-negative synovial fluids were tested on both dPCR instruments. The Absolute Q was negative for 30 (61%) and indeterminate for 18 (37%). The QIAcuity was negative for 34 (70%) and indeterminate for 14 (29%). When compared to Gram stain, 9 of 16 culture-positive specimens with a negative Gram stain, were positive by dPCR.

CONCLUSION: This study demonstrated that dPCR can be performed directly on synovial fluids, requiring low specimen volume. Performance for the detection of bacteria was comparable between two dPCR instruments and real-time PCR. dPCR demonstrated superior sensitivity to Gram stain, but culture remains the most sensitive method.

TP009

Change in the *Streptococcus pyogenes* (group A streptococcus, GAS) positivity rates among throat swabs submitted from community settings in British Columbia

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OBJECTIVE: *Streptococcus pyogenes*, the group A streptococcus (GAS), is known to cause pharyngitis predominantly in the 3–14 years age group. However, in our community microbiology laboratories in British Columbia, we noticed an increase of the GAS positivity rate among throat swabs, from 8.76% in December 2022 to 12.49% in January 2023. The current study aimed to investigate whether the epidemiology changed among the throat swab GAS positivity rate in 2022 versus 2023.

METHODS: A total of 48,008 and 59,322 throat swabs were processed in our three community regional microbiology laboratories in 2022 (January to December) and 2023 (January to September). Microorganisms were isolated in blood agar culture plates after 18 hours in reduced oxygen incubators. Suspicious colonies (beta-hemolytic) were identified using Bruker matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS), followed by latex agglutination test PathoDX Strep Grouping Kit. Any number of colonies identified to be GAS by MALDI-TOF MS, in addition to Lancefield Group A would be reported.

RESULTS: The throat swab GAS positivity rate increased from 8.51% (2022) to 21.77% (2023). The GAS positivity rates in different age groups (divided using the Centor/modified McIssac criteria) were as follows in Table TP009-1.

Table TP009-1: Throat swab GAS positivity rates.

Age Groups	GAS Positivity Rate in 2023 January to October	GAS Positivity Rate in 2022 January to December
Age <3	13.35%	1.65%
Age 3-14	36.20%	8.28%
Age 15-44	19.71%	10.38%
Age >44	9.76%	3.16%

CONCLUSION: The throat swab GAS positivity rate was significantly higher in 2023 than 2022. This corresponds with the increase in invasive GAS infections in Canada and elsewhere in the winter of 2022/2023. GAS typing could help identifying a relationship between pharyngeal colonization and invasive disease. In 2023, GAS positivity remained highest among the 3–14 years age group, in keeping with clinical diagnostic criteria for GAS pharyngitis; however, positivity in the adult age group was significantly higher than the previous year.

TP010

To beat or not to beat—An exploratory assessment of two commercial fecal DNA extraction methods with and without bead-beating for quantitative polymerase chain reaction-based detection of gastrointestinal protozoa

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OBJECTIVE: Optimization of stool DNA extraction is critical for accurate detection of parasitic protozoa. The inhibitory nature of stool matrix combined with the resilience of protozoan cysts pose unique challenges for effective extraction. This study aimed to investigate the added value of bead-beating as a pretreatment prior to DNA extraction by two commercial stool extraction kits for detecting gastrointestinal (GI) protozoa by quantitative polymerase chain reaction (qPCR).

METHODS: Nine positive clinical unpreserved stool samples were prepared into COPAN FecalSwab with a defined concentration (*Entamoeba histolytica* [$n = 3$]; *Giardia lamblia* [$n = 3$]; *Cryptosporidium* spp [$n = 3$]). The fecal swabs were then extracted in triplicate across four experimental setups: Seegene STARMag Universal Cartridge Kit and KingFisher MagMAX Ultra Microbiome Kit, each with and without bead-beating. Bead-beating was performed prior to extraction with Bead Ruptor Elite 96 (Omni International, Inc., United States) for a total of 1 min. Extraction performance was evaluated by comparing the qPCR cycle threshold (Ct) values of the same sample from each experimental setup, using RIDA GENE Parasitic Stool Panel I.

RESULTS: The two commercial DNA extraction methods performed similarly for most protozoa tested, except for two samples for which the KingFisher showed favourable performance. These included one *E. histolytica*, which showed up to a 5.7 Ct difference, and one *G. lamblia*, which showed up to a 5.1 Ct difference. There was no systematic trend in performance with or without bead-beating. However, greater benefit was observed with bead-beating in samples with dry and/or mucous consistency.

CONCLUSION: These findings from a limited sample set demonstrated similar performance of two commercial DNA extraction methods and variable impact of bead-beating for the detection of GI protozoa from fecal swab specimens. This preliminary study supports the need for a more comprehensive assessment, including consideration of a sample-dependent approach for bead-beating from fecal swab specimens.

TP011

Cerebrospinal fluid galactomannan detection for the diagnosis of central nervous system aspergillosis: A diagnostic test accuracy systematic review and meta-analysis

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OBJECTIVE: Our primary objective was to evaluate the diagnostic test accuracy of cerebrospinal fluid (CSF) galactomannan testing to diagnose central nervous (CNS) as-

pergillosis, alone or in combination with other tests. Our secondary objective was to determine the test characteristics in immunocompromised patients.

METHODS: We systematically searched MEDLINE, Embase, Web of Science and Scopus from inception to February 24, 2023. Abstract and full-text screening, data extraction, and risk of bias assessments occurred blinded and in duplicate. We included prospective and retrospective case-control and cohort studies using any galactomannan assay on the CSF, alone or in combination, to diagnose neuroaspergillosis. We included adult and/or paediatric patients, regardless of immune status. The galactomannan index test(s) were compared to EORTC/MSG diagnostic criteria. We assessed risk of bias using QUADAS-2 and QUADAS-C. We used bivariate-restricted maximum-likelihood estimation random-effects meta-analysis, using forest and summary receiver-operator characteristic plots to synthesize data. We explored heterogeneity using bivariate meta-regression. Subgroup effects and methodologic choices were explored using subgroup and sensitivity analyses (PROSPERO registration: CRD42022296331).

RESULTS: Eight studies totalling 342 participants were included. The pooled sensitivity of CSF galactomannan was 69.0% (95% CI 57.2% to 78.7%), with a pooled specificity of 94.4% (95% CI 82.8% to 98.3%). Galactomannan cut-off ($p = 0.38$), EORTC/MSGERC criteria version used ($p = 0.48$), or how the comparator was defined ($p = 0.48$) did not explain observed heterogeneity. No subgroup effects were demonstrated by analyzing how the comparator was defined or whether paediatric patients were included. We were unable to assess test characteristics in immunocompromised patients. Diagnostic sensitivity was improved when using a galactomannan cut-off of 1.0 compared to 0.5, and by excluding a high risk of bias and cohort studies.

CONCLUSION: CSF galactomannan is a highly specific but poorly sensitive test that can be used to assist in neuroaspergillosis diagnosis. Few included studies, few included prospective studies, and study limitations were a high risk of bias.

TP012

Low-level (<1 × 10⁶ CFU/L) *Streptococcus agalactiae* bacteriuria in pregnancy is significantly associated with antepartum colonization

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OBJECTIVE: Recto-vaginal *Streptococcus agalactiae* (GBS) colonization poses a risk of neonatal GBS disease. Intrapartum prophylaxis is recommended for antepartum GBS colonization detected by screening between 36 weeks and 37 weeks 6 days gestation and for GBS bacteriuria detected anytime during pregnancy. Because traditional urine culture methods use an inoculum of 1 mL, the risk of antepartum colonization with GBS bacteriuria at levels below 1×10^6 CFU/L remains unclear. This study aimed to assess this risk.

METHODS: A 10-mL urine inoculum on the Kiestra InoqulA was placed on ChromAgar Orientation medium. GBS bacteriuria below 1×10^6 CFU/L was not reported by the laboratory. Pregnant women screened for asymptomatic bacteriuria between November 2020 and May 2022 with low-level GBS bacteriuria (between 1×10^5 and 1×10^6 CFU/L) underwent routine antepartum recto-vaginal GBS screening, and results were determined by review of birth records. Antepartum colonization rates in women with low-level GBS bacteriuria were compared with a contemporaneous control group of pregnant women who underwent antepartum recto-vaginal screening without a history of GBS bacteriuria.

RESULTS: Among 126 women with low-level GBS bacteriuria, 101 had antepartum screening results available of which 41 (40.6%) were GBS colonized. In the control group, 550/3,982 samples (13.8%) were GBS-positive. The relative risk of very low-level bacteriuria for antepartum GBS colonization was 2.939 (95% CI 2.2927 to 3.7676; $p < 0.0001$).

CONCLUSION: Women with very low-level GBS bacteriuria had about 3× greater risk of antepartum GBS colonization than those without a history of GBS bacteriuria. This compares with a higher relative risk of 5.6 for GBS bacteriuria $>1 \times 10^6$ CFU/L reported in a similar study. As the use of automated inoculation methods using larger volumes of urine becomes more common in microbiology laboratories, further evaluation is warranted to determine whether low-level GBS bacteriuria justifies universal intrapartum GBS prophylaxis.

TP013

Evaluation of the NG-Test CTX-M MULTI lateral flow immunoassay

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OBJECTIVE: With increasing incidence of extended-spectrum β-lactamase (ESBL) producing Enterobacterales, rapid ESBL identification can facilitate early antimicrobial optimization. NG-Test® CTX-M MULTI (NG-BIOTECH, Guipry-Messac, France) is a rapid, qualitative multiplex immunochromatographic assay detecting CTX-M ESBL (groups 1, 2, 8, 9, 25) with a previously reported sensitivity of 90%–100% and specificity of 96%–100%. We evaluated the NG-Test® performance compared to two PCR-based CTX-M detection methods.

METHODS: Seventy-eight frozen gram-negative isolates (2013–2023) recovered from previous submitted multidrug-resistant and non-ESBL clinical samples, along with carbapenemase-screening specimens, were subcultured to blood agar plates. After 48 hours incubation, 3 colonies were suspended in the NG-Test® commercial buffer and applied to the test cassette as per the manufacturer's instructions. Results were compared to reference standard: either commercial BioFire BCID2 FilmArray (bioMérieux, Marcy-l'Étoile, France) (n = 32), or an internally validated, laboratory-developed PCR (n = 46). All discrepant results were reviewed with repeat NG-Test®, phenotypic combination discs, and an alternative PCR platform.

RESULTS: NG-Test® detected CTX-M in 26/78 isolates (33.3%), compared with 30/78 (38.5%) by PCR methods. Postdiscordance analysis revealed: PPA 89.7% (95% CI 71.5% to 97.2%), NPA 100% (95% CI 90.9% to 100%) and overall agreement 96.2% (95% CI 88.4% to 99.0%). Only three false negatives were identified, possibly due to freezing-related plasmid loss or low-level enzyme expression: *Raoultella ornithinolytica* (n = 2), *Klebsiella oxytoca* (n = 1). One *Escherichia coli* was phenotypically negative for CTX-M (NG-Test and ESBL combination disc) but PCR positive; whole-genome sequencing confirmed the presence of a nonfunctional $bla_{\text{CTX-M}}$ gene.

CONCLUSION: NG-Test CTX-M MULTI performed well with categorical 96.2% agreement for CTX-M detection compared to PCR tests, consistent with published characteristics. Although limited to CTX-M, rapid turnaround time and minimal technical expertise could support earlier escalation to carbapenem therapy for ESBL infections. Further studies are needed to support clinical implementation through diverse testing methodology (e.g., directly from blood culture) and correlation with patient outcomes.

TP014
Investigating the performance of typhoid diagnostics and molecular analysis of *Salmonella enterica* virulence

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OBJECTIVE: Typhoid fever, a systemic bacterial infection caused by the microbe *Salmonella enterica* serovar Typhi, remains a significant public health problem. The minimal data on the accuracy of typhi-dot test kit, coupled with its design as a screening tool is a great hurdle for typhoid diagnosis. This test method is, nevertheless, used to decide on antibiotic administration contributing to larger problem of antimicrobial resistance due to misdiagnosis. This study aims to improve upon typhoid diagnosis and identify genetic mediators of *Salmonella enterica* virulence.

METHODS: A total of 258 blood and stool samples were collected from patients clinically diagnosed of typhoid fever at 7 hospitals. Samples were cultured and isolates were biochemically identified. PCR and cultures were used as gold standard for diagnostic assessment through comparative analysis with typhi-dot(RDT) kits, where plasma was used for typhoid IgG/IgM serological analysis. Disc diffusion antibiotic sensitivity testing was performed to determine the overall resistance pattern of isolates against antibiotics conventionally prescribed for treatment. Whole genome sequencing (WGS) and bioinformatic analysis were performed on identified isolates to determine circulating sequence types (STs), plasmids, and markers of antimicrobial resistance and virulence of *S. enterica* causing typhoid within the population.

RESULTS: The data suggest an overall typhi-dot test kit's sensitivity and specificity of 60% and 53%, respectively, relative molecular detection. In total, 29 *S. enterica* isolates were confirmed. Generally, isolates were sensitive to conventional tested antibiotics. Markers of resistance and plasmids identified from WGS analysis predicted resistance

to aminoglycosides tetracyclines and penicillin class phenotypes. Typhoid toxins and Vi antigens confirmed serological virulence of isolates.

CONCLUSION: Our study showed that typhi-dot test kit used in typhoid diagnosis performs nonoptimally. The data also suggest clonal diversity expansion, which emphasizes the need for intense molecular epidemiological surveillance to understand the evolutional occurrence in the typhoid domain.

TP015

Evaluation of the Seegene STARlet-AIOS compared to the conventional STARlet system using the Allplex Entero-DR Assay

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OBJECTIVE: Technological advances have allowed diagnostics to gain efficiency through automation. Seegene's PCR diagnostics utilizes robotics to automate extraction using the STARlet system followed by manual loading and data extraction using Bio-Rad CFX96 thermocyclers. The new Seegene STARlet-AIOS adds automation integrating STARlet extraction and Bio-Rad CFX96 amplification and data extraction limiting hands-on time to one single setup step. The goal of this work was to compare the hands-on-time, walk-away time, and turnaround time associated with the use of the STARlet-AIOS compared with the conventional STARlet system using the Allplex Entero-DR Assay.

METHODS: Duplicate testing was completed on the STARlet-AIOS and the conventional STARlet system using a convenience sample of 208 mock samples that were prepared for a limit of detection analysis using the Allplex Entero-DR Assay using 10 clinical isolates (NDM, OXA-48, KPC, or VIM-positive *Escherichia coli* and *Klebsiella pneumoniae* and vanA or vanB-positive *Enterococcus faecium* and *Enterococcus faecalis*). Eight parallel runs were completed. Mean hands-on-time, walk-away time, and turnaround time to results were measured and compared along with sensitivity, specificity, cycle threshold differences, and reproducibility.

RESULTS: The STARlet-AIOS was associated with a significant decrease in hands-on time compared to the conventional STARlet (average 26 min/run versus 40 min/run) with an increased mean walk-away time/run (average 185-min single walk-away time versus two 89-min and 85-min walk-away time). Turnaround time to results were comparable for the two systems (average 214 versus 211 min/run for the STARlet-AIOS and conventional STARlet, respectively). Sensitivity, specificity, Ct differences, and CoV were comparable for both systems.

CONCLUSION: Using the Entero-DR PCR Assay, compared with the conventional Seegene STARlet system, the Seegene-AIOS provided automation that reduced hands-on-time and increased walk-away time while providing comparable turnaround time, accuracy, limited of detection, and reproducibility, providing another option for laboratories to automate processes and become more efficient.

TP016

Monitoring of *Legionella pneumophila* outbreaks through next-generation sequencing-based genotyping: Comparison assessment with PFGE and SBT

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OBJECTIVE: Improve tools to monitor *Legionella pneumophila* outbreaks by developing an easy-to-use, highly reproducible, and efficient next-generation sequencing (NGS)-based protocol and benchmarking our findings to PFGE and SBT.

METHODS: The Public Health Laboratory of Québec (LSPQ) had historically used PFGE and SBT to compare clinical and environmental strains of *Legionella pneumophila* that had been linked epidemiologically. We used a first selection of strains representing seven epidemiological and molecular investigations with related profiles to compare and evaluate previously employed molecular epidemiology benchmark techniques (PFGE and SBT) to more recent investigative tools (Legiocluster, Legsta, mompS, KSNP3, and chewBBACA) based on single nucleotide polymorphisms (SNPs), kmer, and MLST NGS approaches.

RESULTS: In comparing past investigations with PFGE and SBT, we found SBT to be less discriminant compared

to PFGE. Data from NGS analyzed by Legsta coupled with mompS programs confirmed equivalent allelic and ST results to first-generation SBT. Legiocluster, KSNP3, and chewBBACA, respectively, show differences of <20 SNP, <30 SNP, and <2 locus for strains with the same or related PFGE patterns.

CONCLUSION: NGS-based protocols for outbreak investigation led to similar conclusions, as previously employed PFGE and SBT techniques. There, the advantage lies in being more efficient and providing detailed information regarding molecular evolution and allelic profiles. NGS-based detection protocols for *Legionella pneumophila* allow easily scalable analysis of clinical and environmental strains of *Legionella pneumophila* and may lead to more efficient and proactive surveillance.

TP017

Candida auris identification using CHROMagar Candida Plus and qPCR

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OBJECTIVE: *Candida auris* is a yeast with high outbreak potential that is often multi-drug resistant and was recently categorized by the World Health Organization as a critical priority fungal pathogen. Here we validated methods of identification of *C. auris* using isolates from Canadian patients.

METHODS: We selected two methods of identification based on availability and ease of use and tested them with clinical and colonization *C. auris* isolates from clades I to IV, along with a variety of related *Candida* species. We examined the ability of commercially available pre-made plates of CHROMagar Candida Plus (CCP) agar, and CCP agar sold in powder form to differentiate *C. auris* cultures from other *Candida* species. We also adapted and tested a real-time quantitative PCR test developed by the CDC with isolates of *C. auris*.

RESULTS: Thirty-three *Candida* isolates were screened using CCP. All *C. auris* isolates ($n = 10$) produced expected phenotypes after 48 h of incubation. Five additional *Candida* species that were not listed by the manufacturer (including *Candida haemulonii* and *Candida duobushaemulonii*) produced phenotypes that were easily differentiated from *C. auris*. When mixed cultures containing a variety of *Candida* species were plated on CCP; both the premade and in-house prepared plates enabled identification of putative *C. auris* colonies and subsequent confirmation using matrix-assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry. A slightly modified version of the qPCR assay developed by the CDC was tested with a variety of *Candida* species and showed accurate identification of *C. auris* isolates and no cross-reactivity with non-*auris* Candida species. To accommodate our workflow for the qPCR, we substituted a different fluorogenic probe and used a synthetic DNA fragment for the internal positive control.

CONCLUSION: CCP agar with MALDI-TOF and qPCR were reliable methods for the accurate identification of *C. auris* from the four major clades (I-IV).

TP018

Performance evaluation of complete urine culture categorization by WASPLab PhenoMATRIX

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OBJECTIVE: WASPLab PhenoMATRIX offers clinical microbiology laboratories the ability to leverage deep learning algorithms and digital image analysis for assessing, sorting, and segregating bacterial cultures according to user defined rules. The objective of this study was to evaluate the performance of PhenoMATRIX digital analysis compared to manual interpretation of significant and insignificant urine cultures.

METHODS: Plate images of urine cultures processed on Brilliance UTI Clarity and incubated at 37°C were produced at 0 and 16 hours and used by PhenoMATRIX to segregate cultures into result categories. Manual interpretation by two blinded MLTs was performed. A third interpreta-

tion was performed when manual interpretations disagreed. Agreement was obtained if PhenoMATRIX and two manual interpretations agreed.

RESULTS: Postadjusted agreements of 79% (157/200), 73% (145/200), 73% (145/200), 97% (194/200), 84% (168/200), 84% (167/200), 65% (130/200), and 99% (198/200) were obtained for cultures identified by the PhenoMATRIX as no growth (NG), no significant growth (NSG), mixed growth (MG), pure growth of *E. coli*, pure growth of gram-negative bacilli (GNB), pure growth of *Enterococcus* sp, growth of multiple organisms of significance (2-or-more), and pure or predominant growth of white or translucent colonies (other).

CONCLUSION: Agreement between manual interpretation and PhenoMATRIX was highest for scenarios involving pure growth of *E. coli*, GNB, or *Enterococcus* sp, and Other. Agreement was lowest for categorizations with complex interpretive algorithms involving multiple organisms and those identified as NSG and NG. MLTs disagreed with 70 PhenoMATRIX 2-or-more and 50 MG identifications and reclassified 64% and 67% as MG, and other, respectively. All 55 cultures identified as NSG were reclassified as other. The algorithms inability to detect microscopic pinpoint hazes consistent with *Lactobacillus* and *Aerococcus* growth, coupled with the selected microcolony setting of <20 impacted NG and NSG identifications.

TP019

Xpert MTB/RIF Ultra performance on bronchoscopy specimens for tuberculosis (TB) diagnosis in a low-incidence setting

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OBJECTIVE: Xpert MTB/RIF Ultra ("Ultra"), a rapid molecular assay for TB diagnosis, has improved performance over the previous version of Xpert MTB/RIF. Ultra has been extensively validated and approved for testing on sputum. However, if sputum is nondiagnostic or unavailable, and there is moderate to high suspicion for TB, bronchoscopy is typically pursued. We aimed to evaluate the performance of Ultra for TB diagnosis on bronchoscopy specimens in a low-incidence setting.

