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CALGARY TELUS CONVENTION CENTRE
CALGARY, ALBERTA

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ORAL PRESENTATIONS

Session A (Student Competition)
Wednesday, April 30

A01
Understanding infection kinetics and clinical outcomes in participants enrolled in a *Bordetella pertussis* controlled human infection model

Ashley Osa-Peters, May ElSherif, Scott Halperin, Wade Blanchard

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OBJECTIVE: *Bordetella pertussis* causes whooping cough, a respiratory illness dangerous to newborns and unvaccinated infants under 1 year old who can suffer severe complications, including death. Despite decades of acellular pertussis (aP) and/or whole-cell pertussis (wP) vaccine programs, there has been a rise in cases over recent years. A controlled human infection model (CHIM) was developed to study pertussis infection in healthy adults. This study focuses on differences in infection kinetics and clinical outcomes between participants who were aP primed versus wP primed. The results could inform future *B. pertussis* vaccine development and public health vaccination initiatives.

METHOD: Healthy adults were screened and admitted to a challenge unit from the day of challenge to treatment. Vaccination priming (aP or wP) and pre-challenge antibody titers were recorded. Participants were intranasally inoculated with a saline suspension of *B. pertussis*. Nasal wash (NW) samples collected on post-challenge days 6 to 16 were used to assess bacterial shedding by both culture and qPCR. Participants were examined daily for signs and symptoms of infection. Mean qPCR Ct values and geometric mean bacterial colony counts from NW samples of aP- and wP-primed participants were compared using ANOVA (*t*-test). Fishers exact test was used to analyze the difference in clinical outcomes between aP- and wP-primed participants.

RESULTS: aP-primed participants showed greater bacterial shedding on average by both culture and qPCR. Sixty-four percent of the aP-primed participants became symptomatic, compared with 38% of wP-primed participants. Thirty-two percent of the aP-primed participants developed cough, whereas 16% of wP participants developed cough.

CONCLUSION: Bacterial shedding could be used as a proxy for propensity for transmission in the natural infection setting. Similarly, the higher likelihood of becoming symptomatic and developing cough could be used as a measure of increased risk of severe infection in aP-primed individuals.

A02
ResaCPE: a rapid, low-cost colourimetric assay for the clinical detection of carbapenemase-producing *Enterobacterales*

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OBJECTIVE: Infections caused by carbapenemase-producing *Enterobacterales* (CPE) are associated with poor patient outcomes and high mortality rates. Thus, early detection of these pathogens is vital to ensure timely administration of appropriate antimicrobial therapy and infection control practices. Current phenotypic CPE detection strategies suffer from limitations such as long turnaround time (eg, modified carbapenem inactivation method), lower sensitivity for carbapenemases with weak hydrolytic activity (eg, CARBA-NP), and a high cost per test (eg, NG-CARBA-5). Thus, the objective of this study was to develop and validate a rapid, novel colourimetric CPE detection method that exhibits a high degree of sensitivity across carbapenemase subtypes at a low cost.

METHOD: The ResaCPE assay was performed on colonies of test isolates following overnight growth. The performance of the test was assessed using a panel of 46 CPE and 29 non-CPE clinical isolates obtained from Kingston General Hospital (Kingston, ON) and Shared Hospital Lab (Toronto, ON), respectively. The same isolates were also tested with the CARBA-NP assay to compare the sensitivity to the ResaCPE.

RESULTS: The ResaCPE assay demonstrated a sensitivity of 100%, with 13/13 VIM-, 12/12 NDM-, 1/1 NDM- & KPC-, 13/13 KPC-, and 7/7 OXA-48-like-producing isolates testing positive. The assay also yielded a specificity of 100%, with 29/29 non-CPE isolates testing negative. The performance of the resaCPE was superior to the CARBA-NP, which yielded a sensitivity of 95.6% with false negatives obtained for the two OXA-48-like-producers.

CONCLUSION: Due to the high sensitivity, rapid turnaround time (approx. 3.5 h), and low cost per test

(approx. $1.50 CAD), the resaCPE assay is an attractive alternative to the currently used CPE detection strategies. Ongoing and future work is aimed at evaluating the performance of the assay in several clinical microbiology labs in Ontario.