METHODS: Patients with a clinical suspicion of TB with bronchoscopy performed between March 2019 and September 2023 at two hospitals were included in the study. Bronchoscopy specimens comprised bronchoalveolar lavages, bronchial washings, and endobronchial ultrasound (EBUS) lymph node biopsies. All specimens underwent acid-fast bacilli (AFB) smear and mycobacterial culture. Ultra (Cepheid, Sunnyvale, California) was performed upon clinical request by respirologists. Mycobacterial culture was considered a reference standard for diagnosis of TB.

RESULTS: 136 bronchoscopy samples from 127 patients were included in the study. Cultures were positive in 49/127 (38.6%) of included patients. Of culture-positive patients, 20/49 (40.8%) were smear-positive and 29/49 (59.2%) smear-negative. Overall agreement between Ultra and culture was 96.8%. Positive percent agreement (PPA) and negative percent agreement (NPA) of Ultra compared with culture were 93.9% and 98.7%, respectively. In smear-positive cases, Ultra had 100% PPA and NPA, while in smear-negative cases PPA and NPA were 89.7% and 98.6%, respectively. On average, results of positive cultures were available after 14.5 days incubation (range, 5–42 days) versus 24 h for Ultra. Ultra cycle threshold (Ct) values correlated strongly with AFB-smear grade and time-to-culture positivity.

CONCLUSION: Ultra performed on bronchoscopy collected specimens demonstrated excellent agreement with culture and ≥90% PPA and NPA, even in smear negative cases. Our results support the use of the Ultra on bronchoscopy specimens for accurate and rapid TB diagnosis in a low-incidence setting.

TP020

TaqMan PACMAN: A simple molecular approach for positive rapid antigen test confirmation during periods of low prevalence

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OBJECTIVE: Antigen-based rapid diagnostic tests (Ag-RDTs) were widely deployed to enhance SARS-CoV-2 testing capacity during the COVID-19 pandemic. Consistent with national guidance for low prevalence settings, positive Ag-RDTs were confirmed using nucleic acid amplification tests (NAATs) to avoid false-positive results. However, increasing demands for positive Ag-RDT confirmation competed with other testing priorities in clinical laboratories. This work hypothesized that real-time RT-PCR without nucleic acid extraction (NAE) would be sufficiently sensitive to support positive Ag-RDT confirmation.

METHODS: Ag-RDT and NAAT results from community-based asymptomatic testing sites prior to the Omicron variant wave were compared to calculate the weekly false positive rate (FPR) and false detection rate (FDR). Real-time RT-PCR was compared with and without NAE using 752 specimens previously tested positive for SARS-CoV-2 using commercial NAATs and 344 specimens from Ag-RDT-positive individuals. The impact of SARS-CoV-2 prevalence on laboratory resources required to sustain Ag-RDT confirmation was modelled for the RT-PCR with and without NAE.

RESULTS: Overall, FPR was low [0.07% (222/330,763)] in asymptomatic testing sites, but FDR was high [30.7% (222/724)]. When RT-PCR was compared with and without NAE, 100% concordance was obtained with NAAT-positive specimens, including those from Ag-RDT-positive individuals. NAE-free RT-PCR significantly reduced time to results, human resources, and overall costs.

CONCLUSION: A 30.7% FDR reaffirms the need for NAAT-based confirmation of positive Ag-RDT results during low SARS-CoV-2 prevalence. NAE-free RT-PCR was shown to be a simple and cost-sparing NAAT-based solution for positive Ag-RDT confirmation, and its implementation supported data-driven broader Ag-RDT deployment into communities, workplaces, and households.

TP021

Incidence rates and serotype distribution of human enteroviruses in patients with central nervous system (CNSI) infections in south-central Ontario

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OBJECTIVE: Human enteroviruses account for up to 95% of recognizable, aseptic meningitis cases. There is limited data on the epidemiology of enteroviruses in south-central Ontario. The objective of this study was to assess the incidence and serotype distribution of enteroviruses implicated in CNSI in this region from 2019–2023.

METHODS: Cerebrospinal fluid (CSF) specimens submitted to the Hamilton Regional Laboratory Medicine Program (HRLMP), which serves south-central Ontario, were tested for enterovirus using a validated, lab developed PCR test. Retrospective data on enterovirus PCR performed on CSF specimens collected between January 2019 and December 2023 were retrieved from LIS and analyzed. Molecular serotyping was performed on a subset of specimens that were positive for enteroviruses by Sanger sequencing.

RESULTS: The detection rate of Enteroviruses in CSF fell to almost 0 during 2020 and 2021 with 0.5% (5/962) and 0.1% (1/1066), respectively, which coincides with the periods of social and travel restrictions during COVID-19 pandemic. In 2022, the incidence rose to 2.3% (24/1031) and rose again in 2023 to 4.1% (41/997), which was comparable to the last prepandemic year, 2019, at 3.6% (41/1134). Detection rate of enteroviruses in CSF was unexpectedly high in October 2023 (12/98 or 12.2%), the highest incidence for a single month in the study period. We were able to successfully type 11 species from October and November (11/15), and detected a high proportion (6/11, 55%) of Coxsackievirus B3 among different serotypes. Strikingly, the Coxsackievirus B3 sequences we obtained were identical at the nucleotide level despite being from 6 different patients at 6 different hospitals spanning south-central Ontario.

CONCLUSION: Incidence rates of enterovirus associated CNSI have returned to prepandemic levels in south-central Ontario with an unusual surge of cases in October-November 2023 driven by widespread transmission of a single strain of coxsackievirus B3.

TP022

Comparison of fosfomycin MICs generated by reference agar dilution (AD) testing and

Etest for pathogens submitted to a Canadian fosfomycin susceptibility testing service

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OBJECTIVE: Intravenous (IV) fosfomycin (FOS) sodium was approved for use in Canada in 2019. Oral FOS was reintroduced in Canada in 2017. Clinical microbiology laboratories that report FOS MICs commonly test using Etest® (bioMérieux).

METHODS: FOS MICs were determined by CLSI AD [Mueller Hinton Agar (BD BBL)] and Etest [Mueller Hinton Agar Plus (Oxoid)] for 122 gram-positive and Gram-negative isolates submitted to a Fosfomycin Susceptibility Testing Service offered through the Winnipeg HSC Clinical Microbiology Laboratory. MICs were interpreted by CLSI (M100, 2023) and EUCAST (v.13.1, 2023) breakpoint criteria where applicable.

RESULTS:

Table TP022-1

	CLSI[1]		EUCAST[2]		
Pathogen (*n*)	**% EA**	**% CA**	**% CA**	**% ME**	**% VME**
A. baumannii (1)	100	NA	NA	NA	NA
C. freundii (2)	100	NA	100	0	0
E. cloacae complex (19)	74	NA	95	0	11
E. coli (12)	100	100	100	0	0
K. aerogenes (1)	100	NA	0	0	100
K. pneumoniae (36)	86	NA	86	0	17
P. aeruginosa (47)	79	NA	NA	NA	NA
S. marcescens (2)	100	NA	100	0	0
S. aureus (2)	100	NA	100	0	0

Abbreviations: EA, essential agreement; CA, categorical agreement; ME, major errors; VME, very major errors; NA, not applicable.
[1]CLSI breakpoints: MIC (≤64 [S], 128 [I], ≥256 [R] µg/mL) apply to UTI isolates of *E. coli* and *E. faecalis* only.
[2]EUCAST breakpoints: MIC (≤32 [S], >32 [R] µg/mL) apply to IV FOS for Enterobacterales and *Staphylococcus* spp only.

CONCLUSION: EA between FOS Etest and AD was 86%–100% for all species except *E. cloacae* complex and *P. aeruginosa*. CA for FOS Etest and AD MICs was 86%–100% where CLSI and EUCAST MIC breakpoints could be applied. Seven VMEs (all with *Klebsiella* spp and *E. cloacae* complex isolates with Etest MICs of 16 or 32 µg/mL) were identified where EUCAST IV breakpoints were applicable.

TP023

Performance of a novel chromogenic agar for primary isolation of pathogenic β-hemolytic streptococci from throat swabs

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OBJECTIVE: Group A *Streptococcus* (GAS), group C and G streptococci (GCS/GGS) are common causes of bacterial pharyngitis. Chromogenic media are well established and have been proposed to streamline high-throughput diagnostic workflow. This study aimed to validate the Colorex StrepACG developed to facilitate detection of pathogenic beta-hemolytic streptococci (β-HS) from throat samples.

METHODS: Clinical validation was conducted using 239 throat swabs collected between November 6, 2023, and December 2, 2023. Additionally, 56 spiked Eswabs (Copan Eswab) (15-GAS; 7-GCS; 10-GGS; 24 other commensals of pharyngeal flora) were included. Swabs were plated onto Colorex and blood agar plates (BAP) and incubated for 18–24 hours at 35–37°C in CO_2. Colorex plates were examined for colorimetric suspected growth of GAS (orange/red colonies) or GCS/GGS (light mauve to purple colonies) by a trained technologist, blinded to results from BAP. Chromogenic agar results were compared with those from BAP. Presumptive growth of β-HS was verified by MALDI-TOF. Samples were considered true-positive (TP) if ≥1 media yielded growth of β-HS, confirmed by MALDI-TOF.

RESULTS: In total, 100 Colorex plates were read as positive, while 195 were negative. Positive and negative-percent agreements with BAP for presumptive growth of β-HS were 82.6% (95% CI 74.4% to 89.0%) and 97.2% (95% CI 93.6% to 99.9%), respectively. As per MALDI-TOF identification, 109 of 295 swabs were considered TP (85 TP-GAS; 24 TP-GCS/GGS. 10.9% (8/73) of Colorex with TP GAS yielded brown-purple-colonies. After discrepant analysis, sensitivity of Colorex™ and standard BAP were 95.4% (95% CI 89.7% to 98.5%) and 97.3% (95% CI 92.1% to 99.4%) respectively; whereas specificities were 97.6% (95% CI 94.6% to 99.4%) and 94.6% (95% CI 90.3% to 97.4%), respectively.

CONCLUSION: These findings suggest that Colorex StrepACG should be used in combination with BAP for throat samples. Further assessment would be required to establish if this holds true in the context of total laboratory automation paired with artificial intelligence-powered digital plate interpretation modules.

TP024

Evaluation of the Seegene STARlet-AIOS automation system for respiratory virus testing

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OBJECTIVE: The Seegene STARlet-AIOS is a complete automation system that offers the promise of minimal hands-on time for complete sample-to-result processing of respiratory specimens. Using existing STARlet and CFX96 Real-time PCR hardware, the added AIOS component offers a bridge between the devices to automate transfer of 96-well plates. We sought to evaluate 1) categorical agreement of viral respiratory specimens between the AIOS and existing STARlet/CFX96 combination; 2) potential carry-over and environmental contamination introduced by the new hardware; and 3) hands-on and walk-away times for operators of the instrument.

METHODS: Eleven influenza A, 11 influenza B, 11 RSV, and 14 SARS-CoV-2-positive and 47 negative nasopharyngeal swab specimens (previously tested using the Allplex SARS-CoV-2/FluA/FluB/RSV assay on the STARlet and CFX96 systems) were tested on the AIOS system in a checkerboard pattern to assess for categorical agreement and presence of carry-over contamination. Hands-on and walk-away times were recorded during testing. Fifteen environmental swabs, collected from a variety of internal instrument surfaces, were tested on an alternate platform.

RESULTS: The AIOS demonstrated 100% categorical agreement for known positive samples. Two influenza A/B positive samples produced an isolated S gene positive result (Ct > 36) for SARS-CoV-2 that had not been previously characterized. One RSV positive sample produced an influenza B positive result (Ct = 35.3) that had not been previously characterized. There was no evidence of carry-over contamination. Environmental swabs all tested negative for influenza A/B/RSV/SARS-CoV-2. Hands-on time for the AIOS was 24 min, and walk-away time was 4 hours and 35 minutes (compared to 33 min and 4 h and 30 min, respectively, for the STARlet/CFX96).

CONCLUSION: The AIOS produces concordant results for "quadplex" respiratory testing compared to the original STARlet/CFX96 combination system, with no evidence of carry-over or environmental contamination being introduced by the added robotics. There was a modest reduction in hands-on time of 7 minutes per run, but no appreciable difference in walk-away time.

TP025

Evaluation and comparison of five commercial stool antigen assays for the diagnosis of *Helicobacter pylori*

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OBJECTIVE: Timely and accurate diagnosis of *Helicobacter pylori* is important to guide treatment and prevent patient harm. This study aims to verify methodologies and results of commercially available enzyme immunoassays for the detection of *H. pylori* antigen in human fecal specimens.

METHODS: 220 patient samples were tested with five different commercial assays. Two rapid lateral flow immunoassays (Techlab *H. pylori* Quik Chek and Meridian Immunocard STAT!) and three traditional EIA assays (Meridian Premiere Platinum, Techlab *H. pylori* Chek EIA, and IDK *H. pylori* Antigen ELISA) were compared. A Biorad Evolis Twin Plus analyzer was used for the traditional EIA assays. Discrepant results were considered resolved when 4 out of the 5 assays were in agreement.

RESULTS: The TechLab *H. pylori* Quik Chek and Meridian Immunocard STAT! assays both demonstrated a sensitivity and specificity of 93% and 100, respectively. The IDK *H. pylori* antigen ELISA assay had a sensitivity of 93.3% and a specificity of 98.3%. Following the manufacturer's cut-off values provided in the package inserts of the TechLab *H. pylori* Chek EIA and the Meridian Premiere Platinum, both assays had a sensitivity of 100%; however, the specificities were only 29.1% and 79.9%, respectively. Reinterpreting the results using independent previously established optimized cut-off values increased the specificity of both the TechLab *H. pylori* Chek EIA and the Meridian Premiere

Platinum assays to 99.4%, and the sensitivities remained high at 100% and 97.7%, respectively.

CONCLUSION: The performance of the rapid lateral flow immunoassays was acceptable. For two of the three traditional EIA assays, optimized cut-off values were required to achieve satisfactory results with the Evolis Twin Plus analyzer. Commercial manufacturers should work to optimize cut-off values for specific instruments to ensure test accuracy.

TP026

Comparison of genetic resolution in clinical *Mycobacterium tuberculosis* complex isolates by genotyping and whole-genome sequencing methods

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OBJECTIVE: Historically, genotyping of *Mycobacterium tuberculosis* complex (MTBC) has been achieved by the methods spoligotyping and mycobacterial interspersed repetitive unit variable number tandem repeat (MRIU-VNTR). With recent technological advances, whole genome sequencing (WGS) of MTBC is steadily being adopted across public health laboratories for tuberculosis surveillance. The objective of this study was to compare the performance of WGS to conventional genotyping for determination of genetic relatedness in MTBC isolates identified in a public health laboratory between the years of 2011 and 2023.

METHODS: MTBC genotyping was performed on 896 MTBC isolates identified from 2011 to 2023. Of this collection, WGS data corresponding to 385 isolates were available for determination of the number of single nucleotide polymorphism (SNP) differences between samples (SNP distance) and cluster identification. Isolates with both WGS and conventional genotyping data were compared for genetic relatedness, clustering resolution, and lineage classification.

RESULTS: Of the MTBC isolates included in this study, the most frequently observed genotypes were genotypes 2 ($n = 342$), 76 ($n = 140$), 7 ($n = 87$), 6 ($n = 64$), 98 ($n = 60$), 5 ($n = 53$), 14 ($n = 41$), 246 ($n = 40$), 100 ($n = 37$), and 38 ($n = 32$). Average SNP distances calculated by WGS between samples within the same genotype cluster ranged from 2 to 188. Isolates clustering within genotypes 7, 6, 98, and 100 possessed the largest average SNP distances between samples corresponding to 112, 145, 179, and 188, respectively, suggesting potential overclustering of isolates by conventional genotyping methods. MTBC lineages—4, Euro-American; 1, Indo-Oceanic; 2, East Asian/Beijing; and 3, East-African Indian—were identified from the isolates included in the study.

CONCLUSION: Determination of genetic relatedness between MTBC isolates is a critical component of tuberculosis transmission surveillance and outbreak investigation. WGS provides the advantages of higher resolution and increased genome coverage, facilitating more accurate detection of clusters.

TP027

Bruker MALDI-ToF MS Compass Library Revision K accurately discriminates *Streptococcus pyogenes* from *Streptococcus dysgalactiae/canis*

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OBJECTIVE: *Streptococcus pyogenes*, *S. dysgalactiae*, and *S. canis* are related streptococci with similar MALDI-ToF spectra. Previously, the Bruker MBT Compass library could not reliably discriminate between these species, but in 2022, it updated its library (revision K) and claimed that *S. pyogenes* could be distinguished from *S. dysgalactiae/canis* without additional testing. We sought to evaluate this claim on overnight cultures and short-incubation (4-hour) blood subculture smudge plates.

METHODS: Beta-haemolytic streptococci in three laboratories were identified by MALDI-ToF (Bruker BioTyper with MBT Compass 11897 MSP). *S. pyogenes* was identified when any of the following criteria were met by extraction from an overnight culture: *S. pyogenes* identified with a score $\geq$2.00 and $\geq$0.3 higher than *S. dysgalactiae/canis*, *S. pyogenes* identified with a score $\geq$2.00 and no other species reported in the top 10 identifications or, *S. pyogenes*, *S. dysgalactiae*, or *S. canis* was identified with a score of $\geq$2.00 and the organism was PYR positive. Definitive results were compared with initial MALDI-ToF results obtained from on-plate extraction from smudge plates (blood cultures) and overnight cultures (all other specimen types).

RESULTS: Forty-one smudge plates and 311 overnight cultures were included. Of 26 *S. pyogenes* from blood culture

smudge plates, 25 (96.2%) were correctly initially identified by MALDI-ToF with one (3.8%) misidentified as *S. dysgalactiae/canis*. Of 15 confirmed *S. dysgalactiae/canis* from smudge plates, all were correctly identified initially (accuracy 97.6%). Of 257 *S. pyogenes* from overnight cultures, 255 (99.2%) were correctly initially identified by MALDI-ToF with two (0.8%) misidentified as *S. dysgalactiae/canis*. Of 54 confirmed *S. dysgalactiae/canis* from overnight cultures, all were correctly identified (accuracy 99.4%).

CONCLUSION: Initial identification of *S. pyogenes* and *S. dysgalactiae/canis* by MALDI-ToF using the MBT Compass is accurate from smudge plates and overnight incubation, eliminating the requirement for off-line testing or review of results to confirm identification.

TP028

Evaluation of the Xpert MTB/RIF Ultra for the detection of *Mycobacterium tuberculosis* in cerebrospinal fluids

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OBJECTIVE: This study aims to evaluate the performance of the Xpert MTB/RIF Ultra assay (Ultra), a rapid molecular assay for the simultaneous detection of *Mycobacterium tuberculosis* complex (MTB) and rifampin (RIF) resistance, in CSF specimens.

METHODS: The limit of detection (LoD) of Ultra for CSF was determined using a commercial MTB organism spiked into MTB culture-negative CSF specimens at concentrations near the assay's LoD for sputum. The positive percent agreement (PPA) was assessed using contrived MTB positive CSF and one smear positive, MTB culture-positive CSF. MTB culture-negative CSF were spiked with dilutions of an inactivated MTB strain. A laboratory-developed, real-time PCR was used as the reference result. Negative percent agreement (NPA) was assessed using MTB culture-negative CSF, some spiked with inactivated culture lysates of nontuberculous mycobacteria, and compared to the AFB culture result. Samples with >2 mL volume were concentrated by centrifugation, and 0.5 mL of the concentrate was tested. For specimens with <2 mL volume, 0.25 mL of the neat sample was tested on Ultra.

RESULTS: The LoD of Ultra for the detection of MTB in CSF (26 genome copies/mL) was similar to the LoD for sputum (16 CFU/mL). In 18 of 19 positive CSF (concentrated, $n = 9$ | neat, $n = 10$), MTB was detected (94.7% PPA). One contrived specimen gave an initial discordant negative result on Ultra, with MTB detected on repeat testing. For all 19 MTB culture-negative CSF, a concordant negative result (100% NPA) was observed. The overall agreement between the Ultra and reference methods was 97%.

CONCLUSION: The Xpert MTB/RIF Ultra demonstrated good PPA and NPA with the reference method for the detection of MTB in CSF. Additional testing of clinical MTB-positive CSF is needed for a complete validation of this specimen type. The detection of RIF resistance in CSF was not evaluated as part of this study.

TP029

Increased seroprevalence of Lyme disease in Nova Scotia: A 10-year update

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OBJECTIVE: Reports of Lyme disease in Nova Scotia have increased over the past 20 years, with expanding areas of higher risk. In the spring and summer of 2012, residual sera (originally collected for other clinical indications) were tested for seropositivity to *Borrelia burgdorferi*, stratified by age, sex, and region. At that time, almost all 1,855 samples were negative, with only two borderline-positive Western blots (0.1% seropositivity). The serosurvey was repeated in 2022 and 2023 to determine any changes in seroprevalence in the interim.

METHODS: From October 2022 to November 2023, a total of 1,872 residual serum samples were tested for Lyme positivity using the current testing algorithm (modified two-tier method). Samples were selected using a proportional representation of males and females, ages 10–64, from each region. Serum was subjected to an initial screening enzyme immunoassay (EIA) for VlsE1/pepC10 IgG/IgM (Zeus), and those that were positive or indeterminate were confirmed with a whole-cell lysate EIA (Zeus).

RESULTS: Ninety-three samples were either positive or indeterminate on the first EIA. Thirty of those samples confirmed as positive by the second EIA, with an overall Lyme disease seroprevalence in our population of 1.6%. The sero-

prevalence varied based on the region of the province, ranging from 1.92% to 6.53% in areas historically considered the highest risk, and 0% to 1.35% elsewhere in the province.

CONCLUSION: The current study demonstrates an increase in the seroprevalence of Lyme disease in Nova Scotia over the past 10 years. This is consistent with an increase in clinical cases. Disproportionately affected areas of the province align with the clinical reports. These findings support that Lyme disease is increasing in all areas of the province and highlight the need for continued provincially targeted messaging. Future work will focus on testing the archived sera for determining seroprevalence of other emerging zoonotic and communicable diseases in NS.

TP030

Optimizing *Leishmania* diagnostics: An integrated molecular approach for accurate detection and species identification

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OBJECTIVE: Leishmaniasis is caused by a protozoan parasite that includes over 20 species. Species identification is recommended to inform therapeutic management, but testing availability may be challenging. We aimed to investigate a comprehensive integrated molecular testing approach to enable timely and accurate *Leishmania* detection and species differentiation.

METHODS: Reference laboratory positive culture material and in-house positive clinical samples were tested. These were tested on the basis of two previously published assays: a 18S quantitative polymerase chain reaction (qPCR) for Leishmania detection, and a SYBR green-based qPCR assays for species differentiation by grouping. In addition, because of the lack of publicly available high-quality genomic data, in-house whole genome sequencing (WGS) was performed to inform next-generation sequencing (NGS) target selection. Whole-genome draft assemblies were built using de novo sequence assembler SPAdes. Amplicon-based NGS candidate targets were selected and trialed for species identification.

RESULTS: The 18S qPCR assay successfully detected all culture isolates ($n = 30$) and clinical samples ($n = 2$) tested, with a limit of detection (LOD) of 2 copies/µL. The SYBR green-based assay showed a LOD of 2 copies/µL and misidentified the species grouping of 3/25 culture isolates and 1/2 clinical samples. HSP70 was identified as a promising NGS target for species identification. Sequence database limitations restricted the options for NGS target selection.

CONCLUSION: The 18S qPCR assay enabled rapid and accurate detection of *Leishmania*, whereas the SYBR green-based assay demonstrated suboptimal performance in species grouping differentiation. Furthermore, this study identified that HSP70 is a promising target for species differentiation. Because of the rarity of leishmaniasis cases in Canada, these findings are preliminary, and we are collaborating with other centres to expand the clinical validation of the presented assays. Further research is needed to identify optimal amplicon size, and to assess performance by different sample types.

TP031

Workflow comparison and evaluation of an automated instrument for handling sample preparation in clinical laboratory

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OBJECTIVE: Laboratory testing is a multistep process that often involves repetitive tasks, such as sample labeling and aliquoting. Errors tend to occur during manual procedures that may impact the accuracy of results. We evaluated the performance of an automated instrument, Copan UniVerse, for preanalytical processing of clinical samples and the potential workflow improvements.

METHODS: Custom protocols are programmed on the UniVerse instrument for processing specific sample collection containers. Experiments were designed to compare Copan UniVerse's labeling and pipetting accuracy of transferring samples from primary sample container to secondary container, and its efficiency against manual procedures. Two primary containers tested were the Copan sample collection kits with universal transport medium and nasopharyngeal swabs, and the clinical oral gargle collection kits with sterile saline. Primary containers were prepared as samples in vitro, and as two groups: 1) negative samples, which were uninoculated, and 2) positive samples, which were inoculated with SARS-CoV-2 virus. Both

groups of samples were aliquoted to secondary container, Hologic Fusion lysis tube, by the UniVerse and manually, which were subsequently tested on Panther Fusion system for SARS-CoV-2 virus. Time study was performed to compare the hands-on time of the automated and manual process. Additional types of sample containers were used in the time study.

RESULTS: The accuracy for saline gargle samples ($n = 24$) and Copan swabs ($n = 24$) were both 100%, with average delta cycle threshold 0.15 and 0.18, respectively between the UniVerse and manual results. Hands-on time of sample preparation was reduced by 50% using UniVerse. With the integration of UniVerse in DNA/RNA extraction workflow, a pretesting step of aliquoting primary sample into secondary container can be eliminated to streamline the testing process.

CONCLUSION: Copan UniVerse can help improve laboratory's preanalytical workflow by automating repetitive manual procedures, which reduces the hands-on time required and possible human errors. A clinical validation is in progress.

TP032

Comparing routine *C. difficile* testing methods to identify *C. difficile* colonization in asymptomatic patients prior to hematopoietic cell transplantation

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OBJECTIVE: Patients undergoing hematopoietic cell transplant (HCT) are at high risk for infection, including *Clostridiodes difficile* infection (CDI). Colonization with *C. difficile* is associated with subsequent CDI, yet there are no routinely used methods to identify patients who may benefit most from prophylactic treatment. Here, we compared existing *C. difficile* stool detection methods at the time of pretransplant planning to identify individuals at high risk of developing CDI.

METHODS: We performed a prospective cohort study of patients undergoing HCT with data collected up to 3 months post-transplant. *C. difficile* colonization was assessed on baseline stools by using the laboratory's standard two-step algorithm: 1) a glutamine dehydrogenase (GDH) enzyme immunoassay screen, and 2) toxin B gene (*tcdB*) PCR on GDH+ samples only. A modified one-step *tcdB* PCR approach was also performed on DNA extractions (QIAGEN PowerFecal Pro) from a separately aliquoted stool sample.

RESULTS: We used baseline stool testing in our cohort, and 6/60 (10%) patients were GDH positive, 3/60 (5%) were both GDH and *tcdB* PCR positive, and 8/60 (13%) were *tcdB* PCR positive using our modified PCR protocol. 10/60 (18.3%) patients developed laboratory-confirmed CDI post-transplant [CB1]. The overall sensitivity and specificity of using *C. difficile* colonization (GDH+) as a screening test for identifying patients at risk of developing CDI were 50% and 98%, respectively. The modified *tcdB* PCR-only approach had a sensitivity of 60% and specificity of 96% for CDI.

CONCLUSION: Using routine and short-turnaround time diagnostic tools for *C. difficile*, we identified a subgroup of patients undergoing HCT that was at high risk for developing CDI during their peri-transplant period that could benefit from targeted CDI prophylaxis. Omitting the GDH screen and altering the *tcdB* PCR protocol improved sensitivity with minimal impact of specificity in this patient population.

TP033

Enhancing influenza surveillance through whole genome sequencing: Implications for local, national, and global pathogen control

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OBJECTIVE: Whole Genome Sequencing (WGS) is a robust tool in surveillance, enhancing our ability to monitor, track, and respond to infectious diseases with unprecedented precision. In the post-SARS-CoV-2 pandemic era, influenza re-emerged as a formidable public health challenge, coupled with a notable increase in paediatric infections during the 2022–2023 respiratory season, illustrating the need for understanding the genetic diversity, refining diagnostics, and ensuring the accuracy of surveillance efforts. In this study, we investigated the application of WGS to the enhancement of influenza virus surveillance in Saskatchewan.

METHODS: Libraries were prepared from 257 Influenza A and from 21 Influenza B nasopharyngeal swab extracts. Illumina's DNA prep kit and MiSeq platform were used to sequence 138 specimens, while Oxford Nanopore's ligation sequencing kit and MinION Mk1C platform were used to sequence 140 specimens. All genomes were assembled and analyzed using the nf-flu pipeline, with clades being assigned through Nextclade analysis.

RESULTS: There were 278 Saskatchewan influenza genomes generated and shared internationally to GISAID.org. Amid the resurgence in Saskatchewan, WGS data not only aided in identifying circulating strains but also contributed to crucial information to guide public health responses. The high incidence of infections among children was a focal point, guiding interventions aimed at mitigating the impact on this vulnerable population.

CONCLUSION: The integration of WGS into influenza virus surveillance in Saskatchewan during the 2022–2023 season was a powerful tool for understanding and addressing the challenges posed by the resurgence of influenza, offering a comprehensive strategy for emerging infectious threats. In addition, collaboration aspects remain crucial, as Influenza virus WGS data sharing contributes to the global understanding of viral dynamics. By actively participating both federally and internationally, this approach helps formulate a coordinated response in mitigating the resurgence of influenza infections on a global scale, thus enhancing the preparedness and resilience of health systems worldwide.

TP034

Comparative performance of the BioFire FilmArray respiratory panel 2.1 and the GeneXpert Xpert SARS-CoV-2/Flu/RSV assays for the detection of respiratory viruses in children using nasopharyngeal swabs

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OBJECTIVE: We assessed the performance of the BioFire FilmArray respiratory panel 2.1 (RP 2.1) and the GeneXpert Xpert SARS-CoV-2/Flu/RSV assays using health care worker (HCW)-collected nasopharyngeal (NP) swab samples for the molecular detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza, and respiratory syncytial virus (RSV) in children presenting for testing in the emergency department.

METHODS: Children who were symptomatic and had clinical indications for respiratory virus testing were recruited from a paediatric emergency department (ED). All participants had a HCW-collected NP swab tested with both assays. Samples that had both assays test positive for a target were considered positive for that target and those that had both test negative were considered negative for that target. Discrepant results were resolved through parallel molecular testing of matched alternate respiratory samples (either oral/nasal swabs or saline gargle samples) collected at the same time.

RESULTS: A total of 184 children were enrolled in the 2022/2023 and 2023/2024 respiratory seasons. 60.9% were males and the median age was 59 months (interquartile range 17 to 109). There were 13 SARS-CoV-2, 33 influenza A cases, and 26 RSV positive cases. Only one child tested positive for influenza B, so this target was not assessed. The GeneXpert assay had sensitivities and specificities of 100% and 100% for RSV, 100% and 100% for influenza A, and 100% and 99.4% for SARS-CoV-2, respectively. The BioFire RP 2.1 panel had sensitivities and specificities of 100% and 98.7% for RSV, 100% and 100% for influenza A, and 100% and 100% for SARS-CoV-2, respectively.

CONCLUSION: The BioFire FilmArray respiratory panel 2.1 and GeneXpert Xpert SARS-CoV-2/Flu/RSV assays demonstrated similar performance in detecting respiratory viruses in children. These relatively low complexity, rapid sample to answer automated assays may allow for reliable, comparable respiratory virus diagnostics for pediatric patients outside of molecular microbiology laboratory settings.

TP035

Detection of atypical bacteria, including *Mycoplasma pneumoniae*, 2013–2023

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OBJECTIVE: Etiological causes of respiratory tract infections are often clinically indistinguishable; thus, surveillance measures depend on pathogen-specific lab diagnosis. The purpose of this study was to evaluate the efficacy of the syndromic NxTAG Respiratory Pathogen Panel (RPP; Luminex), and to assess trends in detection of atypical bacteria (AB) during and after the COVID-19 pandemic. Testing is based on physician requests.

METHODS: Dates for analysis were divided into periods reflecting different testing strategies and COVID-19 restrictions. In period 1, the NxTAG Respiratory Viral Panel V2 (Luminex) and in-house developed multiplex NAT for AB (*Mycoplasma pneumoniae* [Mp], *Chlamydophila pneumoniae* [Cp], *Legionella pneumophila* [Lp]) were used. Samples were tested by either the viral or AB panel upon request. In period 2, the updated NxTAG RPP, which incorporates AB targets was adopted. Samples were tested by this panel whether viral or atypical pathogens were requested. These periods reflected prepandemic phases. Periods 3 and 4 reflected the pandemic and postpandemic period, respectively, and had the same testing practices as period 2.

RESULTS: During period 1, a bacterial pathogen test positivity rate of 2.4% (49/2001) was observed, while test positivity was 0.52% (157/30,203) in period 2. A significant increase in identification of AB-associated infections (49 versus 157; $p \leq 0.0001$) was observed following NxTAG RPP implementation, primarily due to an 11-fold and 4-fold increase in Cp and Mp cases, respectively. An overall decrease in AB-associated infections was observed in periods 3 and 4, with an increase in cases only occurring as of fall 2023.

CONCLUSION: This study suggests that implementation of the NxTAG panel enhanced identification of AB via syndromic approach instead of physician request. COVID-19 measures affected AB frequency, which then increased in period 4 signalling a return to endemic state. It is critical that comprehensive laboratory methods reflecting seasonal circulating pathogens are available for patient care and surveillance strategies.

TP036

Multicentre experience on the diagnostic yield of multiplex bacterial PCR for sterile site infections

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OBJECTIVE: To assess the diagnostic yield of multiplex PCR for bacterial pathogens (mPCR) on sterile site specimens (excluding blood and CSF) in adult and paediatric populations, utilizing data from two different laboratories.

METHODS: Lab-developed mPCR panels were independently validated by the laboratories at Hamilton Regional Laboratory Medicine Program (HRLMP), ON, Canada, and Sidra Medicine, Qatar. At Sidra, all sterile site specimens from paediatric patients were tested by culture and PCR ($n = 118$). At HRLMP, adult and paediatric specimens that tested negative by culture after 24 hours and upon physician request were tested by PCR ($n = 184$). Retrospective culture and PCR testing data for over a year were retrieved from the respective laboratory information systems. The diagnostic yield of PCR in different populations was assessed by the Chi-square test.

RESULTS: Combining results from both laboratories, out of 302 specimens from 267 patients, 20 (6.6%) were positive by culture, and 117 (38.7%) were positive by PCR for the target organisms. At Sidra, the diagnostic yield of PCR was significantly higher than culture (52.5% versus 10.2%; $p < 0.001$). At HRLMP, diagnostic yield of PCR was significantly higher than culture in both adult (3.8% versus 15.2%; $p < 0.003$) and paediatric (5.8% versus 67.3%; $p < 0.001$) populations. Additionally, diagnostic yield of PCR over culture was significantly higher in the paediatric population compared to adults (67.3% versus 15.2%; $p < 0.001$). Pathogen detection rates by PCR were similar for the paediatric populations of HRLMP and Sidra ($p = 0.07$). The most common pathogens detected by PCR but not by culture were *Streptococcus pneumoniae* (19.2%) and *S. pyogenes* (10.3%) and the most common specimen type where a pathogen was detected was pleural fluid (20.9%).

CONCLUSION: The detection rate of bacterial pathogens is greatly increased by PCR, particularly in the paediatric population. PCR testing should be used alongside culture to improve the diagnosis and management of sterile site infections.

TP037

Public Health Agency of Canada's measles and mumps molecular proficiency panel program: A retrospective study examining past results from Canadian laboratories

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OBJECTIVE: In order to identify factors that impact measles and mumps (MM) detection assays, we analyzed yearly proficiency panels completed by Canadian Laboratories from 2010 to 2023. The goal of this study was to combine participant submitted data from multiple years and examine the data for trends.

METHODS: We performed a retrospective analysis of results from participants that submitted measles and/or mumps detection results from 2010 to 2023. Data collected included sample type, gene target, qualitative result, Cp/Ct value, extraction platform, detection platform, detection kit, and reaction volume.

RESULTS: The number of laboratories participating in the proficiency panel for the detection of measles rose from 4 in 2010 to 8 in 2023 and from 6 in 2010 to 8 in 2023 for the detection of mumps. Consistently, all participating laboratories have achieved 100% concordance. Throughout the years, many institutions have made modifications to their testing methods, such as the addition of a vaccine-specific assay for measles ($n = 3$) and the addition/modification of a hemagglutinin (H) probe to detect measles viruses of the B3-Harare lineage ($n = 5$). By 2023, gene targets for measles include H (87.5%), N (71.4%), vaccine specific (37.5%), F (12.5%), and L (12.5%). Gene targets for mumps include F (87.5%), SH (37.5%), and N (25%). For measles detection, 100% of the laboratories have at least 2 gene targets, and for mumps, 50% of the laboratories have at least 2 gene targets. Extraction platforms for MM include the NUCLISENS easyMAG (50%) followed by the MagNA Pure instruments (28%), the Qiagen Viral RNA Mini Kit (16%), and the Maxwell Total Nucleic Acid Purification (6%).

CONCLUSION: This study examines the evolution of the MM detection practices in Canada from 2010 to 2023 and highlights the trends and optimizations. Canadian laboratories are proficient in detecting MM.

TP038

Development and validation of a low-cost semi-automated high-throughput direct qualitative loop-mediated amplification assay for the detection of *Streptococcus pyogenes* from throat swab specimens

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OBJECTIVE: Accurate and prompt testing for bacterial pharyngitis caused by *Streptococcus pyogenes* allows for more appropriate clinical decision making, avoidance of unnecessary antibiotics, and improved patient outcomes. We developed and validated a high-throughput direct loop-mediated amplification (LAMP) assay for the detection of *S. pyogenes* from clinical throat swab samples to maintain rapid results turnaround in a high-volume community laboratory setting.

METHODS: Crude heat lysis of aliquoted liquid amies transport media from flocked swab samples was performed in Tris-EDTA (TE) buffer at 95°C. Direct LAMP reactions with crude lysate templates were prepared using New England Biolabs WarmStart LAMP kit and primers targeting *S. pyogenes* Spy1258 transcriptional regulator and human β-actin (internal control) genes based on previously published sequences. Hamilton Nimbus/Starlet robotic liquid handlers were used for automated pipetting. Isothermal (65°C) LAMP reactions were run on CFX96 Touch Real-Time PCR Detection instruments. Endpoint melt-curve analysis to detect Spy1258 and β-actin amplification products was used for result determination. 33 non-*S. pyogenes* bacterial and yeast species commonly found in the human oropharynx were tested by direct lysis of colonies in TE buffer to confirm analytical specificity. Assay limit-of-detection was established by testing replicates of *S. pyogenes* quality control isolate serially diluted in pooled negative patient samples. Assay reproducibility was determined by repeated testing of known positive and known negative patient sample replicates. 276 patient throat swabs were tested in parallel with culture-based methods to determine clinical accuracy.

RESULTS: LAMP assay limit-of-detection was established between 1,500 and 15,000 colony forming units/mL. Analytical specificity and intra-/inter- assay reproducibility were 100% with no evidence of carry-over or cross-contamination. LAMP was 100% sensitive and 98.8% specific compared to culture.

CONCLUSION: High-throughput semiautomated direct LAMP is a cost-effective way to accurately detect *S. pyogenes* from clinical throat swab samples with less than 24-h results turnaround in high-volume centralized laboratory models.

TP039

Development of a real-time PCR assay for the detection of *Aspergillus* species from bronchial specimens

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OBJECTIVE: We aimed to establish a multiplex real-time PCR assay for the simultaneous detection of the most common medically relevant *Aspergillus* pathogens (*A. fumigatus*, *A. flavus*, *A. niger*, and *A. terreus*) from bronchial specimens.

METHODS: Primers and probes targeting the *Aspergillus* ITS1 regions, including an internal control, were evaluated. Spores from *Aspergillus* isolates and synthetic DNA were used to evaluate PCR efficiency, linearity, analytical sensitivity, and reproducibility. The analytical specificity was tested using non-*Aspergillus* DNA samples. Nucleic acid extraction was performed with the automated MagNa Pure 24 system (ROCHE). After optimization, accuracy was evaluated in 67 clinical specimens that underwent culture, including 31 *Aspergillus* positive (23 *A. fumigatus*, 5 *A. flavus*, 3 *A. niger*), and 38 *Aspergillus* negative with 18 of those positive for other fungi or bacteria).

RESULTS: One assay with two PCR reactions was established on the ABI 7500 Fast System. PCR efficiency was acceptable for all targets 90%–94.6%. Linearity (r^2) values were greater than 0.99 and dynamic range was 2×10^6 to 5 spores/reaction. Reproducibility was 100%. Analytical sensitivity was 8 to 20 spores/reaction. Analytical specificity was 100% in a panel of 30 samples, including other filamentous fungi, yeast, and bacteria. The PCR assays demonstrated 72.4% (21/29) sensitivity and 94.7 % (36/38) specificity compared to culture results. Some specimens with growth of one colony were undetected. One culture negative specimen, with *A. fumigatus* DNA detected, had a galactomannan-positive result. Overall, the PCR assays had a substantial agreement with culture results ($\kappa = 0.681$ [95% CI 0.502 to 0.859]).

CONCLUSION: PCR detection assays for *Aspergillus* species in bronchial specimens were established. The assays will be further validated prospectively in comparison to clinical information to determine a diagnostic algorithm.

TP040

Carbapenemase-producing Enterobacterales in Alberta from 2013 to 2023

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OBJECTIVE: Carbapenemase-producing Enterobacterales (CPEs) poses a significant global health challenge, marked by increased drug resistance resulting in treatment failures, elevated hospital mortality rates, prolonged hospital stays, and increased medical costs. Despite the widespread impact of CPEs, a comprehensive analysis of their prevalence in Alberta has not been undertaken in the past decade, rendering the current status of CPEs in the province largely unknown. This study aims to fill this gap by characterizing CPEs isolated from January 2013 to April 2023.

METHODS: Descriptive data was summarized for each CPE, including carbapenemase type (bla_{GES}, bla_{IMP}, bla_{KPC}, bla_{NDM}, bla_{NMC}, $bla_{\text{OXA-48}}$, bla_{VIM}), organism, specimen type, and collection year. Duplicate organisms carrying the same carbapenemase were removed if they were isolated from the same patient in the same year. Carbapenemase gene screening was completed by PCR at the National Microbiology Laboratory, and whole genome sequencing was performed by the National Microbiology Laboratory or Alberta Precision Laboratories.

RESULTS: A total of 589 CPEs were identified in Alberta. CPE numbers increased throughout the study period, with a maximum of 125 cases in 2022. Nineteen different taxonomic groups harbouring carbapenemase genes were identified, with *E. coli* ($n = 254$) and *K. pneumoniae* complex ($n = 158$) being the most common. The predominant carbapenemases were bla_{NDM} ($n = 359$) and $bla_{\text{OXA-48}}$ ($n = 165$), with 45 isolates carrying more

than one carbapenemase gene. The CPEs were isolated from a variety of body sites, with the majority from urine ($n = 240$) and rectal sites ($n = 178$).