A03

Characterization of methicillin-resistant *Staphylococcus aureus* in Canadian hospitals: 17 years of the CANWARD study, 2007–2023

Anissa Brahami[1], James A Karlowsky[1,2], Melissa McCracken[3], George Golding[3], Kimberly A Nichol[2], Melanie Baxter[1], Heather J Adam[1,2], Philippe R S Lagacé-Wiens[1,2], George G Zhanel[1]

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OBJECTIVE: This study assessed the demographic and molecular characteristics of community-associated (CA) and health care–associated (HA) methicillin-resistant *Staphylococcus aureus* (MRSA) strain types in Canadian hospitals between 2007 and 2023.

METHOD: MRSA (a total of 12,734) were collected from inpatients and outpatients presenting to Canadian tertiary care medical centers. Antimicrobial susceptibility testing was performed by broth microdilution (CLSI M07, 2024); MICs were interpreted using CLSI M100 (2024) breakpoints when available. PCR was used to detect the Panton-Valentine leukocidin (PVL) gene and sequencing to generate *spa* types.

RESULTS: The annual proportion of MRSA decreased significantly from 2007 (26.1%) to 2016 (16.9%) and then increased to 24.2% in 2023 ($p < .0001$). t008 (associated with CA types) and t002 (associated with HA strain types) were the predominant *spa* types identified among all study isolates at 24% and 36%, respectively. Between 2007 and 2023, CA-MRSA strain types increased significantly from 20.8% to 75.0%, and HA-MRSA decreased from 79.2% to 25.0%. The *PVL* gene was detected in 36.0% of all MRSA (76.3% of CA-MRSA; 2.7% of HA-MRSA). Resistance rates for CA- and HA-MRSA strain types were as follows: 60.6% and 91.1% for ciprofloxacin; 67.9% and 91.3% for clarithromycin; 13.0% and 61.1% for clindamycin; and 1.2% and 8.6% for trimethoprim-sulfamethoxazole. All MRSA (CA and HA combined) were 99.7% ceftobiprole susceptible (EUCAST v14, 2024), 99.9% daptomycin susceptible, >99.9% dalbavancin susceptible, 99.9% vancomycin susceptible, and >99.9% linezolid susceptible.

CONCLUSION: In Canada, the annual proportions of *S. aureus* isolates cultured from samples submitted to hospital microbiology laboratories that were MRSA decreased between 2007 and 2016, then returned close to the 2007 proportion by 2023. Over the 17 years, CA-MRSA strains, particularly spa type t008, increased from 2007 to 2023 and are now the most common MRSA isolates recovered in Canadian hospital laboratories. Almost all MRSA (≥99.8%) were susceptible to ceftobiprole, linezolid, dalbavancin, vancomycin, and daptomycin, and 98.8% of CA-MRSA were susceptible to trimethoprim-sulfamethoxazole.

A04

Comparison of pharyngeal and invasive isolates of *Streptococcus pyogenes* by whole-genome sequencing

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OBJECTIVE: To explore the *Streptococcus pyogenes* population during an invasive Group A Streptococcus (iGAS) outbreak and identify potential genetic and phenotypic factors influencing this trend.

METHOD: We analyzed 38 blood and 117 pharyngeal GAS isolates collected between January and May 2023 using whole-genome sequencing. We compared our isolates to ~2,000 genomes available in the NCBI database to gain a better understanding of our local epidemiology in a global context. Additionally, we performed genome-wide association analyses and specifically looked for the presence of 63 relevant virulence factors and adhesins, typing schemes (*emm*-type), antimicrobial resistance (AMR) genes, as well as deletion mutations the critical CovRS two-component system to determine if there were genetic signatures that may explain this iGAS disease increase. Concurrently, we

performed phenotypic functional assays to assess the ability of our isolates to produce relevant virulence factors.