CONCLUSION: CPEs have been increasing in number in Alberta since 2013. Characterization of provincial CPEs provides valuable information about the local epidemiology, which can be used to inform IPC policy within the province and contribute to global CPE surveillance. Genomic characterization of these isolates is under way.

TP041

Status of detection of *Pneumocystis jiroveci* in Canadian clinical microbiology laboratories by the National Molecular Group (NMG) survey

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OBJECTIVE: *Pneumocystis jiroveci* pneumonia (PJP) is a disease with a mortality of 27 to 65%. We conducted a national survey through the National Molecular Group (NMG) to understand and improve PJP detection in Canadian clinical microbiology laboratories.

METHODS: We conducted the survey using an online questionnaire. There were 19 questions with a combination of multiple-choice and free texting. The survey was open to the 225 attendees of the 2023 NMG Conference in November 2023. The survey results were pooled and analyzed.

RESULTS: The survey uptake rate was 27% and represented 20 institutes from at least seven provinces. A similar number of respondents performed on-site testing through reference laboratories. A microbiologist's approval was required in some institutes for various reasons. For the institutes providing onsite testing, the monthly volume varied from 1–5 specimens/month to >50 specimens/month. Bronchial lavage/washing or induced sputum were routine specimens for Pneumocystis detection. Other types of specimens acceptable in some institutes included routine sputum, endotracheal fluid, lung tissue, pleural fluid, and nasopharyngeal swabs. Both LDT and commercial PCR assays detecting mtLSU gene were employed in institutes offering molecular detection of Pneumocystis. About 2/3 of these institutes offered daily testing. A qualitative result was reported while most of such institutes also provided a comment on the likelihood of infection versus colonization based on various Ct cut-off values. For the institutes detecting Pneumocystis by staining, Calcofluor white was most commonly used.

CONCLUSION: A sensitive assay with a fast turnaround time is desired for the diagnosis of PJP. A scan of the availability of PJP diagnostics in Canada revealed the need for onsite testing with faster TAT in many institutes. Differentiating colonization from infection from a PCR result varied. In addition, serum beta-D-glucan readily available in other countries to determine infection was not evidently used in Canada.

TP042

Evaluation of a commercial lateral flow immunochromatographic assay, the Alere SA penicillin binding protein 2a (PBP2a) test, for detection of PBP2a in coagulase negative *Staphylococcus* species

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OBJECTIVE: Infections with coagulase negative staphylococcal species (CNST) is increasing, and their antibiotic treatment can be impeded by their ability to acquire oxacillin resistance, due to penicillin-binding protein 2a (PBP2a) encoded by mecA gene. Because the Clinical and Laboratory Standards Institute's (CLSI) oxacillin breakpoints can overcall resistance in CNST with minimum inhibitory concentration (MIC) values between 1 and 2 µg/ml, the purpose of our study is to evaluate the diagnostic performance of a rapid immunochromatographic assay to detect PBP2a in CNST.

METHODS: Twenty-seven previously characterized CNST clinical isolates (other than *S. lugdunensis*, *S. epidermidis*, *S. pseudintermedius*, and *S. schleiferi*) were tested. A range of oxacillin VITEK 2 MIC was included: 6 isolates with an MIC ≤0.25 µg/mL (susceptible to oxacillin), 16 isolates with MIC between 0.5 and 2 µg/mL (variable susceptibility to oxacillin), and 5 isolates with an MIC of ≥4 µg/mL (resistant to oxacillin). All 27 isolates were tested with the Alere PBP2a SA test from growth on sheep blood agar following 24 h induction with 30 µg cefoxitin disc, while mecA PCR was performed by the reference laboratory for the category with an MIC of 0.5–2 µg/mL.

RESULTS: All 6 isolates with oxacillin MIC of ≤0.25 µg/mL tested negative for PBP2a. All five isolates with an MIC

of ≥4 µg/mL tested positive to PBP2a. Of the remaining 16 isolates, 3 isolates tested positive for both PBP2a and mecA PCR, and the other 13 isolates tested negative for both PBP2a and mecA PCR.

CONCLUSION: Agreement between the methods was 100%. Consequently, the PBP2a SA test is a rapid, reliable, and inexpensive method to detect PBP2a in clinically significant CNST isolates. These test results provide the opportunity to utilize β-lactams for the treatment in PBP2a-negative isolates that fall within the CLSI breakpoint resistant range 1–2 µg/mL.

TP043 - WITHDRAWN

TP044

Validation of the VITEK 2 AST-N391 susceptibility testing card compared to disc diffusion following 2022 CLSI M100

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OBJECTIVE: The VITEK 2 AST-N391 susceptibility card (bioMérieux) replaced discontinued cards but regulatory requirements restricted approval on a number of drug-organism combinations. Because validating their performance is difficult and resource-intensive, many laboratories supplement the limitations with ancillary testing, such as disc diffusion (DD) testing. This study compared the performance of the AST-N391 card against parallel DD for a number of drug-organism combinations that had limited validation or verification data upon initiating use of the card.

METHODS: SPICE organisms (n = 277), *Escherichia coli* (n = 403), *Klebsiella pneumoniae* (n = 162), *Klebsiella oxytoca* (n = 43), *Proteus mirabilis* (n = 43), *Pseudomonas aeruginosa* (n = 40), and *Acinetobacter* spp (n = 43) were tested against both AST-N391 and disc diffusion following the 2022 M100 CLSI. Drugs of interest included amikacin (an), ceftazidime (taz), tobramycin (tob), ampicillin (am), amoxicillin-clavulanic acid (amc), ciprofloxacin (cip), ertapenem (etp), fosfomycin (fos), gentamicin (gm), tetracycline (tet), and piperacillin-tazobactam (tzp). Very major errors (VME), major errors (ME), minor errors (MinE), and categorical agreements (CA) were calculated, with DD results as the CLSI accepted gold standard. Acceptability thresholds followed CLSI M52 and 95% confidence intervals were calculated using GraphPad's QuickCalcs.

Organism	Average number of isolates/drug	an	taz	tob	am	amc	cip	etp	fos	gm	tet	tzp
SPICE	477											
Escherichia coli	403											
Klebsiella pneumoniae	162											
Klebsiella oxytoca	43											
Proteus mirabilis	43											
Pseudomonas aeruginosa	40											
Acinetobacter spp.	43											

Organism	Average number of isolates/drug	an	taz	tob	am	amc	cip	etp	fos	gm	tet	tzp
SPICE	477											
Escherichia coli	403											
Klebsiella pneumoniae	162											
Klebsiella oxytoca	43											
Proteus mirabilis	43											
Pseudomonas aeruginosa	40											
Acinetobacter spp.	43											

KEY:
Green = Optimal (no errors, OR only 1 instance of point estimate disagreement with CLSI thresholds for CA, VME, ME + minor errors, but agreement within 95% CIs).
Yellow = Acceptable (2 or more instances of point estimate disagreement with CLSI thresholds but agreement within 95% CIs, OR 1 or 2 instances of point estimate disagreement (excluding VME) with CLSI thresholds and 95% CIs).
Red = Unacceptable (Instance of a VME OR 3 or more instances of point estimate disagreement with CLSI thresholds and 95% CIs).
Grey = Not tested
Blue = Recommended
Black = Not recommended

Figure TP044-1: Validation of the VITEK®2 AST-N391 susceptibility testing card, compared to disk diffusion following 2022 CLSI M100.

RESULTS: Compared to KB, performance of AST-N391 was acceptable across all drugs tested for *K. oxytoca, P. aeruginosa*, and *Acinetobacter* spp Performance for *P. mirabilis* was acceptable for all drugs, except ampicillin and piperacillin-tazobactam, while *K. pneumoniae* was acceptable for all, except amikacin, amoxicillin-clavulanic acid, ertapenem, and piperacillin-tazobactam. *E. coli* had VMEs for all except amoxicillin and ciprofloxacin and SPICE organisms had VMEs across all drugs (Figure TP044-1).

CONCLUSION: Performance of VITEK 2 AST-N391 is comparable to DD for all drugs listed when testing *K. oxytoca, P. aeruginosa*, and *Acinetobacter* spp AST-N391 may also be used to test *P. mirabilis, K. pneumoniae*, and *E. coli*, with notable specific exceptions. However, VITEK 2 AST-N391 performs poorly for SPICE organisms and continued use of DD is recommended.

TP045

Trends in antimicrobial resistance among gram-negative organisms in Toronto, Canada, between January 2013 and December 2022 – A notable rise in MDRO and XDRO *Klebsiella pneumoniae*

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OBJECTIVE: The emergence of multi-drug resistant gram-negative organisms (MDR-GN) is a growing threat. There is a need to understand the current trends to inform empiric treatment. This study analyzes the trends in MDR-GN between January 2013 and December 2022 in a tertiary-care academic clinical laboratory serving four acute care hospitals in Toronto, Canada.

METHODS: Susceptibility testing results were collated for *Enterobacter* spp (avg. $n = 8{,}239$/yr), *Pseudomonas aeruginosa* (avg. $n = 690$/yr), and *Acinetobacter* spp (avg. $n = 37$/yr). Among *Enterobacterales* spp, predominant species included *E. coli* (avg. $n = 4{,}842$/yr) and *K. pneumoniae* (avg. $n=1253$/yr). For each category of organisms, an individual patient was represented only once per year. Adhering to CPHLN and CACMID guidelines, *Enterobacterales* spp isolates were classified as either multi-drug-resistant (MDRO), or extensively drug-resistant (XDRO), while *P. aeruginosa* and *Acinetobacter* spp isolates were classified as XDRO. Ninety-five percent confidence intervals were calculated using the modified Wald method with a test for trends calculated using Chi-square.

RESULTS: Hospital-wide MDRO and XDRO resistance among Enterobacterales increased modestly between 2013 and 2019, from 13% to 16% ($p = 0.03$), with a slight decrease to 14% in 2022 ($p = 0.002$). The trends for MDRO and XDRO *E. coli* reflects the overall *Enterobacterales* trend. However, hospital-wide MDRO and XDRO resistance across *K. pneumoniae* increased dramatically between 2013 and 2017, from 6% to 16% ($p = 0.002$), with a nonsignificant decrease to 13% in 2022 ($p = 0.3$). The proportion of XDRO *P. aeruginosa* decreased hospital-wide, from 5% in 2013 to 0.5% in 2022 ($p = 0.005$). The proportion of XDRO *Acinetobacter* spp displayed no significant trends, owing to insufficient data.

CONCLUSION: From 2019 to 2022, MDRO and XDRO *Enterobacter* spp- and *E. coli* increased modestly overall with a drop in XDRO *P. aeruginosa*. However, the significant increase in MDRO and XDRO *K. pneumoniae* resistance in this time period indicates a need for heightened surveillance and stewardship for this organism.

TP046

Investigating clinical microbiology performance in an external quality assessment program: A 5-year cross-sectional analysis

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OBJECTIVE: Laboratory participation in external quality assessment (EQA) programs including proficiency testing (PT) is a requirement of clinical laboratory conformance to ISO 15189:2022. Established in 1982, the Canadian Microbiology Proficiency Testing (CMPT) program is an ISO 17043:2012 accredited, peer-directed, non-for-profit service that provides EQA schemes and PT samples for microbiology testing laboratories around the world. Samples for all the EQA schemes are designed in CMPT's laboratory facility and are formulated to simulate real specimens (e.g., stool, blood). Detailed clinical scenario cases are provided alongside PT samples, and detailed critiques are provided after each challenge round. EQA program subscribers must characterize the organisms present in the sample and

provide a report of their results. This cross-sectional study aims to investigate the impact of using MALDI-TOF MS compared to conventional phenotypic biochemical testing on laboratory performance by analyzing the results from 111 challenges reported by Canadian laboratories during a 6-year period (2017–2022).

METHODS: Multiple logistic regression techniques were employed for a complete case analysis to explore the association between the testing method and lab performance. The sterility of each sample type and mode of respiration used by challenge organisms were included as relevant confounders based on existing literature, while the challenge year was included as a risk factor for the outcome.

RESULTS: Labs using MALDI-TOF MS performed significantly better than labs using phenotypic biochemical testing (OR 5.68 [CI 3.92, 8.22]) regardless of sample type and mode of respiration. Notably, our analysis also identified a significant association between anaerobic organisms and laboratory performance (OR 0.24 [CI 0.17 to 0.35]), suggesting culturing fastidious organisms is a significant obstacle for many clinical laboratories.

CONCLUSION: These results from actively operating laboratories across Canada strengthen the call for clinical laboratories to invest in MALDI-TOF MS testing systems for more timely and improved diagnostic results.

TP047

Hemophilus influenzae screening and isolation in asymptomatic cystic fibrosis patients: Is it worth it? A narrative review

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OBJECTIVE: *Hemophilus influenzae* is a gram-negative bacillus that is a pathogen and commensal of the human upper respiratory tract. In patients with cystic fibrosis (CF) most Canadian Clinical Microbiology laboratories isolate and report any *H. influenzae* in sputum samples from CF patients, independent of clinical context (i.e., including asymptomatic outpatients undergoing surveillance). We aim to elucidate the evidence for this widespread practice.

METHODS: A single reviewer screened three databases (OVID-Medline, Embase, CENTRAL Registry of Controlled Trials) using a combination of keywords and subject headings including "cystic fibrosis" and "*Hemophilus influenzae*" using both British and American spellings. Reviews, guidelines, statements regarding *H. influenzae* in CF patients, and observational/experimental studies involving CF patients with *H. influenzae* isolated from the respiratory tract were evaluated. Case reports, abstracts, or qualitative studies were excluded. Covidence screening software was used studies were individually evaluated for evidence.

RESULTS: 1,356 studies were extracted from the three databases on Dec 7th, 2023. Duplicates ($n = 175$) were removed and 1,151 were found irrelevant following abstract screening. Thirty publications underwent full-text review. Of these, 21/30 were excluded for being either abstracts, commentaries, letters to the editor, studies that did not differentiate between CF and non-CF patients or had outcomes unrelated to morbidity/mortality. The remaining 9/30 studies were selected for data extraction. Included studies were published between 1989 and 2023 and included 4 prospective studies, 2 retrospective analyses, and 3 review papers, which included 9,501 patients.

CONCLUSION: Only 3 review papers and 6 studies were published on this topic in the past 60 years, suggesting that the clinical implications of isolating *H. influenzae* in the sputum of asymptomatic patients with CF are still poorly understood, with the pendulum swinging back and forth over time about whether clinicians should consider this a significant pathogen with limited data on whether its isolation correlates to patient morbidity and mortality outcomes.

TP048

Mycobacterium tuberculosis pseudo-outbreak due to laboratory cross-contamination—An epidemiological investigation and phylogenetic analysis

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OBJECTIVE: Five patients from distinct institutions for whom clinical samples had been processed in a centralized mycobacteria laboratory were diagnosed with culture-positive tuberculosis (TB). Laboratory cross-contamination was suspected due to culture positivity in an organ donor for which TB pretest probability was low but routine testing was performed. We describe a TB *pseudo outbreak* due to laboratory cross-contamination and assess the role of conventional typing (MIRU-VNTR) and whole genome sequencing (WGS) in supporting the investigation.

METHODS: Clinical data were collected to assess patients' epidemiological risk factors and clinical manifestations' compatibility with TB disease. Pre- and per-analytic trajectories of samples were retraced to identify potential cross-contamination events. TB isolates were characterized by MIRU-VNTR and sequenced on Oxford Nanopore (ONT). The novel bioinformatic pipeline TBPore Cluster was used for phylogenetic analyses.

RESULTS: Two patients had previous exposure to endemic settings and clinical symptoms compatible with TB disease. The three others had no follow-up samples positive for TB. Laboratory reception and sample processing overlapped in time for 4 patients, including one with clinical TB. MIRU typing was identical for isolates grown from those patients' samples. WGS replicated this clustering pattern with zero single nucleotide polymorphism (SNP) between the 4 isolates. The clinically suspected TB patient within this cluster presented with pulmonary cavitary disease and had multiple 3+ AFB smear-positive sputum samples processed on the suspected cross-contamination period. Only one TB patient diagnosed in 2013 shared the MIRU-type with the putative contamination isolate but had a 15 SNP distance, confirming the higher resolution of WGS.

CONCLUSION: Clinical, laboratory, and molecular typing data, including results from the novel ONT WGS pipeline, were considered sufficiently robust by clinicians to discontinue TB therapy, including in organ transplant recipients. Comprehensive sample-processing timelines and phylogenetic tree analyses will be presented as tables and figures.

TP049

Transmission of *Mycobacterium tuberculosis*, a problem inside Colombian prisons

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OBJECTIVE: People deprived of liberty (PDL) are at high risk of contracting tuberculosis (TB) infection and progressing to TB disease. In Central and South American countries, the number of PDLs and people diagnosed with TB (PDTB) has increased up to 269%. This study aimed to describe the transmission dynamics and genotypic diversity of *M. tuberculosis* in PDL from four prisons in Colombia and identify potential risk factors associated with clusters within prisons.

METHODS: We included 64 PDL with microbiology-confirmed pulmonary TB from a prospective cohort study involving four Colombian prisons. The isolates were genotyped by MIRUs-VNTR and analyzed with BioNumerics®. A cluster was defined when two or more isolates from different PDTB shared the same genotype. A person was considered infected in prison when two or more PDTB had the same genotype and an epidemiological link. The relapses, reinfection, and mixed infection percentages were evaluated; PDL diagnosed with TB were geo-referenced in the community and prisons, and the overcrowding and ventilation conditions were assessed in one prison.

RESULTS: LAM (56.8%) and Haarlem (36.4%) were the most frequent genotypes. Evidence of prison-acquired infection was demonstrated in 19% of people diagnosed with TB, 9.4% mixed infection, 3.1% reinfection, and 1.6% relapse. Most PDTB came from neighborhoods with a high incidence of TB in Medellín. 45.3% of the isolates was clustered, and clusters only appeared in one prison. Clusters appeared in cell blocks with overcrowding >100%. The ventilation conditions in those patios were inadequate, with air flows of 0.3 m/s.

CONCLUSION: There is evidence of *M. tuberculosis* transmission inside Colombian prisons. Overcrowding, poor ventilation, and the epidemiology of the city influence the dynamic of TB disease. It is urgent to implement effective measures to control TB in prisons.

TP050

Evaluation of a provincial hepatitis C virus nucleic acid testing reflex program

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OBJECTIVE: A strategy identified as being critical for hepatitis C virus (HCV) elimination is the utilization of reflex testing of serum samples, initially collected for anti-HCV antibody, by nucleic acid testing (NAT). In 2020, the provincial implementation of HCV reflex NAT has enabled reduction of the previous two-step method, which required additional clinic visits and plasma sample collection to confirm an active HCV infection. Individuals at high-risk of active HCV infection are also often hard to reach and NAT detection of HCV RNA is required for initiation of antiviral treatment. This study evaluates the impact of this implementation and turnaround times (TAT) for samples submitted for diagnostic testing.

METHODS: We analyzed data from 38,808 samples submitted for HCV diagnosis by NAT over 3.5 years using statistical software, and TAT was measured from the time of a positive serology result to the time of a NAT result.

RESULTS: We found that reflexing serum samples to NAT reduced the number of persons lost to follow-up testing and eliminated the need to recollect samples for 3,325 individuals. The median TAT of all HCV NAT results improved from 6 to 5 days between January 2020 and June 2023. The median TAT for HCV NAT when plasma samples needed to be recollected was 22 days (99% CI 20.31 to 23.69), while the median TAT for serum reflex HCV NAT was 4 days (99% CI 3.96 to 4.34).

CONCLUSION: It is crucial to diagnose active HCV infection at an early stage, allowing infected individuals to receive timely treatment, thereby increasing their chance of recovery. Our findings show that HCV NAT TAT has decreased between 2020 and 2023 in part due to reflex NAT testing. This research provides a basis for further studies to be done to determine the degree to which improved diagnosis translates to cost savings, linkage to care, and patient recovery.

TP051 - WITHDRAWN

TP052

Evaluation of digital PCR technology for the detection of *Mycobacterium tuberculosis* DNA in formalin-fixed paraffin-embedded tissues

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OBJECTIVE: We aimed to evaluate the use of digital polymerase chain reaction (dPCR) technology to improve the detection of *M. tuberculosis* complex (MTB) from formalin-fixed paraffin-embedded (FFPE) tissue.

METHODS: An existing real-time PCR (RT-PCR) assay was transitioned to the Quant Studio Absolute Q dPCR system (ThermoFisher). Archived DNA extracts from FFPE tissue were examined by both dPCR and RT-PCR targeting the MTB-*IS6110*. Digital PCR results were expressed as the number of positive microchambers. Results were considered concordant positive if one of the following methods were positive: Ziehl Neelsen (ZN) stain of the tissue or MTB culture from the same or different specimen. Results were regarded concordant negative if the MTB culture from the same tissue was negative.

RESULTS: The analytical sensitivity of dPCR for the detection of MTB was 2.5 fg of genomic DNA (~0.5 MTB genome/reaction). This concentration was lower than with RT-PCR that detected 5 fg (~1 genome/reaction). Seventy-seven FFPE tissues, 38 positive (10 ZN stain, 18 culture from the same tissue and 6 culture from different tissue) and 39 negatives by culture, were tested to assess accuracy. The dPCR demonstrated 89.5% (34/38) sensitivity and 89.7% (35/39) specificity. The dPCR had almost perfect agreement compared to RT-PCR (Cohen's $\kappa = 0.974$ [95% CI 0.924 to 1.000]), and there was a negative strong correlation between the number of positive microchambers with Ct values at least up to ~1.8 positive microchambers, which corresponded to ~34.5 Ct (Spearman's correlation $r = -0.9153$ [95% CI −0.9613 to −0.8195]; $p < 0.0001$). Samples at the limit of detection by dPCR were also at the limit of detection by RT-PCR.