RESULTS: Results demonstrated limited clustering of our samples with both invasive and noninvasive isolates represented across a diverse set of lineages. Noninvasive isolates were predominantly *emm12* (70.1%) whereas invasive isolates included emm*12* (26.32%), *emm49* (23.68%), and *emm1* (13.16%). Although there were no differences in the presence of total virulence factors/adhesin genes, there were statistically more superantigen and DNase genes in noninvasive isolates, and a rare phage gene was associated with invasiveness across three *emm* types. The prevalence of individual genes also differed, including a higher likelihood of *speA, enn, mrp, ideS/Mac, fbaA,* and *fbaB* in invasive isolates. There were no significant differences across 11 AMR genes. Lastly, pharyngeal isolates had larger hemolysis and hydrolysis zones, and *covS* deletions were observed in only seven invasive strains.

CONCLUSION: Despite there being no genetic signature that differentiated our isolates, we observed several predominant features in invasive strains, which provides further insights into the factors that contribute to GAS invasiveness.

ORAL PRESENTATIONS

Session B
Wednesday, April 30

B01
Characterization of Carbapenemase-producing *Enterobacterales* and *Pseudomonas aeruginosa* in Manitoba hospitals between 2014 and 2024

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OBJECTIVE: Carbapenemase-producing organisms (CPO), including *Enterobacterales* (CPE) and *Pseudomonas aeruginosa* (CPPA), represent significant clinical challenges. Until recently, few CPO infections occurred in Manitoba. The purpose of this study was to describe and characterize the recent emergence of these pathogens in Manitoba between April 2014 and November 2024.

METHOD: Only clinical nonduplicate isolates were included in the study. Screening specimens were not included. Isolates were identified by MALDI-TOF and CPO was suspected when the Vitek™ 2 reported any carbapenem non-susceptibility. Carbapenem non-susceptibility was confirmed by Kirby-Bauer disk diffusion. Carbapenem-non-susceptible *Enterobacterales* and *P. aeruginosa* that were additionally ceftolozane/tazobactam resistant (2019 onwards) were investigated for carbapenemase-production using the CarbaNP test or immunoassay for VIM, IMP, NDM, KPC, and OXA-48-like enzymes. All confirmed CPE and CPPA were forwarded to a reference laboratory for PCR to determine the specific carbapenemases enzymes present.

RESULTS: Two hundred twenty-eight CPOs were detected during the study period. CPO detections increased from 3 in 2014 to a peak of 62 in 2023, with CPE counts increasing rapidly in the past 3 years. The most common species was *P. aeruginosa* (24.6%), followed by *Klebsiella pneumoniae* (18.4%), *Enterobacter cloacae* complex (17.5%), *Escherichia coli* (17.5%), and *Citrobacter freundii* complex (11.4%). Most (96.9%) isolates had a single carbapenemase gene. The most common genes detected were NDM (59.6%), IMP (19.3%), OXA-48-like (4.8%), KPC (3.9%), and SME (3.9%). The most common sites of isolation were urine (65.1%), lower respiratory tract (11.4%), skin/soft tissue (11.4%), and bloodstream (10.3%).

CONCLUSION: There has been a significant increase in CPO detections in Manitoba in the past 3 years with CPPA being the most common species and CPEs increasing most rapidly. There is heterogeneity in CPE species with diverse *Enterobacterales* accounting for ~75% of CPO detections in Manitoba. CPOs in Manitoba are largely NDM producing and recovered from the urinary tract.

B02
The Bridge outreach infectious diseases clinic: A quality improvement community partnership initiative in Halifax, Nova Scotia

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OBJECTIVE: Access to outpatient infectious diseases care can be challenging for people who inject drugs and are insecurely housed, who face barriers to traditional outpatient clinic settings. With community partners, we developed a novel outreach infectious disease care model in Halifax, Nova Scotia. As part of a pragmatic evaluation, we aimed to describe the model of care including the population served and the reasons for outreach infectious diseases consultations.

METHOD: Beginning in November 2023, outpatient visits were coordinated at an all-gender shelter in conjunction with the Mobile Outreach Street Health (MOSH) team for patients identified during inpatient hospitalizations to have infectious disease issues that would benefit from coordinated outreach follow-up. Hepatitis C consultations were excluded due to an existing care pathway. Clinics were scheduled monthly and as needed based on identified patient need. New referrals were accepted from primary care team members for patients unable to attend traditional outpatient appointments. Data was extracted and summarized via retrospective chart review.