CONCLUSION: The dPCR provided high analytical sensitivity. The dPCR performance was comparable to RT-PCR for the detection of MTB in FFPE tissue. The dPCR and RT-PCR are valuable tools for MTB detection, especially when culture is unavailable.

TP053

Replacing the CLSI disk potentiation assay with a semi-automated, cost-effective molecular assay for the identification of ESBL producing *Escherichia coli, Klebsiellae* spp, and *Proteus mirabilis* from surveillance specimens

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OBJECTIVE: Automation and molecular methods can improve detection and decrease the burden on the bacteriology laboratory performing the Disk Potentiation assay for the identification of ESBL producing organisms in surveillance specimens. Moving to molecular-made use of robotics acquired for the SARS-CoV-2 pandemic.

METHODS: Surveillance specimens are cultured to ChromAgar ESBL/CRE biplates. Color differentiates *E. coli* from *Klebisellae* and *Proteus* spp MALDI-TOF MS is used to identify *Klebsiellae* spp and *Proteus mirabilis* for molecular testing. Isolates are submitted in a lysis buffer (Tween 20/Brij58) by gently touching the top of two colonies. Lysis tubes are loaded onto the Hamilton Star by MLAs. The Star scans the sample barcodes (creating a plate file for the CFX), transfers 100 µL of each sample to a deep 96-well plate and heats the plate for 10 min at 80°C. The Star dispenses master mix in a PCR plate and adds the crude eluates. The plate is sealed and spun. PCR is done on a CFX 96 (Bio-Rad) using Luna M3004 (New England Biolabs). The assay targets TEM, SHV, all CTX-M groups with 16S as the internal control using TaqMan probes. PCR takes 45 min to complete.

RESULTS: After validation, 98 nonduplicate clinical samples were tested. Sensitivity and specificity for CTX-M were 100% compared with disk testing. PCR was also able to detect ESBLs missed by disk testing in two *E. coli* strains that were ampC positive. The incidence of ESBL targets was CTX-M (76.5%), TEM (30.6%), and SHV (11.2%). The disk test costs $31.20 per sample, most of which is MLT labour. PCR costs $3.20 per sample.

CONCLUSION: Molecular methods using robotics compared to traditional CLSI disk methods to detect ESBL are accurate, less costly, can improve turnaround time, and make good use of robotics to relieve the bacteriology lab during the current MLT staffing crisis.

TP054

Evaluation of the utility of secondary confirmatory testing for *Neisseria gonorrhoeae* identification from culture

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OBJECTIVE: Culture-based detection of *Neisseria gonorrhoeae* is required for antimicrobial susceptibility testing and strain typing. Historically, distinguishing *N. gonorrhoeae* from other *Neisseria* species was challenging and led to the recommendation that confirmatory testing should be performed. This recommendation has persisted despite advancements in technology, particularly matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) for rapid species identification. In this study, we aimed to establish whether there is

added value in the continued use of confirmatory methods following identification by MALDI-TOF MS.

METHODS: Multiyear data (2017–2023) for isolates from anogenital and non-anogenital sites from six Clinical Microbiology laboratories in Ontario were used to compare the performance of MALDI-TOF MS and secondary testing assays for the identification of *N. gonorrhoeae*. Additionally, 42 isolates of known identity, including *Neisseria* species ($n = 34$) and similar gram-negative organisms ($n = 8$), were used for a direct comparison of three commonly used commercial gonococcal confirmatory tests (BactiCard, RapID NH and NET test).

RESULTS: All *N. gonorrhoeae* isolates identified by MALDI-TOF MS were confirmed by the reference laboratory ($n = 288$). However, secondary confirmatory testing misidentified 9.4% (27/288) of isolates tested that were correctly identified by MALDI-TOF MS. Direct head-to-head comparison of tests used for secondary confirmation and MALDI-TOF MS showed a range of diagnostic specificity (67%–86%) and positive percent agreement (75%–88%) for *N. gonorrhoeae*, although diagnostic sensitivity and negative percent agreement were both 100%.

CONCLUSION: These data demonstrate that secondary biochemical testing shows low agreement with MALDI-TOF MS and does not add diagnostic value for the identification of *N. gonorrhoeae*. Thus, discontinuation of confirmatory tests for *N. gonorrhoeae* already identified with high confidence using a validated MALDI-TOF MS is recommended for hospital laboratories.

TP055

Road to efficient HIV diagnostic testing: An evaluation of first-time HIV antibody-positive patients receiving follow-up testing in Alberta, Canada, from 2018 to 2023

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OBJECTIVE: The current HIV diagnostic algorithm in Alberta uses a fourth-generation antigen/antibody (Ag/Ab) screening assay; should the assay be positive, a HIV-1/HIV-2 antibody differentiation immunoassay is performed. If the immunoassay is negative or indeterminate, a nucleic acid test (NAT) is required to ensure an individual is not in the diagnostic window period. We aimed to identify patients who received a first-time antigen/antibody (Ag/Ab) positive HIV test, estimate the proportion receiving NAT follow-up testing, and calculate the average diagnostic turnaround times between antibody and NAT results.

METHODS: HIV testing (Ag/Ab immunoassay, Ab differentiation, NAT) performed between 2018 and 2023 ($n =$ 1,600,853) were analyzed to assess diagnostic HIV follow-up practices. Patients testing positive for HIV Ag/Ab were used to investigate the proportion of individuals receiving NAT follow-up testing after their first-time HIV diagnosis and calculate turnaround times (TAT). All statistical analyses were performed using STATAv17.

RESULTS: We identified 793 first-time HIV Ag/Ab positives; 398 (50.1%) received NAT within 6 months of diagnosis. Mean TAT of 65 days (95% CI 59.7 to 70.3) from HIV Ag/Ab sample collection to HIV NAT result was observed. Of those receiving HIV NAT within 6 months from initial screen-positive, 138 (34.7%) were female and 260 (65.3%) were male. For those not receiving HIV NAT, 161 (40.8%) were female and 234 (59.2%) were male.

CONCLUSION: Although first-time positive patients remain to be confirmed in this study, findings show efforts need to focus on retaining first-time HIV-positive patients in care for follow-up testing. HIV reflex testing could significantly decrease average TAT for first-time patients receiving HIV NAT follow-up testing in Alberta, and prompt linkage-to-care for therapy initiation. Our group has successfully implemented HCV reflex testing, which significantly improved HCV NAT TAT and linkage to care in Alberta's Public Health Laboratory, promoting the potential for HIV reflex testing.

TP056

An enhanced National SARS-CoV-2 Surveillance Program: Bringing together genetic and functional characterization of circulating strains to monitor viral antigenicity and the effectiveness of current antiviral therapeutics

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OBJECTIVE: In late December 2019, a novel coronavirus, SARS-CoV-2, emerged and was the causative agent of the COVID-19 pandemic. While still a public health concern, the COVID-19 pandemic was declared over in May 2023. With the availability of vaccines and therapeutic treatments, there is a need to adapt our current methods for monitoring this virus to better reflect what is of public health concern. In September 2023, the National Microbiology Laboratory Branch (NMLB) launched a new Enhanced National SARS-CoV-2 Surveillance Program in collaboration with the Canadian Public Health Laboratory Network, which integrates both genomic and functional assays to identify and characterize circulating strains.

METHODS: With an emphasis on viral antigenicity, a high-throughput focus reduction neutralization assay has been implemented to assess viral antigenicity and compare the reactivity of circulating isolates to antiserum generated against the current vaccine strain, XBB.1.5. Similarly, the effectiveness of current antiviral therapeutics, Paxlovid (nirmatrelvir/ritonavir) and Veklury (remdesivir), was evaluated using a focus reduction assay.

RESULTS: As of December 31, 2023, the NMLB has received 218 isolates from three provincial participants. Of these isolates, 200 were cultured and fully characterized, and 195 isolates were reactive against XBB.1.5 antiserum, while 5 isolates demonstrated reduced reactivity against the XBB.1.5 antiserum. All of the isolates tested are susceptible to both Paxlovid (nirmatrelvir/ritonavir) and Veklury (remdesivir).

CONCLUSION: The results presented show the added value of antigenic characterization and antiviral susceptibility testing of SARS-CoV-2 circulating isolates to existing genomic-based surveillance systems. In order to have an effective representation of the Canadian picture, increased participation across all provincial and territorial jurisdictions would be beneficial.

TP057

A pilot study to use a viability real-time PCR assay as a diagnostic tool for patients experiencing Salmonellosis

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OBJECTIVE: Frontline laboratories are adapting culture-independent diagnostic testing like real-time polymerized chain reaction assays (qPCR) due to numerous advantages over culture-based tests. Paradoxically, the viability of pathogens, a crucial factor that determines active infections, cannot be confirmed with current qPCR assays alone. To address this limitation, viability-qPCR (vPCR) was recently developed, where a DNA-intercalating dye was used to irreversibly remove the free and dead cell DNA to selectively amplify live-cell DNA. The objective of this pilot study was to test the applicability of the vPCR assay on stools from diarrheal patients to detect viable *Salmonella* spp in a clinical setting.

METHODS: Eighty-five stools confirmed by PCR using the BD MAXÔ platform and culture for Salmonellosis were used. Ten percent stool suspensions were subjected to qPCR analysis using in-house primers and probe targeting the *invA* gene with and without the viability dye treatment-PMAxx. All vPCR-negative stools (Ct cut-off value >31) were enriched in mannitol selenite broth (MSB) to verify the presence of a low bacterial load undetected by the vPCR assay.

RESULTS: The sensitivity of the vPCR assay was ~89% (76/85 qPCR and vPCR-positive), and 9/85 (11%) stools were vPCR-negative (5 were qPCR-positive; 4 were qPCR-negative). All vPCR-negative stools were culture-positive post-MSB enrichment and confirmed the presence of viable bacterial cells initially at an undetectable level.

CONCLUSION: The discordant results between qPCR and vPCR could be due to initial low bacterial loads, time lag between initial stool collection, and in-house analysis, and sampling error. The preliminary data generated by this pilot study demonstrated the feasibility of the stool vPCR assay to assess pathogen viability in a clinical setting, especially when culture-based testing is unavailable. Further studies are warranted to examine the vPCR assay conditions and stool factors that can affect the sensitivity of the vPCR assay.

TP058

Testing for extragenital *Neisseria gonorrhoeae* and *Chlamydia trachomatis*: At-home pharyngeal and rectal self-swabs are noninferior to those completed in health care settings

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INTRODUCTION: The rates of gonorrhea and chlamydia have been increasing in the years preceding the COVID-19 pandemic. Because most gonorrhea and chlamydia infections are located in the oropharynx and rectum for men who have sex with men (MSM) and because at-home self-collected swabs for these infections are not licensed by Health Canada or the United States Food and Drug Administration, decreased access to in-person care during and since the COVID-19 pandemic potentially means missed case finding.

OBJECTIVES: To evaluate the performance of at-home self-collected pharyngeal and rectal swabs for gonorrhea and chlamydia nucleic acid amplification testing.

METHODS: All persons who contacted the sexual health clinic and who had a clinical indication to complete oral and/or rectal swabs for gonorrhea and chlamydia were invited to complete at-home swabs in advance of their scheduled appointments. We mailed swabs and instructions to those who consented. Participants brought these swabs to their scheduled appointments, where we repeated the same swabs. All matching swabs were sent to the laboratory for analysis to determine concordance.

RESULTS: From September 8, 2022, to July 18, 2023, we enrolled 296 eligible participants who provided 1,184 swabs. For analysis, cancelled specimens and specimens with invalid results were excluded, leaving 1,032 swabs for comparison. We identified 66 infections in 47 unique participants. Overall accuracy was high (>99.0%), except for rectal chlamydia, which was 96.0%. Although the performance of self-swabs for chlamydia was lower compared to gonorrhea, at-home swabs identified six chlamydia infections that were missed by in-clinic collected swabs (two pharyngeal, four rectal). Removing these six cases as "false positives" increased overall accuracy for chlamydia detection to 99.7% (pharyngeal) and 97.8% (rectal), and increased specificity to 100%.

CONCLUSION: Self-collected at-home swabs had good performance acceptable for gonorrhea and chlamydia nucleic acid amplification testing.

TP059
A challenging O166:H15 STEC strain isolation from patients' stools

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OBJECTIVE: Two patients with acute gastroenteritis tested positive for Shiga-toxin producing *Escherichia coli* (STEC) by polymerase chain reaction, and both strains carried the Shiga-toxin 2 encoding gene. Since routine culture using CHROMagar STEC failed to recover these isolates from stools and enriched broths, immunomagnetic separation (IMS) targeting the top 6 non-O157:H7 was experimented as a novel approach for STEC isolate recovery.

METHODS: Stools were inoculated into trypticase soy broth (TSB) and were enriched overnight. IMS run-1 was performed on the enriched stool-TSB, and the captured STEC were plated on MacConkey agar (MAC). MAC Quadrant sweeps were inoculated into TSB the next day, and IMS run-2 was performed without an overnight enrichment. Isolated colonies from the captured STEC on MAC were passed on to sheep blood agar (BAP) for serotyping based on whole genome sequencing (WGS). Colony morphology was observed on CHROMagar STEC and BAP after overnight incubation at 37°C and room temperature thereafter for 2 weeks.

RESULTS: Both patients carried the strain O166:H15 STEC that was recovered by IMS. The immunomagnetic beads were targeted toward the top 6 non-O157, and O166:H15 recovery was indicative of the cross-reactivity of the immunobeads with other *E. coli* serotypes. Two distinct colony sizes were apparent on CHROMagar STEC and BAP, which were noncomparable to O157:H7. After 1 week, the larger colonies showed concentric ring structures on CHROMagar STEC and a "fried egg" resembling structure with a raised circular centre and a flat surrounding on BAP. Both colony types remained morphologically different on CHROMagar STEC throughout the 15 days. However, on BAP, their appearance was comparable by day 7.

CONCLUSION: Alternate approaches to culture are crucial for non-O157:H7 STEC strain recovery from patient stools. Further investigations are under way to characterize the virulence factors of these two STEC strains to understand their possible disease outcomes.

TP060

Post-pandemic recrudescence of invasive streptococcal infection: The new epidemiology of pneumococcal bacteremia

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OBJECTIVE: Invasive pneumococcal disease (IPD) caused by *Streptococcus pneumoniae* is a spectrum of severe infections for which children and elderly are most at risk. Conjugate vaccines have been effective at reducing IPD incidence. Recent national data have demonstrated further decreased *S. pneumoniae* rates during the COVID-19 pandemic. As restrictions lift, this observational study reports a notable increase in cases in a Western Canadian health authority.

METHODS: A retrospective review of laboratory results identified blood cultures positive for *S. pneumoniae*. Demographic and immunological data were reviewed: date of collection, sex (male; female), age (5–14 years; 15–49 years; 50–64 years; ≥65 years), and HIV status (vaccinated yes; no). Susceptibility testing, serotype, viral coinfections, and first respiratory culture results were included. Descriptive statistics comparing 2023 to previous years (2012–2022) were summarized using Microsoft Excel.

RESULTS: Sixty-nine cases were identified for 2023, the highest recorded year. Mean age was 57 years. Around two-thirds of cases were in age groups 15-49 (38%) and ≥65 (35%), with cases most frequently seen in males (72%). Where available, a quarter of the cases (n = 15/59) were serotypes not covered by PCV-13 or PPV-23. The serotype 3 was most common (17%) followed by 9V (14%). Eleven of 58 (19%) cases tested for viruses were positive for RSV, SARS-CoV-2, or influenza A. All isolates were susceptible to β-lactams by nonmeningitis breakpoints; for meningitis breakpoints, 25% and 1% were penicillin and ceftriaxone resistant, respectively.

CONCLUSION: With the COVID-19 pandemic and associated restrictions declining, attention has been focused on group A *Streptococcus* invasive cases. Surveillance of epidemiologic changes of *S. pneumoniae* is necessary, as it may influence public health interventions. Respiratory viruses have been described as potential triggers of IPD, increased exposure risks with the easing of COVID-19 restrictions may have contributed to the increase in cases. Further investigation is needed to characterize this recrudescence and monitor resistance.

TP061

Diagnosis of *Helicobacter pylori* infection in British Columbia—Serology versus urea breath test

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OBJECTIVE: The objective was to compare the performance of *Helicobacter pylori* serology against urea breath test (UBT) using population-level laboratory data to ascertain an optimal diagnostic strategy.

METHODS: *H. pylori* diagnostic test results for serology and UBT from two laboratories over a 12 year period (2006-2017) were extracted, linked, and analyzed. A subset of this population underwent both methods of testing within days of each other, enabling a direct comparison of the two methods.

RESULTS: Average prevalence of *H. pylori* positivity by serology was 21.3% and by UBT it was 17.5%. There were 2,612 individuals who had serology performed first followed by UBT within 14 days. For this subset, the sensitivity of serology compared with UBT was 96.5%, with specificity of 79.2%. The negative predictive value for serology was 98.4%.

CONCLUSION: Although serology does not distinguish between active and past infection, these data show it is sensitive enough to be used as an initial screening test in a low-moderate prevalence population. Negative serology can be used with confidence to rule out active infection, whereas a positive serology could be followed up with a

UBT or a similar performing test, such as stool antigen to differentiate active from past infection. For population-based diagnostic recommendations, such a strategy may be ideal since serology generally costs less than UBT and may be combined with a blood draw being done for other diagnostic tests.

TP062

Discordance in rifampin resistance determination between a commercial molecular test, whole genome sequencing, and phenotypic testing, for a provincially circulating *Mycobacterium tuberculosis* strain

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OBJECTIVE: *Mycobacterium tuberculosis* (MTB) continues to circulate in Canada. One MTB strain has continuously grown in numbers since 2006 and has been seen in all regions of our province. Isolates in this cluster share an upstream mutation in the promoter region of the i*nhA* gene, predicted to confer resistance to isoniazid and ethionamide. A recently detected MTB case attributable to this strain was predicted to be resistant to rifampin using the Xpert MTB/RIF Ultra test (Cepheid). This assay detects MTB resistance to rifampin directly from patient sputum by interrogating the rifampin-resistance determining region (RRDR) of the *rpoB* gene. On further testing, this isolate was phenotypically sensitive to rifampin, a concerning discordance with the Xpert MTB/RIF Ultra test, with implications for patient care, which we sought to investigate.

METHODS: We investigated, via whole genome sequencing, whether this isolate and the others in the cluster share a mutation that potentially disrupts the Xpert MTB/RIF Ultra assay. Mutation profiles for 83 isolates collected over 17 years from all provincial health authorities were generated by the TB-Profiler tool and compared. An additional 10 isolates were tested with Xpert MTB/RIF Ultra.

RESULTS: All 83 isolates had a synonymous mutation in the *rpoB* gene (c.1341C > T; both states encode for arginine), reported by TB-Profiler as "synonymous variant," under the "other variants" section and not associated with drug resistance. This mutation is located between the H526 and S531 positions of the RRDR and may interfere with probes 3 and 4 of the Xpert MTB/RIF Ultra test. All additional 10 strain isolates tested with Xpert MTB/RIF Ultra were predicted rifampin resistant by the test.

CONCLUSION: The c.1341C > T synonymous mutation in *rpoB* shared by the strain isolates might be causing the Xpert MTB/RIF Ultra assay to falsely call rifampin resistance, underscoring the importance of confirmatory resistance/susceptibility testing for optimal patient management.

TP063

Impact on turnaround time for Herpes simplex virus (HSV-1/2) testing following implementation of the BioFire FilmArray Meningitis/Encephalitis Panel in a paediatric hospital

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OBJECTIVE: Meningitis and encephalitis are severe, potentially life-threatening infections that disproportionately affect children. To assess for these infections, cerebrospinal fluid (CSF) is collected for culture and limited molecular testing. These tests, however, often take multiple days to completely determine the result. In 2021, our tertiary care paediatric hospital introduced the BioFire FilmArray Meningitis/Encephalitis (ME) Panel assay, which detects the 14 most common central nervous system pathogens. Our primary objective was to evaluate the HSV detection turnaround time (TAT) following implementation of the ME Panel within our laboratory. Our secondary objective was to determine the accuracy of bacterial detection via the ME Panel.

METHODS: Preimplementation (August 2019 to 2021), batched HSV testing of CSF was performed using a laboratory-developed molecular assay. Postimplementation (August 2021 to 2022), all samples were routinely tested using the ME Panel. TAT data were extracted from our laboratory information system (LIS) for all samples originating from our hospital's emergency department and inpatient units. For samples where the ME Panel detected a bacterial

target, Gram stain, culture, and molecular testing results were manually reviewed in the LIS.

RESULTS: In both periods, most samples were from patients aged <12 months. Preimplementation, 399 CSF samples were received for HSV testing; the TAT (calculated each month) averaged 11.4 hours. Postimplementation, 404 samples were received; the TAT averaged 3 h. The positivity rate post-implementation was 3.9%; the detected bacterial pathogens included *Escherichia coli* K1 (5), *Haemophilus influenzae* (1), *Neisseria meningitidis* (2), *Streptococcus agalactiae* (3), and *Streptococcus pneumoniae* (2). All bacterial detections via the ME Panel correlated with CSF/blood culture positivity, laboratory-developed molecular assay, or 16S sequencing.

CONCLUSION: The ME Panel significantly decreases the TAT for HSV testing of CSF, which is an immediately actionable result for clinicians and has potential implications for antimicrobial stewardship. Furthermore, our data demonstrate no false-positive results for bacterial targets.