RESULTS: Between November 2023 and December 2024, a total of 27 patients were seen over 68 visits. The average age was 43, and 16 (59%) were male identifying. Sixteen (59%) patients were identified for follow-up during inpatient admissions, and 11 new consults were performed. The most common reason for visit was osteomyelitis (44%), followed by endocarditis and skin/soft tissue infection, each 26%. Nine patients had multiple issues to be followed (33%). Seven patients with HIV were engaged or reconnected to care.

CONCLUSION: This patient-centred and outreach approach to infectious diseases consultation provided access to care for people who inject drugs who were previously excluded, and was associated with high likelihood of follow-up. Partnership with community health programs, with established patient relationships, is essential for success including continuity of care and resource allocation.

B03

Evaluation of a mobile, community-based point-of-care test-and-treat model to address the syphilis epidemic in Saskatchewan: High uptake of immediate intramuscular Penicillin G Benzathine through community-based interventions in underserved populations

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OBJECTIVE: Syphilis is a growing public health concern in Saskatchewan, with rates increasing by 1,346% between 2017 and 2021. The point-of-care (POC) test-and-treat model provides rapid, on-site results, eliminating barriers such as travel and lab processing. This approach is particularly beneficial in rural, remote, and Indigenous communities with limited health care access, offering immediate diagnosis and treatment in trusted, familiar settings. This study aimed to evaluate treatment outcomes in individuals with reactive syphilis POC test results.

METHOD: The POC test-and-treat model was implemented from February 2023 to November 2024 at various community-based locations across Saskatchewan. The mobile and adaptive approach leveraged partnerships to use trusted community spaces. Sites were staffed by health professionals, outreach workers, and peer support workers. Participants were offered both POC testing and standard serological testing. Syphilis treatment was provided when indicated based on POC results, with follow-up testing and treatment arranged as needed. Patients were identified using the Wellness Wheel EMR. Patient demographics, POC test results, disease stage, and treatment date were evaluated.

RESULTS: One hundred fifty-eight participants had a reactive result on their POC test. Of these, 92 participants (58.2%) received their first dose of treatment during their visit. Nineteen participants (12.0%) were informed of their result but refused treatment. Treatment at time of visit for 17 participants (10.8%) was not provided due to limited public health access for history. Thirty participants (19.0%) did not require treatment.

CONCLUSION: The POC test-and-treat model in Saskatchewan showed promising results in addressing syphilis infections. Over half of participants with reactive results received immediate treatment while others refused treatment or had prior treatment. Improved access to treatment history would reduce missed opportunities to treat. Despite reported challenges, the model shows

potential for improving syphilis diagnosis and treatment in underserved populations.

B04

Decoding bloodstream infections: Insights from the Calgary BSI cohort show minimal co-segregation between microbial traits and clinical outcomes

Annegret Ulke-Lemee[1], Rory Gilliland[1], Mario Valdés-Tresanco[1], Morgan Hepburn[1], Ryan Groves[1], Anika Westlund[1], Andrey Plakhotnyk[1], Gopal Ramamourthy[1], Daniel B Gregson[1], Thi Mui Pham[2], Tatum Mortimer[3], Josh Smith[4], Bruce Walker[4], Yonatan Grad[2], Ashlee Earl[4], Hallgrimur Benediktsson[1], Ethan MacDonald[1], Ian A Lewis[1]

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OBJECTIVE: Bloodstream infections (BSI) cause over 500,000 cases annually in North America, resulting in 90,000 deaths. A wide range of human factors contribute to the clinical trajectory of these infections, but the contribution of microbial traits, such as protein virulence factors, remains poorly understood. A significant barrier to understanding this impact is the requirement for quantitative assessment of individual proteins. Additionally, we are lacking a systematic map of microbial diversity and its link to affected patients.

METHOD: To address these deficiencies, we acquired the Calgary BSI Cohort, comprising the 12 most common BSI pathogens occurring between 2006 and 2022 in the greater Calgary region. For each of the 38,000 BSI isolates we obtained whole-genome sequencing data, quantitative TMT proteomics, metabolomics, and extensive electronic medical records linked to each infection. Robust data integration resulted in a massive multi-omic data resource that enables detailed research into the long-term relationship between BSI microbes and human health (ResistanceDB.org).

RESULTS: Using the Calgary BSI cohort data, we systematically mapped the impact of every gene, protein, and metabolite on infection outcomes, constructing the first systematic map of microbial virulence, linked to patient factors. We show that quantitative proteomics is a robust mechanism for identifying and quantifying virulence factors and an important complement to whole genome sequencing data. We next examined all presently annotated virulence factors for their relationship between gene presence and expression level and for their co-segregation with clinical outcomes. Our results suggest that minimal co-segregation was observed between patient outcomes and the expression of known virulence factors.

CONCLUSION: Collectively, outcomes of blood stream infections are only minimally linked to microbial multi-omic traits when patient factors such as comorbidities were taken into account. Lastly, the Calgary BSI Cohort dataset will enable extensive research into BSI with the goal of improving human health.

ORAL PRESENTATIONS

Session C (Student Competition)
Thursday, May 1

C01

Validation of agar-based methodologies compared to broth disc elution for the detection of aztreonam-avibactam susceptibility among MDR gram-negative organisms

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OBJECTIVE: Aztreonam and ceftazidime-avibactam can be used in combination for the treatment of multidrug-resistant gram-negative organisms. Restoration of aztreonam susceptibility in the presence of avibactam can be confirmed using the CLSI broth disc elution method (BDE); however, the high workload and large material footprint of this assay make it difficult to implement in a high-throughput clinical laboratory. We validated two agar-based methods to evaluate aztreonam susceptibility in the presence of avibactam, using BDE as our gold standard in lieu of broth microdilution.

METHOD: Ninety-seven clinical isolates comprised of metallo-beta-lactamase-expressing Enterobacterales, *Pseudomonas aeruginosa, Stenotrophomonas maltophila*, *Acine-*

tobacter spp., and other non-fermenting gram-negative organisms (*Pseudomonas putida, Sphingomonas koreensis*) were selected. Susceptibility to aztreonam-avibactam was evaluated using BDE, double-disc diffusion, and E-test/disc diffusion. For agar-based methods, an aztreonam disc was placed at a specified distance from either a ceftazidime-avibactam disc or E-test strip, and the resulting zone of clearance between discs or disc/E-test strip was measured. Restoration of aztreonam susceptibility was confirmed by applying CLSI zone measurement breakpoints for aztreonam. Calculation of percent categorical agreement (CA), very major errors (VME), major errors (ME), and minor errors (MinE) was performed as per CLSI M52 and Cumitech 31A.

RESULTS: By BDE, 74% of Enterobacterales and 79% of *S. maltophila* isolates were susceptible to aztreonam in the presence of avibactam, whereas all *P. aeruginosa, Acinetobacter* spp, and other non-fermenting gram-negative isolates remained aztreonam-avibactam resistant. Compared to BDE, CA for double-disc diffusion and E-test/disc diffusion methods was 95% (95% CI 88.20–98.07) and 92% (95% CI 84.35–95.97), respectively. No VMEs or MEs were recorded for either method. MinE rate was 5% (95% CI 1.93–11.80) for double-disc diffusion and 8% (95% CI 4.03–15.65) for E-test/disc diffusion.

CONCLUSION: Both double-disc diffusion and E-test/disc diffusion methods met validation thresholds when using CLSI zone breakpoints to determine aztreonam susceptibility in the presence of avibactam.

C02

Monitoring microbial populations using a LC/MS-machine learning combined method

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OBJECTIVE: The global spread of antimicrobial resistance has brought the need for large-scale microbial monitoring into sharp focus. Current clinical laboratory tests cannot distinguish microbial pathogens at the strain level. This limitation hampers our ability to track the emergence and spread of specific microbial lineages across the entire population. Traditional genomic approaches effectively define microbial population structure but fail to capture protein expression levels, a critical determinant of antimicrobial resistance phenotypes and virulence. Here, we leveraged high-resolution quantitative proteomics of 30,000 clinical isolates from 12 bacterial species and machine learning to identify and track clinically relevant clones.