TP064

Theoretical assessment of BioFire Blood Culture Identification Panel 2 for positive blood culture identification in a tertiary care pediatric/obstetric hospital

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OBJECTIVE: BioFire BCID2 panel for rapid identification of positive blood cultures (BCx) contains an expanded roster of pathogens and molecular resistance markers. The performance and clinical implications of BCID2 have been thoroughly evaluated, although primarily in adult hospital settings. We undertook a theoretical assessment of BCID2 use in a tertiary paediatric/obstetric hospital.

METHODS: Positive BCx over a 5-year period were reviewed. The current method of rapid identification (MALDI Sepsityper method) and rapid resistance detection (β-LACTA colorimetric test for third-generation cephalosporin susceptibility testing) were compared against the theoretical use of BCID2.

RESULTS: There were 1,818 positive BCx in the 5-year period, including both single pathogens and mixed cultures. Bacterial BCx had: 813 gram-positive cocci in clusters (GPCCl), with 72% on BCID2 to species level; 493 gram-positive cocci in pairs/chains (GPCCh), with 36% on BCID2 to species level; 500 gram-negative rods (GNR), with 84% on BCID2 to species level; ~30% of tested *E. coli* and *Klebsiella* spp were positive on β-LACTA test. Analysis of 1 years' data (n = 383) demonstrated that BCx from obstetric patients or with >24 hours' time to positivity (TTP) were more likely to have organisms not on BCID2. Examination of Sepsityper results demonstrated high success rate for bacterial organisms on BCID2, as well as many [JS1] bacterial organisms not on BCID2 panel, in single-pathogen BCx, but lower success rate for yeast organisms.

CONCLUSION: Stratified use of BCID2 for only pediatric BCx with ≤24 h of TTP and either GPCCl, GNR, or mixed organisms, or yeast at any TTP, would result in most effective use of BCID2. However, given the overall high success rate and rapidity of Sepsityper-based identification at a much lower cost, the cost effectiveness versus clinical impact of BCID2 becomes questionable.

TP065

Development of high-throughput extraction methodology for *Legionella pneumophila* to support outbreak response in Canada

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OBJECTIVE: *Legionella pneumophila* (Lp), a bacterial pathogen endemic in waterways worldwide, can cause a serious form of pneumonia called Legionnaires' Disease (LD). The National Microbiology Laboratory (NML) of the Public Health Agency of Canada (PHAC) serves as the reference centre for this agent, providing support for Lp identification and outbreak investigation(s). With incidence rates increasing and point-source outbreaks having

the potential to affect a large number of individuals, high-throughput (HTP) methodologies for outbreak response to this organism, and other emerging pathogens are required. Herein, we describe the development of methodology for HTP processing of Lp isolates for emergency preparedness.

METHODS: At the NML, a custom robotics system leveraging the KingFisher platform is employed for centralized HTP extractions. The MagMAX Viral/Pathogen II (MVP II) Nucleic Acid Isolation Kit and Mag-Bind Universal Pathogen DNA Kit (Omega Bio-Tek [OBT]) were compared on this platform using 30 Lp isolates. For this comparison, a subset of 12 and 18 isolates was selected for high- and low- inoculum testing, respectively. Multiple methods were used to analyze the quality of the extractions. Subsequent whole genome sequencing (WGS) was conducted (Illumina platform) for further quality assessments.

RESULTS: In the low-inoculum comparisons, both MVPII and OBT kits generated comparable quality and WGS results; however, RNA contamination was noted with the MVPII kit. Upon increasing the inoculum density, the OBT kit generated significantly higher DNA concentrations via Qubit analyses than the MVPII kit. The genomic DNA concentrations obtained from the MVPII kit were not sufficient for downstream WGS-based analyses.

CONCLUSION: On the basis of the comparative analyses, the OBT kit was selected to perform Lp culture extractions, via the KingFisher platform. HTP extractions for Lp have been established at the NML to support outbreak response and support our GRDI-funded project to establish WGS-based surveillance tools for the future.

TP066

Factors associated with paediatric COVID-19 mortality: A Paediatric Investigators Collaborative Network on Infections in Canada (PICNIC) Study

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OBJECTIVE: A previous Canadian paediatric study reported the underlying disorders associated with severe COVID-19, including medical technology dependence, neurological conditions, respiratory conditions, and obesity, but did not report on mortality. Indeed, data on children who have died of SARS-CoV-2-related disease are lacking worldwide. This study's primary objectives were to describe the characteristics of children who died of COVID-19 or multisystem inflammatory syndrome in children (MIS-C) and factors associated with mortality. Estimating the prevalence of death was a secondary objective.

METHODS: Following ethics approval at each site, we conducted a retrospective case-control study at 14 centres in Canada and the Caribbean. Children <18 years old admitted April 1, 2020, through December 31. 2022, with a primary cause of death of COVID-19 or MIS-C were identified using ICD-10 codes. Cases were matched 1:3 with controls based on site, diagnosis, age, and date of admission. Univariate and multivariable conditional logistic regression will be used to determine, which covariates are associated with mortality. The number of inpatients with positive SARS-CoV-2 tests, or a discharge diagnosis of MIS-C was recorded to estimate mortality prevalence.

RESULTS: At the time of this interim report, data collection is complete at 4 Canadian sites and is ongoing at 10 sites (5 Caribbean; 5 Canadian). At the 4 sites with complete data, 14 children died of COVID-19 out of 1,916 inpatients who tested positive for SARS-CoV-2 (0.7%). The median age of these children was 3 years (0.1 to 15 years). Eleven out of 14 (79%) children had 1 or more underlying chronic medical condition. There were no deaths in 352 admissions for MIS-C.

CONCLUSION: Mortality is rare in children with SARS-CoV-2 infection or MIS-C. Further data collection should allow us to report risk factors for death.

TP067

Evaluation of self/parent collected oral nasal swabs for respiratory illness in symptomatic children

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OBJECTIVE: We sought to determine the diagnostic yield and acceptability of self-collected oral nasal (ON) swab samples compared with health care worker (HCW)-collected nasopharyngeal (NP) swabs for respiratory viruses, including severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza, and respiratory syncytial virus (RSV) in children.

METHODS: Symptomatic participants (0–4 years old) were recruited from a paediatric emergency department (ED) where they were undergoing clinical testing with an NP swab. Participants provided an additional ON swab using written self-collection instructions. Caregivers were asked to rate acceptability of ON and NP swab collections on a 5-point Likert scale. Both samples were collected with minitip flocked swabs and were tested with the SARS-CoV-2/Influenza A+B/RSV GeneXpert assay. A portion of matched samples was also tested with the BioFire RP2.1 respiratory panel.

RESULTS: A total of 107 matched sample pairs were tested with the GeneXpert assay and had similar detection for RSV (27 ON positive versus 25 NP positive), influenza A (15 ON positive versus 14 NP positive), and SARS-CoV-2 (8 ON positive versus 10 NP positive). Median Ct values were higher for matched ON positives versus NP positives (25.8 versus 22.8). Fifty-eight pairs were also tested using the RP2.1 assay and showed a similar yield for total respiratory viruses detected (63 positive ON swabs versus 62 positive NP swabs). Caregivers rated higher acceptability of self-collected ON swabs than HCW-collected NP swabs (median acceptability 2 versus 4).

CONCLUSION: The performance of self-collected ON swabs was similar to HCW-collected NP swabs for the detection of a range of respiratory viruses across two commercial molecular assays. Given their significantly higher acceptability ratings, self-collected ON swabs should be considered as a potential less-invasive diagnostic option for children.

TP068

Cytomegalovirus transmission in mismatched paediatric solid organ transplant recipients: What factors are at play?

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OBJECTIVE: Risk factors for CMV transmission in CMV-seronegative paediatric solid organ transplant (SOT) recipients (R−) receiving organs from CMV-seropositive donors (D+) in the era of routine antiviral prophylaxis are unknown.

METHODS: Donor-derived CMV transmission, defined as CMV DNAemia and/or CMV seroconversion in a recipient by 2 years post-transplant, and donor and recipient characteristics were studied in CMV-mismatched (CMV D+/R−) children (<17 years) who had a SOT at the Stollery Children's Hospital from 2000 to 2018. Cox regression was performed to ascertain effects of organ transplanted, donor and recipient age and sex, and donor type on time to donor-derived CMV transmission.

RESULTS: 105 CMV D+/R− paediatric SOT recipients (37% thoracic, 46% liver, 17% kidney) were analyzed. Donor-derived CMV transmission occurred in 58% of recipients. Frequency of transmission was highest in liver (73%), then kidney (61%), and lowest in thoracic recipients (39%). Median time (months) to CMV transmission was 4.32 (IQR 2.16–6.72) for liver, 4.68 (IQR 3.72–9.48) for kidney, and 5.64 (IQR 4.68–8.40) for thoracic recipients. In multivariate Cox regression, risk of CMV transmission was significantly lower in thoracic and kidney recipients compared with liver recipients (HR 0.32 [95% CI 0.16 to 0.62]; $p = 0.001$; HR 0.43 [95% CI 0.19 to 0.98]; $p = 0.04$, respectively). Increasing recipient age was associated with increased CMV transmission (HR 1.07 [95% CI 1.01 to 1.13]; $p = 0.02$). Organ and age effects remained the same when donors <12 months old, with likely false-positive serology due to maternal antibody, were excluded. Among 13 recipients (11 heart, 2 liver) with donors <12 months, only 1 episode of CMV transmission occurred, in a liver recipient with an 11.5-month-old donor. Among liver and kidney recipients, there was no significant difference in CMV transmission between those with living and deceased donors.

CONCLUSION: Understanding risk factors for CMV transmission may allow more targeted use of antiviral prophylaxis in paediatric SOT recipients.

TP069

Increasing frequency of intracranial complications of sinusitis in children: A single centre retrospective study before and after emergence of SARS-CoV-2

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OBJECTIVE: To explore trends in frequency, microbiology, and disease outcomes of intracranial complications of acute rhinosinusitis (IC_ARS) before and after the emergence of SARS-CoV-2.

METHODS: Single tertiary centre retrospective cohort study of children admitted with IC_ARS over a 10-year period (2013–2023). Demographics, microbiology, and outcomes were compared before (era-1) and after emergence (era-2) of SARS-CoV-2 in March 2020. Era-2 was subdivided into pre/post-delta SARS-CoV-2 emergence. Outcome was considered unfavorable at discharge if the stay was >4 weeks, there was neurological or visual deficit, there was an anticonvulsant requirement, required transfer to rehabilitation centre or function below baseline.

RESULTS: IC_ARS occurred in 21 children. Eleven cases occurred in era-1 (1.5/year) versus 10 cases in era-2 (no cases (0/year), and 10 cases (6.0/year) before and after delta phases, respectively). Median age (11.8 versus 12.8 years; $p > 0.05$), male predominance (55% versus 80%; $p > 0.05$) and median time to presentation (8.5 versus 7.5 days; $p > 0.05$) were similar in both eras. Viral triggers were documented historically (8/11 versus 10/10) and by testing (influenza: 1/12 versus SARS-CoV-2: 5/10; $p = 0.03$) in era-1 and era-2, respectively. Bacterial pathogens were polymicrobial (11/21) and detected in 19/21 (90%) of IC_ARS cases, facilitated by multisite cultures. Leading causes were *Streptococcus* spp (71%), *Staphylococcus aureus* (28%), and anaerobes (24%), similar in both eras. Although median hospital stay (20 versus 33 days; $p > 0.05$) was not significantly different, Era-2 IC_ARS had more severe presentations with increased subdural collections, cerebritis, and aphasic strokes ($p < 0.05$), and management practices were similar. Outcome was unfavourable in 5/11 (45%) versus 8/10 (80%; $p = 0.15$) in era-1 and era-2.

CONCLUSION: There is an increasing trend in frequency and severity of IC in older children since emergence of SARS-CoV-2 without notable changes in bacterial pathogens. SARS-CoV-2 was detected in half of postemergence cases, and further studies are required to better explore contributing factors to trending severity and the potential role of SARS-CoV-2 as a facilitator.

TP070

Exploring updates to contact tracing recommendations for potential measles exposure on an airplane

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OBJECTIVE: The "Guidelines for the Prevention and Control of Measles Outbreaks in Canada" is an Advisory Committee Statement endorsed in November 2012. Applying a risk-based approach, the 2012 recommendations include considerations for contact tracing using a passenger manifest, focusing on travellers seated in a two-row radius around a measles case that had travelled by air during the infectious period. These Guidelines are being updated. This abstract explores whether 2012 contact tracing recommendations for potential measles exposure on an airplane remain appropriate, based on evidence.

METHODS: The following activities were undertaken to inform a policy paper: 1) synthesis of provincial/territorial and select international measles guidance; and 2) rapid synthesis of evidence regarding in-flight transmission of measles and contact tracing following potential measles exposure during air travel.

RESULTS: Measles transmission can occur among airplane passengers during flights (regardless of duration), but not

all on-board infectious cases result in secondary cases. Evidence suggests that passenger contact tracing has identified relatively few secondary cases related to in-flight exposure and that, when transmission does occur, secondary cases are often identified beyond the zone typically targeted (i.e., two rows surrounding the index case). Additionally, contact tracing is associated with high resource requirements and vulnerable to delays at multiple steps of the process, limiting its potential effectiveness for reducing measles transmission. Given this, many national and international jurisdictions recommend less intensive strategies, especially in situations with delayed diagnosis and notification, and low probability of secondary cases.

CONCLUSION: Contact tracing recommendations for potential measles exposure on an airplane in the 2012 Guidelines warrant updating, with consideration given to less intensive strategies.

TP071

A rise in the frequency of carbapenemase-producing *Enterobacterales* following an initial decline post-COVID-19

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OBJECTIVE: Carbapenemase-producing Enterobacterales (CPE) is a major health threat. Introduction of CPE is facilitated by international travel from areas of high prevalence. Global travel dramatically reduced during the COVID-19 pandemic. CPE numbers in a tertiary-care clinical microbiology laboratory servicing a metropolitan urban region decreased during this time period and remained low through 2022. The aim of this study was to review changes in the frequency of CPE at this site in 2023.

METHODS: The total number of CPE per year (all CPE per year excluding duplicates) and the total number of individual carbapenemases per year (all carbapenemase per year excluding duplicates) per 1,000,000 bacteriology clinical and CPE screening cultures were graphed from 2009 to 2023. The trend from 2009 to 2019 (pre-COVID-19) was compared to that from 2019 to 2023. Chi-squared test for trend was completed for each time period using GraphPad Instat.

RESULTS: Prior to 2019, the total number of CPEs isolates per 1,000,000 bacteriology clinical and CPE screening cultures rose steadily from 5 (2009) to 130 (2014) and 172 (2019) ($p < 0.0001$). During the pandemic, CPE isolates per 1,000,000 cultures declined from 2019 to 2022, from 172 to 74 ($p = 0.004$). In 2023, CPE isolates increased considerably to 150 per 1,000,000 cultures. The recent increase in CPE correlated with increased frequency of NDM and OXA-48 carbapenemase-producing organisms.

CONCLUSION: The frequency of CPE detection, which declined in the 3 years after the COVID-19 pandemic, has returned to near prepandemic amounts. The return of global flight travel to nearly prepandemic volumes and the ongoing reduction of use of COVID-19 public health measures in the community correlated with this rise in identified CPE.

TP072

Idexx Legiolert for the detection of *Legionella pneumophila*: Benefits and limitations as a potential alternative to agar culture for public health testing of environmental waters

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OBJECTIVE: The performance of Legiolert, an enzyme substrate-based method by Idexx Laboratories, Inc., was verified for the detection and enumeration of *Legionella pneumophila*. The sensitivity, specificity, and the applicability as an alternative to the laboratory-verified agar culture-based method were evaluated with intent for testing environmental waters for public health purposes.

METHODS: For this Legiolert evaluation, we performed sensitivity (and limit of detection) and specificity through sample spikes using various *Legionella* species, including *L. pneumophila* (serogroups 1, 2, 5, 6, 13) and total coliform bacteria using the potable procedure for spike studies. The specificity experiment was expanded using the nonpotable procedure, and a parallel study was conducted to compare Legiolert against the gold-standard culture method ISO 11731 (enumeration of *Legionella*).

RESULTS: Using the 10-mL potable procedure, Legiolert demonstrated a limit of detection of 1.25×10^{-3} CFU/mL for *L. pneumophila*. Specificity tests showed no positive detection in other legionellae, while false-positive detection of nontarget organisms was observed. The parallel study showed generally comparable detection of *L. pneumophila* in cooling tower water samples, but some discrepancies were observed between Legiolert and agar culture, which would require further investigation.

CONCLUSION: While Legiolert showed potential as a rapid and efficient alternative to agar culture, cross-reactivity with common waterborne bacteria remains a concern. Further testing is required to address this issue and to determine the feasibility of incorporating Legiolert into the laboratory for routine *L. pneumophila* detection. Additional confirmation testing may be required to ensure the accuracy of Legiolert results, particularly in the presence of environmental nontarget bacteria.

TP073

Evaluation of test positivity rate for rotavirus in one province from 2013 to 2023

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OBJECTIVE: Infectious disease surveillance, such as for rotavirus (RV), needs to be timely to be effective. RV is one of the leading cases of gastroenteritis (GE) in young infants. In Quebec, a vaccination program was implemented in 2011 using two doses of Rotarix at 2 and 4 months of age. In 2018, this program was modified to use an off-label two-dose schedule of RotaTeq. This study aims to describe percent positivity of RV from 2013 to 2023 in children.

METHODS: Aggregated, anonymized data were retrieved from the laboratory information systems from three teaching hospitals. The number of RV tests and positive cases in children 18 years old or younger were obtained per age groups and per sex. Duplicates for a 28-day period were removed. Percent-positive RV tests were calculated by year, sex, age group, and hospital.

RESULTS: Percent positivity from 2013 to 2019 remained stable and relatively low (4.5%–7.4%), which corresponds with trends reported in the literature. Percent positivity decreased from 2020 to 2022 (0.5%–2.1%), which could be associated with countermeasures during the COVID-19 pandemic. The percentages of positive cases peaked in 2023 (13.5%) during the first 6 months of the year, which could be explained by skewed testing of more severe cases or be linked to a post-pandemic cohort effect. Factors such as sex and age did not show significant correlation with percent positivity ($\alpha = 0.05$).

CONCLUSION: It will be important to maintain surveillance of RV cases, in the context of an off-label vaccine use for RV disease. A timely extension of this study could also provide more information on the impact of the COVID-19 pandemic on RV.

TP074

The effect of antimicrobial copper on pathogenic and environmental microorganisms in high-traffic nonclinical settings

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OBJECTIVE: The COVID-19 pandemic challenged researchers to explore alternative techniques to mitigate the transmission of microorganisms in high-traffic communities. Antimicrobial metals have been investigated due to their self-sanitizing features and ability to disrupt cellular activity. The objective of this project is to determine whether the use of antimicrobial copper in high-traffic settings can reduce the spread of microorganisms that affect the human biome.

METHODS: Antimicrobial copper was implemented into the Thompson Rivers University campus by engineering adhesive copper plates onto door handles in multiple buildings. On campus, the efficacy of antimicrobial copper was tested over a 4-month period, while classes were in session. The antimicrobial copper was swabbed using moistened IsoHelix swabs, and stainless-steel door handles were used as a control. Metals were swabbed, and the microorganisms were extracted under different environmental conditions, cultivated, and plated onto blood agar and brain-heart agar plates that were incubated at 37°C for 24 hours. Additionally, noncultural experiments were performed through 40 DNA extractions of the same swabs used in the cultural experiments, from indoor copper handles, outdoor copper

handles, indoor stainless-steel handles, and outdoor stainless-steel handles.

RESULTS: The cultural approach established the baseline understanding of copper's efficacy in a nonclinical high-traffic setting. Overall, the cultural approach has displayed a reduction in the diversity and concentration of microorganisms on the copper door handles versus stainless-steel. The noncultural approach is ongoing and will be completed by the time of presentation.

CONCLUSION: Supporting past research, copper has demonstrated its ability to reduce the concentration of microorganisms in nonclinical settings. In the future, antimicrobial copper can be used as an agent of antimicrobial resistance.

TP075

Could blood establishments help in evaluating whether HTLV-1/2 screening should be conducted in high-risk pregnant women?

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OBJECTIVE: Mother-to-child HTLV-1 transmission through breastfeeding is associated with increased risk of developing adult T-cell leukemia/lymphoma. Japan pioneered national HTLV-1/2 screening for pregnant women in 2011. Brazil and Iran have since launched similar programs, while Chile suggests voluntary testing. France advises screening for pregnant women from high-risk countries. Blood establishments systematically screen donors for HTLV-1/2 in Canada. This study aims to understand the impact of a targeted screening program for HTLV-1/2 in high-risk pregnant women in Quebec.

METHODS: Héma-Québec screens HTLV-1/2 in blood, cord blood, and human milk donors by chemiluminescent microparticle immunoassay with the PRISM platform (Abbott); infections are confirmed by Western blot analysis. Confirmed positive rates and false positive rates are reported to estimate the impact of testing high-risk pregnant women using 2012–2022 data set for blood and milk donors, and 2012–2014 data set for cord blood donors.

RESULTS: Among 7,750 milk donors, 15 (0.2%) had an unconfirmed positive screening result, 13 (0.2%) had an undetermined confirmation after a positive screening result, and 1 (0.01%) had a confirmed positive screening result. Among 5,169 cord blood donors, 9 (0.2%) had an unconfirmed positive screening result, 4 (0.1%) had an undetermined confirmation after screening positive, and 1 (0.02%) had a confirmed positive test result. Finally, among 266,564 first-time blood donors, 75 (0.03%) had an unconfirmed positive screening result, 124 (0.05%) had an undetermined confirmation after a positive screening result, and 16 (0.006%) had a confirmed positive result. Among blood donors who declared their ethnicity, the highest rate of confirmed positivity was in Black donors (0.2%).