METHOD: We used AMPLE (Automated Microbial Proteomics for Large-scale Experiments) to process clinical isolates. The data were acquired using a Thermo Fusion Lumos Tribrid MS. Proteomic analysis was conducted with Fragpipe using custom pan-proteomes derived from genomic sequencing. Complementary antimicrobial resistance (AMR) and clinical metadata from provincial laboratory records were integrated with the proteomic data.

RESULTS: Remarkably, dendrograms generated from proteomic data mirrored genomic phylogenies and clearly showed the population structure characteristic of these organisms. Feature selection with Stabl method and logistic regression achieved balanced accuracies of over 90% for predicting genomic class from proteomic data. Key predictive proteins were evenly distributed across the core and accessory genomes and often linked to virulence and resistance. A clear example constitutes methicillin-resistant *Staphylococcus aureus* (MRSA) isolates, which were reliably identified by penicillin-binding protein 2a (PBP2a) expression.

CONCLUSION: This study represents the largest proteogenomic analysis of bacterial organisms to date. By combining machine learning with multi-omics data we demonstrate how proteomics complements genomics to shed light on clonal distribution and AMR phenotypes. These findings establish a robust platform for population monitoring and precision diagnostics using microbial proteomics.

C03

Immune recovery and activation among people with HIV on antiretroviral therapy: risk factors associated with delayed CD4+ T-cell and CD4+/CD8+ ratio recovery

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OBJECTIVE: To evaluate CD4+ T-cell recovery (500 cells/mm^3) and CD4+/CD8+ ratio normalization (≥1) following antiretroviral therapy (ART) initiation among people with HIV (PWH) who maintained HIV viral suppression and to identify risk factors associated with delayed recovery.

METHOD: PWH ≥18 years, in a geographically defined population between January 1, 1998 and January 6, 2022 and initiated on ART, were included at the first HIV viral load result of <200 copies/mL (study entry). Study exit was defined as the first date the patient reached the study outcome (CD4+ cell count of ≥500 cells/mm^3 [model 1] or CD4+/CD8+ ratio >1 [model 2]), viral load >200 copies/mL (a proxy for ART adherence), lost-to-follow-up, death, or the trial's concluding date. Continuous time-to-event Cox proportional hazard models estimated crude and adjusted hazards ratios and 95% confidence intervals for factors associated with CD4+ count and CD4+/CD8+ ratio recovery at 10 years.

RESULTS: Among 2,538 PWH, 905 (36%) had a CD4+ count >499 cells/mm^3 at study entry and 392 (15%) had an initial CD4+/CD8+ ratio >1 and were excluded from the analyses. Over 10 years, 84% of PWH achieved a CD4+ count of >499 cells/mm^3 and 55% a CD4+/CD8+ ratio of >1. In adjusted analyses, CD4+ recovery and CD4+/CD8+ normalization were less common among people diagnosed with HIV >50 years old (versus those <30 old), females, and having HIV for >10 years (versus <1 year). Both higher CD4+ counts and CD4+/CD8+ ratios at baseline were associated with both CD4+ cell recovery and CD4+/CD8+ ratio normalization. Factors associated with reduced CD4+/CD8+ normalization included Black race (versus White), CMV co-infection, and taking protease inhibitors (versus NNRTI) at study entry.

CONCLUSION: With HIV viral suppression, most PWH will recover their CD4+ count; however, fewer will reach a CD4+/CD8+ ratio of ≥1. We identified factors associated with delayed immune recovery. Factors associated with delayed CD4+/CD8+ ratio recovery may signal greater immune activation and inflammation.

C04

Consequences of blood culture contamination at a large Canadian hospital network

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OBJECTIVE: Blood culture contamination can cause patient harm by prolonging hospital stays and leading to unnecessary antibiotic exposure. However, little is known about the patient and system impact of blood culture contamination in a Canadian context. We sought to quantify the unnecessary clinical, laboratory, and pharmacy resources that were directly devoted to management of contaminated blood cultures at our institution

METHOD: We performed a retrospective chart review of all contaminated blood culture sets from hospitalized adult patients at two tertiary academic hospitals served by our laboratory between January and April 2024. We documented unnecessary clinical interventions that were directly attributable to the contaminated cultures.

RESULTS: We identified 870 contaminated sets out of 14,035 collected sets (6.2% contamination rate) during the study period. Shockingly, 752 patients were affected by contamination out of the 4,821 patients who had blood cultures drawn (15.6%). Of these patients, 46.8% were exposed to at least one dose of unnecessary antibiotic in response to their contaminated cultures, and a total of 1,351 antibiotic doses were administered (85.0% vancomycin). Unnecessary investigations included 811 repeat blood culture sets (from 50.1% of patients), 202 vancomycin trough levels, and 48 transthoracic echocardiograms. Forty-seven central lines were needlessly removed in patients incorrectly diagnosed with line-associated bloodstream infections. Finally, contaminated blood cultures prompted 67 infectious disease consultations.

CONCLUSION: Blood culture contamination remains a major patient safety issue at our institution. Clinical teams frequently respond to blood culture contaminants with unnecessary interventions that not only strain limited health care resources but also have potential for patient harm. This audit will help inform the cost effectiveness of upcoming quality improvement interventions to reduce our contamination rates. We hope that our work will also serve as a reference for other Canadian laboratories seeking to justify cost effectiveness of their own quality improvement initiatives aimed at reducing contamination rates.

ORAL PRESENTATIONS

Session D
Thursday, May 1

D01
Exploring implementation contexts of immunization assessment tools in three Canadian provinces: Perspectives from policymakers, vaccine administrators, and community members

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OBJECTIVE: Canadian immunization landscapes have evolved significantly in the past 10 years, with increasing numbers of vaccines and growing public engagement in health care decisions. Immunization assessment tools (IATs) personalize vaccine recommendations by comparing individuals' demographics and risk factors to current guidelines and may improve vaccine uptake. They should be user-friendly for both community members (CMs) and health care providers (HCPs). IATs' success depends on early engagement with end-users. The research objective was to contextualize the IAT implementation contexts of Prince Edward Island (PEI) (previously developed-IAT), Nova Scotia (NS) (current-IAT), and Ontario (ON) (future-IAT) from the perspective of end-users. This research is phase 2 of 4, overall aiming to adapt the existing IAT-PEI to improve vaccination practices/outcomes throughout Canada.

METHOD: Semi-structured interviews were conducted with participants from PEI, NS, and ON to describe provincial IAT implementation contexts. Participants were recruited through research team networks, social media, and environmental scan data. Eligible participants included vaccine administrators, policymakers involved in vaccinology, and CMs receiving vaccine recommendations. The i-PARIHS framework was used to guide thematic analysis and interpretation of the data to reflect perspectives across provincial contexts.

RESULTS: Thirty-four participants (PEI $n = 5$; NS $n = 20$; ON $n = 9$) were interviewed: vaccine administrators ($n = 20$); policymakers ($n = 9$); and CMs ($n = 5$). Four generated themes describe provincial contexts and considerations relevant for IAT implementation: (1) establishing trust between HCPs and CMs; (2) creating collaborative/responsive health care; (3) improving resource/information management; and (4) participant recommendations for provincial IATs. Recommendations included the need for intuitive, accessible, and user-friendly IAT design; integrated digital vaccine records; and considering the workload impact for HCPs.

CONCLUSION: Successful implementation of an IAT requires consideration of the CM and HCP trust relationship, the IAT's ability to respond to changing health care needs, and available regional resources (time, funding, personnel). Next steps include piloting an adapted IAT-NS with users in Spring 2025 to assess impact.

D02
Drugs associated with *Clostridioides difficile* infection (CDI) risk in Ontario, Canada: A pharmacopeia-wide case-cohort study

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OBJECTIVE: *Clostridioides difficile* infection (CDI) is a common cause of morbidity and mortality. Our aim was to identify the most important drugs associated with CDI and opportunities for drug stewardship in Ontario.