CONCLUSION: We observed a very low HTLV-1/2 prevalence among donors in Quebec, with higher rates within certain subpopulations. Assuming 2,000 pregnant women per year in Quebec are born in high-risk countries for HTLV-1/2, a targeted screening program could generate 2–10 false positives and 2–4 confirmed positives per year.

TP076

Assessing the public health impact of the adjuvanted respiratory syncytial virus prefusion F (RSVPreF3) vaccine in Canadian older adults

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OBJECTIVE: Respiratory syncytial virus (RSV) is a highly contagious seasonal virus; it is among the most common respiratory infections worldwide. In older adults (OA) and adults with comorbidities, RSV may cause severe infections, complications, hospitalizations, and death. We evaluated the public health impact of the adjuvanted RSV prefusion F (RSVPreF3) vaccine in the Canadian OA population aged ≥60 years.

METHODS: A static multi-cohort Markov model was used to assess the impact of the RSVPreF3 OA vaccine compared with no vaccination (n = 9,970,613). A 3-year time horizon (1-month-long cycle) was applied. Vaccination coverage rates of 25% among those aged 60–74 years and 40% among those aged ≥75 years were applied based on Canadian influenza and pneumococcal vaccination rates. RSV epidemiology (both upper and lower respiratory tract disease) and health care resource utilization were obtained from relevant literature (based on estimates preceding

pandemic public health measures) where available. Vaccination was assumed to occur once in October (assumption verified by clinical experts).

RESULTS: The RSVPreF3 OA vaccine would prevent 149,617 RSV symptomatic cases (64,744 upper and 84,873 lower respiratory tract disease cases), 15,757 hospitalizations, 3,264 emergency department visits, 1,597 deaths, and 68,594 outpatient visits versus no vaccination over 3 years. Furthermore, the RSVPreF3 OA vaccine would prevent 29,700 RSV-related complications (pneumonia, myocardial infarction, and hypoxia), and 55,632 antibiotic prescriptions. The number needed to vaccinate to avoid one case was 20 for RSV symptomatic respiratory infection, 188 for RSV hospitalization, and 1,850 for RSV-related death.

CONCLUSION: The RSVPreF3 OA vaccine can substantially reduce the public health burden of RSV in the Canadian OA population. In this model, vaccination with RSVPreF3 OA reduced RSV-related events, complications, and health care resource utilization. To achieve the full benefit of RSVPreF3 OA in real-world practice, public health efforts (e.g., disease awareness, vaccination programs), will be needed to support RSV vaccination in Canadian OA.

TP077

Improving vaccine uptake: Immunization governance in Atlantic Canada

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OBJECTIVE: 1) To identify aspects of immunization governance that could be improved to foster public trust and acceptability of vaccination programs; 2) To examine the legal, regulatory and guidance policies, programs, and practices for immunization across Atlantic Canadian provinces.

METHODS: Online environmental scan of legislation for immunization and associated regulations and guidance documents in the Atlantic provinces, focuses on eight features critical to immunization: 1) scope of practice, 2) procedural guidance, 3) competency, 4) recording actions, 5) safety, 6) adverse event management, 7) liability, and 8) supports. We corroborated documents by contacting health authorities. 3) Thirty-four semi-structured interviews between September to November 2021 with health policy experts: public health officials ($n = 18$), frontline HCPs ($n = 8$), academic scholars ($n = 5$), and health care union leaders ($n = 3$).

RESULTS: Immunization (particularly school-based) schedules differed across the provinces. Current legislation provides too little guidance for the education, training, and competency of authorized HCPs to vaccinate. Although the responsibility for generating immunization policies and regulations falls on provinces or regional health authorities, too few legal and regulatory tools sufficiently address immunization standards for best practice.

CONCLUSION: Despite a relatively small geographical region compared to the rest of Canada, we found significant differences in immunization policies, programs, and practices across the four Atlantic jurisdictions. The absence of standards for immunization and immunizers contributes to fragmentation of delivery and poor patient experiences in Atlantic Canada. We suggest that significant attention must be given to harmonizing vaccine schedules, standardizing immunization practices, and improving initial and continuing education of HCPs to enhance immunization governance and accessibility across Canada.

TP078

Dried blood spot sampling for HIV, hepatitis C, and syphilis testing: Evaluating provincial implementation of an innovative testing modality

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OBJECTIVE: Dried blood spot (DBS) samples can diagnose new HIV and hepatitis C (HCV) infections and screen for syphilis by using blood from a finger-prick onto paper that is dried and mailed to a laboratory for testing. DBS can improve access to testing, particularly for rural and remote communities, as sampling can be performed outside of a laboratory. Several provinces have accepted confirmatory

results from DBS samples for HIV- and HCV-positive case definition. DBS sampling started in the province in 2019, but a pilot DBS process was launched in 2021.

METHODS: A mixed-methods evaluation was conducted of implementation processes at pilot sites between 2019 and 2022 using provincial data, service provider semi-structured interviews and survey, and a focus group at a community-health agency, including peer workers to explore pilot strengths, limitations, and outcomes.

RESULTS: 335 DBS samples were submitted, 70% of which were from a health region in the North. When comparing DBS and phlebotomy sampling, HIV and HCV antibody positivity rates were 10 times higher with DBS—similar positivity rates for syphilis antibody—but HCV RNA positivity was higher for phlebotomy samples. DBS sampling is a useful, low-barrier tool to engage people who are not being served by standard-of-care testing, including people who use substances, have experienced discrimination in health-care settings, or do not have access to phlebotomists. While an ordering provider is required for DBS to support linkage to care, non-health-care providers, such as peer workers, can take samples. The biggest challenge was turnaround time for results: average 33–34 days, compared to 3.5–6 days for phlebotomy tests, increasing the risk of losing people for follow-up.

CONCLUSION: The results suggest DBS can reach populations at higher risk for HIV, HCV, and syphilis in less urban areas with a high level of satisfaction. The evaluation provides recommendations for improving the current DBS process and for a potential future DBS provincial program.

TP079

The community pop-up clinic: Cascade of care and HCV treatment in a vulnerable population of people who use drugs

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OBJECTIVE: Elimination of HCV infection as a public health concern by the end of this decade will require a concerted effort in all target populations, including vulnerable inner-city populations, many of whom are actively using drugs and facing other issues, including housing and financial insecurity, untreated mental illness, and active untreated addiction. We have evaluated a novel approach of community pop-up clinics (CPCs) as a strategy to promote uptake of HCV therapy and achieve cure among people who use drugs.

METHODS: Weekly events are conducted at places of residence in Vancouver's inner city. Point-of-care testing for HCV is completed (with phlebotomy performed on site to confirm viremia), along with ascertainment of prior HCV infection status, if known. All viremic individuals are then offered access to antiviral therapy delivered within a multidisciplinary program with adherence support.

RESULTS: From January 2021 to August 2023, we conducted 112 CPCs (3.5 events/month, 3 hours/event), evaluating 1,968 individuals, 620 of whom (31.5%) carried HCV antibodies, 474 (76.5%) being viremic. Engagement in HCV care has been secured in 387 (81.6%) cases, with 326 (84.2%) starting treatment and 60 still being in the pretreatment phase, and 1 having died of an overdose. The median time from CPC attendance to HCV treatment initiation was 6 weeks. Of the 326, 302 have completed treatment, 18 remain on treatment, 5 withdrew prematurely, and 1 died of an overdose during treatment. Of those in whom a treatment outcome has been determined, the cure rate is 287/289 (99.3%), with 2 virologic relapses.

CONCLUSION: Our community-based approach is a highly efficient strategy to identify and engage patients in treatment that is almost universally successful. The data validate the need for multidisciplinary programs such as ours to address HCV in vulnerable inner-city populations that must be engaged in care for HCV elimination to become a reality.

TP080

Impact of new sexual-behaviour-based screening practice at Héma-Québec

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OBJECTIVE: In December 2022, Héma-Québec implemented a new sexual-behaviour-based screening practice. The new questionnaire is gender neutral and asks whether blood donors had a new partner or more than one partner in the last 3 months. If donors answer yes to any of these questions, they are asked about anal sex in the last 3

months. If they answer yes to anal sex, a 3-month deferral is applied. This study aims to evaluate the impact of this new questionnaire.

METHODS: Deferrals for high-risk sexual behaviour are described 1 year later. Infectious markers before (April 2021 to March 2022) and after (December 2022 to November 2023) the new questionnaire are compared and risk factors are described.

RESULTS: Among 121,268 donors exposed to the new questionnaire, 3,955 declared a new partner in the last 3 months (3.26%), of which 138 also had anal sex representing 0.11%. Similarly, 1,543 declared more than one partner in the last 3 months (1.27%), of which 93 had anal sex representing 0.08%. Before and after the implementation of the new questionnaire 1 versus 0 donor was positive for HIV, respectively, 7 versus 20 donors were positive for HBV, 10 versus 10 for HCV and 14 versus 19 for syphilis. Thirteen of 17 donors with HBV who accepted to be questioned about risk factors were born in endemic countries. Five of 17 donors with syphilis who accepted to be questioned declared MSM relationship in the previous 3 months; 3 of them should have been deferred for undeclared syphilis history. No one declared a new partner or more than one partner in the previous 3 months.

CONCLUSION: The new sexual-behaviour-based screening practice created a deferral rate of 0.15%, did not increase HIV-positive donation, but increased the number of syphilis-positive donors, 3 of whom should have been deferred because of an undeclared history of syphilis.

TP081

Respiratory syncytial virus: The use of the moving epidemic method to guide the launch of palivizumab immunoprophylaxis campaigns in Québec

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OBJECTIVE: Adapting palivizumab immunoprophylaxis campaign dates during the exceptionally early RSV 2021–2022 season successfully improved coverage of high-risk newborns in Quebec. A mathematical model called "Moving Epidemic Method" (MEM) has been previously described to estimate the RSV epidemic threshold and could be used to guide the launch of future campaigns. However, as incidence rates can be impacted by human behaviour and climatic conditions, evaluation of the MEM in Quebec pre- and post-pandemic conditions is essential before considering its use.

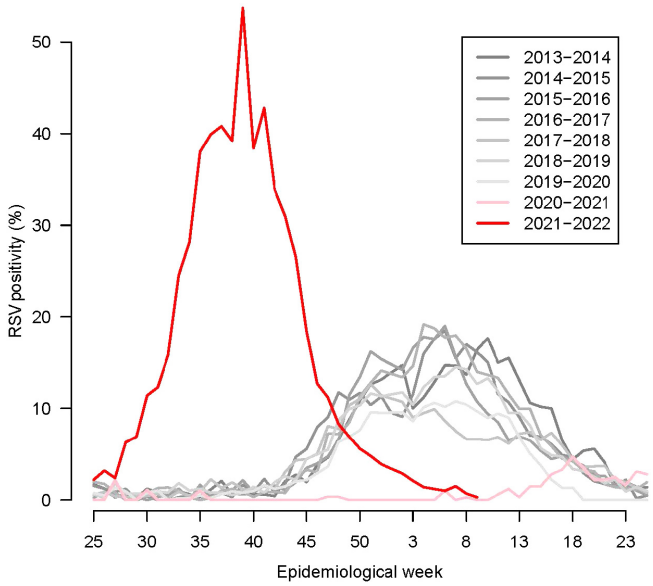

Figure TP081-1: Epidemic periods according to the Moving Epidemic Method and the preestablished approach (fixed dates), seasons 2020–2021 and 2021–2022

METHODS: Quebec RSV surveillance data from 2013 to 2020 were analyzed with the MEM to determine epidemic threshold. MEM performance was explored in season 2021–2022 during which RSV's seasonal pattern was significantly disrupted.

RESULTS: A total of 787,144 RSV tests results were used to fit the model, of which 64,540 (8.2%) were positive. From seasons 2013–2014 to 2019–2020, RSV cases peaked between epidemiological weeks 1 and 8, and all epidemic curves strongly overlapped. The epidemic threshold determined by MEM using those curves was 8.3%. With MEM, the 2021–2022 epidemic period started at week 30 and ended at week 47, covering the vast majority of the epidemic.

CONCLUSION: MEM was reliable during normal RSV seasons and showed robustness to disruptions of RSV's seasonal pattern. MEM is, therefore, promising to guide the launch of future RSV immunoprophylaxis campaigns.

TP082

Molecular screening reveals low prevalence of *Ixodes scapularis* ticks in British Columbia: Implications for tick identification methods

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OBJECTIVE: The aim of this study is to perform an assay using molecular measures to screen for *Ixodes scapularis* and *Ixodes pacificus* ticks, while also determining the prevalence of *Ixodes scapularis* in British Columbia.

METHODS: Samples were selected on the basis of spatial and temporal distributions from the surveillance samples of the British Columbia Centre for Disease Control (BCCDC), encompassing 25% ($n = 209$) of the 2022 samples. The real-time PCR test was adapted from an assay conducted by the National Microbiology Laboratory (NML), with modified cycling protocols. Specific primers targeting the internal transcribed spacer 2 (ITS2) region for both *I. scapularis* and *I. pacificus* were employed. Additionally, sequencing of the mitochondrial cytochrome c oxidase subunit 1 (mtCOI) gene was performed for ticks with positive PCR results for *I. scapularis*. These sequences were then compared to references in a phylogenetic tree.

RESULTS: Our findings indicate that morphologically, 4% of *Ixodes* ticks collected at the BCCDC in 2022 were identified as *I. scapularis*, and 3% had a confirmed travel history outside of BC. Moreover, 1.3% ($n = 2$) of *I. pacificus* ticks were misidentified by morphology, with 75% ($n = 6$) of *I. scapularis* initially categorized as *I. pacificus*. The sequencing of the eight *I. scapularis* ticks provided confidence in the differentiation of *Ixodes* spp, confirming the real-time PCR results. Consequently, these outcomes suggest the absence of an established *I. scapularis* population in BC, emphasizing the potential pitfalls of relying solely on morphologic identification.

CONCLUSION: In summary, real-time PCR proves to be an effective method for screening *I. scapularis* and *I. pacificus* ticks, as confirmed by phylogenetics. This study highlights the importance of supplementing taxonomic techniques with molecular speciation for optimal accuracy. Future work could involve the development of multiplex real-time PCR or next-generation sequencing to encompass a broader range of tick species.

TP083

Motivation to opt-out of quality improvement project for universal third trimester screening of chlamydia and gonorrhea at a single hospital site in Alberta

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OBJECTIVE: Alberta chlamydia and gonorrhea (CT/NG) prenatal screening practice includes universal first-trimester screening and third-trimester screening for those deemed high risk for infection. As part of a quality improvement project, universal CT/NG screening was offered to all women presenting to post-partum units at a single hospital site in Alberta. The objective of this research was to determine motivations for opting out of universal post-partum screening, in an effort to improve inclusion if universal screening strategies should be more widely adopted.

METHODS: Between March 20 and October 17, 2023, all women presenting to post-partum units at a high-risk perinatal hospital for northern Alberta were assessed for CT/NG using urine-based screening. Women opting-out of universal screening were asked for motivation to withdraw, which was documented in opt-out binders at each participating unit by the responsible nurse. Opt-out data were collated and analyzed using STATA v.17.

RESULTS: Seventy-seven individuals were documented to have opted-out of CT/NG screening during the study period, with 76 (98.7%) providing a reason for opt-out. Of those, 63 (82.9%) chose not to give a sample, 5 (6.58%) cited a low likelihood of positivity, 3 (3.95%) were recently tested, 3 (3.95%) provided no reason, 1 (1.32%) withdrew, citing "disbelief in research," and 1 (1.32%) left before a sample could be taken.

CONCLUSION: The primary motivator behind opting out of the current study was an individual's preference not to give a sample. These outcomes provide foundational

framework for understanding patient perspectives on STI screening in post-partum clinical settings. This research indicates that it is crucial to create engaging environments for universal CT/NG screening in clinical contexts. Future research could elucidate key elements supporting an individual's decision to participate in screening programs aimed at prenatal and post-partum populations.

TP084

Characterization of *Mycoplasma genitalium* in Canada from 2022 to 2023

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OBJECTIVE: *Mycoplasma genitalium* (Mgen) is a sexually transmitted pathogenic bacterium commonly found in the urogenital tract of both males and females. To characterize Mgen, a typing scheme was designed consisting of an MgPa adhesion protein (*mgpB)*, and a lipoprotein (*MG309)*. The objective of this study was to utilize the typing scheme to determine the relatedness and spread of Mgen in Canada, and to investigate whether there is an association between sequence type (ST) and antimicrobial resistance (AMR) profiles. Mgen AMR determinants include *23S rRNA* (macrolides) and *gyrA*/*parC* (fluoroquinolones).

METHODS: Between 2022 and 2023, 89 Mgen-positive clinical samples with known AMR profiles were collected from five provinces within Canada. Isolates were tested using PCR and Sanger sequencing methods. The resulting sequences were submitted to PubMLST to determine the STs.

RESULTS: Of the 89 isolates tested, 80 were from Eastern Canada (QC, ON, PEI) and 9 were from Western Canada (BC, AB). A total of 58 STs were identified. ST-27 was the most prevalent type, observed in 11.2% (10/89) of isolates, all of which originated from one province, and had *23S rRNA* and *parC* mutations. Other commonly observed STs include ST-16 (4/89), ST-69 (5/89), and ST-78 (5/89), all of which contain the *mgpB* type seven (mgpB-7) and were from one province. Isolates with mgpB-7 had *23S rRNA* mutations 82.3% (14/17) of the time and were associated with macrolide resistance. Additionally, mgpB-7 was identified in 19.1% (17/89) of isolates. All 58 STs detected were unique to a single province.

CONCLUSION: Mgen typing results indicated high genetic diversity within the *mgpB* and *MG309* genes and showed association with AMR profiles. This typing scheme could be a valuable tool to understand the dissemination of Mgen in a population, and to support outbreak treatment failure investigations, data that can be used to inform public health interventions.

TP085

Mycoplasma genitalium infection in a cohort of adolescents and young women

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OBJECTIVE: This study aimed to determine the clinical and analytical performance of a commercial *M. genitalium* assay and to estimate its prevalence in the female urinary tract among adolescents and young women.

METHODS: Midstream urine samples were collected from participants who reported symptoms consistent with sexually transmitted infections (STIs). Samples were stored at −70°C until processing. Two assays were used for *M. genitalium* detection: the Allplex STI (Seegene), a multiplex real-time PCR that detects seven STI pathogens, and a TaqMan Microbe Detection Assay (ThermoFisher) a real-time PCR that detects *M. genitalium*.

RESULTS: Among 169 midstream urine samples, the Allplex test detected three (2.7%) positive samples for *M. genitalium*. The TaqMan qPCR detected nine (8.0%),

including the three detected by the Allplex test. The analytical limit of detection of TaqMan Microbe assay was confirmed from 0.5 copies/µL, and the detection was linear up to 10,000 copies/µL of the *M. genitalium* genome. Among females with positive results for *M. genitalium*, there were no coinfections with *Chlamydia trachomatis* or *Neisseria gonorrhoeae*.

CONCLUSION: The prevalence of *M. genitalium* in this cohort is lower than in previous studies in other Kenyan and African cohorts. The TaqMan Microbe Detection Assay performed better than Allplex STI to detect *M. genitalium.*

TP086

Ceftriaxone-resistant *Neisseria gonorrhoeae* strains in Canada, 2017–2023

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OBJECTIVE: *Neisseria gonorrhoeae* is the causative agent of the sexually transmitted infection (STI) gonorrhea, which is the second most common reportable bacterial STI in Canada. *N. gonorrhoeae* has developed resistance to many antimicrobials over time, including those in the current recommended treatment regime, either azithromycin and ceftriaxone or azithromycin and cefixime. The National Microbiology Laboratory (NML) uses a minimum inhibitory concentration (MIC) of ≥0.25 mg/L as the resistance cut-off for ceftriaxone (CRO-R). The first strain of CRO-R *N. gonorrhoeae* was identified in Japan in 2009.

METHODS: The CRO-R strains were detected during routine culture surveillance conducted by Canadian provincial laboratories. Strains were tested using agar dilution and whole genome sequencing were performed on each strain to determine the MICs of 10 antimicrobials, *N. gonorrhoeae* MultiAntigen Sequence Types (NG-MAST), *N. gonorrhoeae* Sequence Typing for Antimicrobial Resistance (NG-STAR), and MLST type.

RESULTS: To date, in Canada, there have been eight CRO-R strains, with the first strain detected in 2017 in Quebec. Three were detected in 2018 (Ontario, Alberta), one in 2021 (British Columbia), and three in 2023 (Ontario, British Columbia). Ceftriaxone MICs for the eight strains range between 0.25 mg/L and 2 mg/L. Four of the strains were NG-STAR sequence type (ST) 233, which is associated with the FC428 clone. All eight cases have *penA* alleles associated with cephalosporin resistance, including *penA* 60.001, *penA* 121.002, and *penA* 237.001. NG-MAST and MLSTs are variable among the eight strains. The Canadian CRO-R strains show genetic diversity and cluster with a variety of international CRO-R strains, likely due to separate importations of the strains.

CONCLUSION: To date ceftriaxone remains an effective treatment for gonorrhea but continued surveillance is required to ensure detection and, thus, prevent the further spread of CRO-R *N. gonorrhoeae* in Canada.

TP087

Evaluating the performance of dried blood spot samples for sexually transmitted blood-borne infection testing

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OBJECTIVE: Stigma, trust, and access to testing are three main challenges faced by prevention and treatment efforts of sexually transmitted blood borne infections (STBBIs). Dried blood spot (DBS) samples, collected via fingerpick, are an alternative sample collection method that can be offered to individuals facing one or more of these challenges while efforts to resolve these issues are being made at an institutional and societal level.

METHODS: However, DBS samples are not a validated sample type for most Health Canada-approved STBBI tests. Thus, additional development, optimization, and validation work must be done by testing laboratories. The selection of appropriate elution buffers, DBS punch sizes, and number of DBS punches per test were the first aspects of testing developed. Once sample processing was optimized, DBS sample performance was compared to the gold-standard serum sample through a paired-sample study.

RESULTS: In this study, DBS samples run on the Abbott ARCHITECT Anti-HCV Assay were 97% accurate, 92% sensitive, and 100% specific ($n = 63$). The Hologic Panther Aptima® HCV Quant Dx Assay was 92% accurate, 100% sensitive, and 75% specific for DBS samples ($n = 12$). The Siemens ADVIA Centaur XP Syphilis Assay and the Abbott ARCHITECT HIV Ag/Ab Combo Assay were both 100% accurate, 100% sensitive, and 100% specific for DBS samples ($n = 37$, respectively). For the Hologic Panther Aptima HIV-1 Quant Dx, DBS samples were 75% accurate, 50% sensitive, and 100% specific ($n = 8$). Lastly, the Abbott ARCHITECT HBsAg Qualitative Assay was 100% accurate, 100% sensitive, and 100% specific for DBS samples ($n = 29$).

CONCLUSION: DBS sample performance on the selected STBBI testing platforms depended greatly on the quantity, quality, and diversity of positive paired samples tested. Although DBS samples are not suitable for all STBBI testing scenarios, providing them as an alternate sample type is one way testing laboratories can facilitate greater and more equitable access to health care.

TP088

Multiple syphilis infection episodes in British Columbia: Molecular analysis using enhanced CDC-*rps*A typing and point mutation detection

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OBJECTIVE: In British Columbia, Canada, numerous individuals experienced multiple instances of syphilis infections. This study aimed to assess the effectiveness of enhanced CDC-*rps*A (ECDC+) typing in distinguishing *T. pallidum* strains, providing insights into the transmission network associated with recurrent infections due to reinfection from the same or different sexual partners.

METHODS: The initial screening used real-time polymerase chain reaction, targeting polA and tpp47 genes. To differentiate separate infection episodes within the same patients (PCR test time confined to 3 months), 20 patients were randomly selected from a pool of 55, with two or three infections. ECDC analysis, incorporating *arp*, *tpr*, and *tp*0548 genes along with *rps*A typing, revealed strain characteristics. Point mutation examination in the 23S *r*RNA gene identified instances of macrolide resistance.

RESULTS: Of the 20 patients studied, 30% showed identical ECDC+ profiles in samples taken over 3 months to nearly 4 years, represented by profiles 14d9g, 14d11d, and 8d9g. The remaining 70% demonstrated 11 diverse ECDC+ profiles spanning 4 months to about 4 years, including profiles 14d9g, 14d9f, 13d9g, 12d9g, 14d11d, 9d9g, 15d10f, 19d10c, 14b11d, 13b11d, and 8d9g. All samples exhibited macrolide resistance, with just 5% of patients undergoing the A2059G to A2058G mutation transition over nearly 10 months, while the remaining 95% consistently displayed A2058G mutations.

CONCLUSION: Our findings reveal that about 70% of patients with multiple syphilis infections harbour distinct genotypes, augmenting traditional epidemiology for tracking the transmission network at the STI clinic. Including the *rps*A gene did not significantly enhance discriminatory power, suggesting potential clonal transmission of *T. pallidum* strains in British Columbia. When combined with data on macrolide resistance, strain details from ECDC+ typing, and clinical information, physicians gain valuable insights for evaluating whether patients are experiencing *T. pallidum* persistence or recurrence.

TP089

Genomic characterization of circulating *Treponema pallidum* strains in British Columbia, 2023

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OBJECTIVE: The surge in syphilis cases and macrolide resistance is a significant health concern. In 2023, we comprehensively analyzed circulating syphilis strains, using traditional epidemiological data alongside 4-component CDC typing schemes, MLST, and point mutation detection for macrolide resistance, aiming to understand *T. pallidum* trends in British Columbia.

METHODS: Real-time PCR, targeting *pol*A and *tp*47, was employed as the screening assay ($n = 3,049$) in 2023. Subsequently, 20% of positive samples (81/374) underwent

further analysis in molecular subtyping and drug resistance studies. The process adhered to the CDC typing method, involving the examination of various factors, such as the number of 60-bp repeats in the acidic repeat protein (*arp*) gene, *T. pallidum* repeat (*tpr*) polymorphism, *tp0548* gene sequence typing, and a mononucleotide tandem repeat in *rps*A. Additionally, an integrated multilocus sequence typing (MLST) scheme focused on TP0136, TP0548, and TP0705. The assessment of macrolide resistance included the detection of point mutations in the 23S *r*RNA gene using restriction fragment length polymorphism.

RESULTS: *T. pallidum* strains in circulation were categorized into 12 ECDC subtypes, with subtype 14 d/g prevailing at 54.32%, followed by subtype 14 d/d at 20.99%. In all 81 cases (100%), point mutations in the 23S rRNA linked to macrolide resistance were observed. The A2058G mutation was the most prevalent (97.53%), followed by A2059G (2.47%). Additionally, we successfully determined 7 sequence types from the 78 specimens for which completed MLST profiles were generated.

CONCLUSION: In contrast to the previous year's data, the positive rate of syphilis PCR has slightly dropped. The ECDC demonstrated slightly better discrimination power than MLST. Similar to the preceding year, macrolide resistance remains dominant, underscoring its significance in treatment considerations.

TP090

Investigation of the newly emerging 14d/d *Treponema pallidum* strain in British Columbia using multilocus sequence typing

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OBJECTIVE: In 2019, a novel strain, 14 d/d, emerged in BC and became the second most prevalent strain type (20%). By using multilocus sequence typing, we assess whether it can enhance typing resolution compared to the current Enhanced Centers for Disease Control and Prevention typing method. Additionally, we aim to explore epidemiological analyses using the existing MLST database to gain further insights.

METHODS: The study included 69 recently identified cases of the 14d/d *T. pallidum* strain in British Columbia (2019–2023) through the ECDC method. Three target loci (tp0136, tp0548, and tp0705) underwent Nested PCR before purification and customized Sanger Sequencing with BigDye Terminator chemistry before being placed into the ABI 3500 Genetic Analyzer for analysis. Locus typing occurred on a locally customized BLAST server, including relevant Sequence Type (ST) details. Epidemiological analysis was performed using a consolidated database with information from ECDC, MLST, published articles, and BC data.

RESULTS: All 69 typed samples resulted in an allelic profile of 9.7.3, corresponding to a ST type of 26. Phylogenetic trees were constructed using the combined sequences of all loci fragments of 9.7.3, comparing them with the sequences of all other ST types. Our analysis revealed that these isolates, characterized by 14 d/d and ST 26, formed a cluster closely associated with the Nichols-like group.

CONCLUSION: When analyzing molecular data from ECDC and MLST datasets spanning two decades, the 14 d/d strain has been documented globally before 2010. Higher prevalence in Europe was noted from 2010 to 2020, yet none have emerged as dominant cases in BC. Despite using both ECDC and MLST to target 6 genes, we have encountered challenges discriminating against this strain. Identical 23S macrolide resistance profiles (resistant/A2058G) also suggest a potential clonal complex circulation, prompting further investigations into associated transmission networks.

TP091

Evaluation of the updated cobas SARS-CoV-2 and Influenza A/B Qualitative nucleic acid test (v2) for the detection of influenza A H1N1-containing matrix mutation C124A

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OBJECTIVE: In the 2022 influenza season, influenza A H1N1 strains with matrix mutations C124A ± G141A were identified, leading to potential false-negative results on the cobas SARS-CoV-2 and influenza A/B qualitative nucleic acid test. We evaluated the performance of an updated version of the cobas assay (v2) against H1N1 strains with

matrix mutations in preparation for the 2023 influenza season.

METHODS: Previously confirmed influenza A H1N1 from nasopharyngeal swab samples underwent whole-genome sequencing at the provincial reference laboratory to confirm the presence of matrix mutations C124A and G141A. The cobas assay (previous and v2 versions) were tested on the cobas 6800, with influenza A comparator testing performed on other platforms (Xpert Xpress CoV-2/Flu/RSV *plus* and laboratory-developed assays (LDT) at our clinical laboratory and the provincial reference laboratory).

RESULTS: Using the previous cobas assay compared to the provincial reference LDT, there was an average delay in Ct values of 12.6 for samples with C124A mutation only ($n = 4$), including 1 false-negative. For samples with C124A and G141A ($n = 10$), there was an average delay in Ct values of 16.6 (including 4 false negatives on the cobas). Comparing the cobas v2 assay to the reference LDT, 23 samples with matrix mutations (C124A) were assessed over a range of Ct values (16–31). There were no false-negative results, and Ct values were only an average of 1.5 cycles later with the updated cobas v2 assay.

CONCLUSION: The cobas SARS-CoV-2 & influenza A/B v2 qualitative nucleic acid test resolved previous issues regarding the detection of influenza A H1N1 with matrix mutations (C124A ± G141A) and has been implemented in our clinical laboratory for the 2023 influenza season.

TP092

Targeting hepatitis B virus by pretending to be hepatitis delta virus

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OBJECTIVE: Hepatitis B virus (HBV) is a leading cause of chronic liver disease, chronically infecting over 300 million people globally. An effective *preventative* vaccine exists, but current therapies can only *suppress* the virus, so there remains a strong need for novel anti-HBV approaches. The defective RNA virus, hepatitis delta virus (HDV), requires HBV surface proteins to complete its replication. HDV coinfection is found in ∼5% of HBV-infected individuals. Interestingly, HBV DNA levels appear to be lower in HBV-HDV coinfection compared to HBV monoinfection, suggesting a component of suppression by HDV. It has recently been found that HDV's small hepatitis D (SHD) and large hepatitis D (LHD) proteins can bind HBV pgRNA, which is sufficient to lower HBV levels. The objective of this research is to *characterize the structural interaction between the SHD/LHD and HBV pgRNA to design a novel HBV peptidomimetic*.

METHODS: HDV proteins were recombinantly produced in *E. coli* and purified via affinity and size exclusion chromatography. A consensus sequence for HBV's pgRNA segment of interest was determined using Geneious Prime. The pgRNA is being produced via in vitro transcription for use in pull-down studies between the HDV proteins and the HBV pgRNA to test protein functionality. Binding studies using microscale thermophoresis and structural analysis will follow.

RESULTS: Recombinant HDV proteins have been produced. A consensus sequence of HBV's pgRNA segment of interest has been determined from >13,000 HBV reference sequences and in vitro transcription of HBV pgRNA is under way. The two components will be combined to determine the functional and structural nature of the HDV-HBV interaction.

CONCLUSION: Determining and understanding the molecular interaction between HDV and HBV will provide a foundation for developing small-molecule mimetics of HDV proteins for use as a potential therapeutic against HBV. We would target HBV by pretending to be HDV.

TP093

Detecting proliferation of rubella-specific memory T cells in the prenatal population

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OBJECTIVE: Rubella virus (RuV) infection during pregnancy can result in severe fetal morbidity and mortality. The introduction of MMR-vaccine has reduced the incidence. However, waning antibodies in the adult population have been observed in highly vaccinated cohorts. This study aims to determine the cellular-mediated immune (CMI) response in prenatal population, therefore validating and

developing a CMI assay is the first step to achieve our main goal.

METHODS: Peripheral mononuclear cells (PBMCs) were incubated with RuV (1:20 viral dilution [VD]) for 4, 6, 12, 18, and 24 h (1:10 and 1:20 VD). Memory CD4 T cells and CD8 T cells were isolated and CFSE-labelled cells. After the viral incubation, CFSE-labelled T cells were mixed with infected PBMCs. For the 18- and 24-hour conditions, day 4 to 8 samples were collected and stained with flow antibodies, viability dye, and measured by fluorescence-activated cell sorting (FACS).

RESULTS: The first three incubation times, and particularly those with only 4 and 6 h of virus exposure, didn't show any proliferation. Twelve hours showed an increase in cell frequency (53.4% CD4; 31.2% CD8) compared to the negative control (37.5% CD4; 20.9% CD8). The 18-h incubation at 1:20-VD condition (8.01% CD4; 3.02% CD8) responded better than 1:10-VD (5.67% CD4; 2.51% CD8) on day 7, but that did not reflect in the histogram of each condition. However, 24 h 1:10-VD showed a better proliferation response and profile after 7 days (4.56% CD4; 1.06% CD8) than the negative control (0.011% CD4; 0.016% CD8).

CONCLUSION: The results of the proliferative response after challenging T cells with RuV demonstrated that it could be measured after 24 hours of viral incubation at 7 days post-infection. However, it is necessary to re-evaluate these experiments to confirm the sensitivity of the assay, and eventually be able to use it to measure the proliferative memory response of vaccinated individuals.

TP094

Clinical significance of human herpesvirus 6 detected with the FilmArray Meningitis/Encephalitis Panel in Nova Scotia

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OBJECTIVE: Over the years, syndromic testing using highly multiplexed assays have gained popularity. The Biofire FilmArray Meningitis/Encephalitis (ME) panel allows detection of 6 bacteria, 7 viruses, and a yeast in cerebrospinal fluid (CSF), including human herpesvirus 6 (HHV-6). While HHV-6 encephalitis has been well described among hematopoietic stem cell transplant (HSCT) recipients, it is rare outside this setting, and positive results could simply reflect latency rather than a true infectious cause for disease. After ME panel implementation in Nova Scotia, frequent HHV-6 positive cases were observed. To evaluate the clinical importance of this observation, all HHV-6 positive cases since implementation were reviewed.

METHODS: A retrospective review was conducted on HHV-6 cases detected in CSF using the ME panel between January 1, 2021, and December 31, 2023. A standardized form was used to collect data on patient demographics, outcomes, and management. Cases were reviewed independently by six infectious disease physicians and microbiologists who assigned the possibility of disease as probable (>90% probability), possible (10%–90% probability), or unlikely (<10% probability). Final results were discussed as a group to reach consensus.

RESULTS: Of 17 patients with HHV-6 positive CSF, the age ranged from 2 weeks to 75 years, and 60% were female. None were categorized as probable CNS disease, and disease was unlikely in 16 (94%). A single case who was severely immunocompromised after receiving CAR-T cell therapy with concomitant CMV infection was categorized as possible disease. Only three patients had abnormal CNS parameters, one of whom had meningococcal disease. Three patients received antiviral therapy, but their clinical course was unchanged.

CONCLUSION: Given the majority of the patients had normal CNS parameters and presentations that were not compatible with HHV-6 disease, HHV-6 detection in CSF in immunocompetent patients is often reflective of latency and has limited clinical significance.

TP095

Characterization of live attenuated and UV-inactivated VSV-based influenza universal vaccine targeting the highly conserved M2 ectodomain from different host strains

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OBJECTIVE: The continuous emergence of the influenza virus, causing 290,000 to 650,000 deaths annually despite vaccination, underscores the need for a universal influenza vaccine. A novel approach involves leveraging the immuno-

genic properties of the Ebola glycoprotein (EboGP) to target dendritic cells (DCs). In this study, novel DC-targeting influenza antigens were developed by fusing the EboGP DC-targeting domain (EΔM) with conserved influenza hemagglutinin stalk regions (HA) and the ectodomain of matrix protein (M2e), or four copies of M2e (tM2e), generating EΔM-HM2e or EΔM-tM2e, respectively, and incorporated in the recombinant vesicular stomatitis virus (rVSV) forming rVSV- EΔM-HM2e or rVSV- EΔM-tM2e. Because of safety concerns regarding live vectors in immunocompromised, children, and aged populations, we inactivated the rVSV-EΔM-tM2e using ultraviolet light (UV) and investigated its immunogenicity and potential to protect against the H1N1 virus.

METHODS: In this study, we investigated the immune responses of the rVSV-EΔM-HM2e or EΔM-tM2e against different influenza hosts and its protective ability and H1N1/H3N2 strains. We also examined the immune responses of UV-inactivated rVSV-EΔM-tM2e and its protective ability against H1N1. Additionally, we characterized the ADCC immune response generated by rVSV-EΔM-tM2e.

RESULTS: Results demonstrated that intranasal or intramuscular immunization with rVSV-EΔM-tM2e or EΔM-HM2e significantly boosted immune responses against M2e from human, avian, and swine, providing 100% protection against H3N2 and 60%–100% protection against H1N1. Moreover, the investigation revealed the antigen specificity of the vaccine against diverse influenza strains, demonstrating recognition of antigens from human, swine, and avian influenza. ADCC assays underscored the antibody-dependent survival rate. The UV-inactivated rVSV-EΔM-tM2e maintained its antigenicity, inducing robust immune responses, and providing protection against H1N1 in mice.

CONCLUSION: Using our novel technology, we developed a universal influenza vaccine by fusing influenza-conserved epitopes with EΔM to induce a broader immune response and protect against influenza strains. The UV-inactivated rVSV-EΔM-tM2e retained its antigenicity and protected against H1N1 viral infection.

TP096

Identification of *nsp5* mutations in SARS-CoV-2 isolates from patients after completion of nirmatrelvir-ritonavir therapy through whole-genome sequencing

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OBJECTIVE: The use of nirmatrelvir-ritonavir (NIR-RIT) improves clinical outcomes in individuals infected with SARS-CoV-2 but may put selective pressure on the virus. While antiviral resistance mutations have been rarely reported to date, increasing usage raises concerns regarding the potential selection of novel antiviral-resistant variants. We investigated the emergence of potential antiviral resistance variants in SARS-CoV-2 following treatment with NIR-RIT using whole-genome sequencing.

METHODS: We screened 683 SARS-CoV-2-infected patients being admitted to hospital A from February 2022 to July 2023, and 845 infected patients with emergency department visits (368 admitted) between October 2022 and July 2023 at hospital B to identify persons treated with NIR-RIT prior to testing. Nasopharyngeal samples from patients with sufficient viral RNA were subjected to next-generation sequencing to identify mutations in the viral protease gene (*nsp5*). Bioinformatics analysis was done using artic-network/artic-ncov2019 (Oxford Nanopore) or covid-19-signal (Illumina) and ncov-tools pipelines.

RESULTS: We identified 19 patients with a nasopharyngeal swab yielding SARS-CoV-2 at high enough concentrations for sequencing after exposure to NIR-RIT. Mutations reported to confer high-level resistance to NIR-RIT, such as L50F and E166A/V were not detected. Low-level resistance mutations T21I and P252L were also not detected. Interestingly, two patients had similar patterns with mutations L67V and K90R in *nsp5*. Additionally, nonsynonymous mutations were observed in the majority of samples, with variants being seen most frequently at position D48, which could represent potential spring-board mutations.

CONCLUSION: We did not identify established resistance high- or low-level mutations in our cohort. The identification of novel mutations in the *nsp5* gene requires cell culture studies to assess phenotypic susceptibility. Nonsynonymous mutations that were identified could represent potential spring-board mutations, and further in vitro studies are also needed. The findings underscore the importance of continuous surveillance to monitor the evolution of the virus under ongoing pressure from therapeutic interventions.

TP097

Epidemiology of paediatric invasive pneumococcal disease (IPD) late after introduction of a routine infant PCV13 program

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OBJECTIVE: An infant PCV13 program (2+1) was introduced in our province in December 2010. We assessed the epidemiology of IPD in children in the late post-PCV13 era.

METHODS: We performed a population-based surveillance for IPD (pop. 4.5M). Microbiology labs report sterile site isolates of pneumococci; annual audits ensure completeness. The National Microbiology Laboratory serotypes isolates. Statistics Canada provides population data. Clinical data are from chart review and patient/MD interview. Complete vaccination is defined per NACI. Cases of vaccine serotype (ST) disease are categorized as children ineligible for vaccination, vaccine failure (completely vaccinated children); program failure (unvaccinated or incompletely vaccinated); and partially vaccinated (vaccination up-to-date but incomplete).

RESULTS: From 2014 to 2022, 373 paediatric (age <15 y) IPD cases occurred, with clinical data available for 349 (94%), serotyping for 358 (96%). Thirty-eight (11%) cases required ICU, 26 (7%) had meningitis, and 7 (2%) died. 270/373 (72%) were <5 years; 124 (36%) had an underlying condition predisposing to IPD; 64 (18%) were immunocompromised. Underlying conditions were more common in 5–14-year-olds (49% any, 36% immunocompromised). IPD incidence in 2022 was 12.6/100,000/year among <5-year-olds, 3.3/100,000/year among 5–14-year-olds, not different from incidence in 2014–2019 (Figure). Overall, 84/358 isolates (23%) were PCV13 STs, 47 (13%) were PCV15/notPCV13, 56 (16%) were PCV20/notPCV15, and 48% were non-PCV. PCV13 ST were 41 ST 19A (49%), 32 (38%) ST 3, 6 (7%) 19F, 3 7F and 1 each 14 and 9V. Of 77 (92%) with evaluable vaccine history, 24 were not eligible (5 were <2 months old, 19 were too old to receive PCV13), 34 were vaccine failures, 15 were program failures (8 unvaccinated, 7 no >12 m dose); and 4 were incompletely vaccinated.

CONCLUSION: Post PCV13 implementation, IPD has stabilized, with increased disease due to PCV15 and PCV20 STs and in older and immunocompromised children, although some PCV13 disease persists. Higher-valency vaccines should further reduce IPD; a "catch-up" dose might be considered for immunocompromised older children.

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