METHOD: Among Ontario residents over the age of 66 with no prior CDI, we developed a longitudinal cohort over the period between January 1, 2018 and December 31, 2023. Cases were person-days on which cohort members developed CDI while controls were a 0.01% random sample of person-days on which residents did not develop

CDI. We examined drug exposure (yes = 1, no = 0) in the 1–90 days prior; any individual oral drug used on at least 100 control person-days was included. Covariates included patient age, sex, health care exposures, and comorbidities. Adjusted logistic regression models with case versus control status as the outcome were used to estimate, for each drug exposure, (1) an odds ratios (OR) and (2) the population preventable fraction under a 10% relative reduction of exposure (PPF10); the PPF represents the estimated proportion of CDI that would not have occurred under a given reduction in drug exposure.

RESULTS: We identified 16,196 case person-days and 352,826 control person-days over the 6-year study period; 304 drugs met inclusion criteria. Seven drugs had a PPF10 > 0.5%: amoxicillin-clavulanate (1.2% exposed; OR = 7.7, 95% CI: 7.2–8.2; PPF10 = 1.3%), ciprofloxacin (1.6% exposed; OR = 4.3, 95% CI: 4.0–4.6; PPF10 = 1.0%), pantoprazole (13.6% exposed; OR = 1.4, 95% CI: 1.4–1.5; PPF10 = 0.9%), cephalexin (1.9% exposed; OR = 3.3, 95% CI: 3.1–3.5; PPF10 = 0.9%), clindamycin (0.5% exposed; OR = 16.7, 95% CI: 15.4–18.2; PPF10 = 0.8%), ferrous fumarate (3.1% exposed; OR = 1.9, 95% CI: 1.8–2.0; PPF10 = 0.6%), and furosemide (6.1% exposed; OR = 1.3, 95% CI: 1.2–1.4; PPF10 = 0.6%).

CONCLUSION: "4C" antibiotics (amoxicillin-clavulanate, ciprofloxacin, cephalexin, and clindamycin) continue to be the main drivers of CDI in Ontario; however, several non-antimicrobial drugs may also contribute to CDI incidence and may represent important targets for stewardship efforts. The results of this study can be used to guide stewardship efforts for reducing the burden of CDI.

D03

Real-time detection of loop-mediated isothermal amplification (LAMP) using You Only Look Once (YOLO)-based machine learning algorithm

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OBJECTIVE: Loop-mediated isothermal amplification (LAMP) is a rapid, cost-effective method for DNA amplification that requires minimal resource. However, visual interpretation of results can be subjective, leading to potential false-positive and false-negative outcomes. To address this limitation, a machine-learning approach is proposed for automated LAMP classification based on digital images. This method employs You Only Look Once (YOLOv8), a fast and robust object detection algorithm to locate and classify tubes within LAMP images, enabling automated categorization as positive or negative. The trained model has been applied to LAMP images acquired under different imaging conditions, demonstrating its applicability for real-time disease diagnosis.

METHOD: In this work, YOLOv8 was trained with annotated LAMP images of sizes 640 × 640 pixels, with the location of each tube sample in the LAMP images being marked by bounding box coordinates. The training dataset first underwent a preprocessing step, such as normalization, to address data quality issues. Once the preprocessing was completed, the datasets were split into training (85%) and testing (15%) sets. The model's performance was assessed using different matrices such as accuracy and mAP@50.

RESULTS: The trained model achieved a high overall accuracy of 95.5% in classifying LAMP images into positive or negative. The results were further supported by strong performance metrics, with mAP@50 values of 0.988 and 0.97 for positive and negative classifications, respectively, demonstrating its potential for real-time LAMP diagnosis and enhanced assay performance.

CONCLUSION: We have shown that the YOLOv8 object detection algorithm can effectively classify LAMP images with high accuracy on edge devices under field conditions. This approach enhances the interpretation and automation of molecular techniques and contributes to the potential scalability of LAMP applications.

D04

Increased incidence of vancomycin-resistant *Enterococcus faecalis* in a large hospital network, 2022–2024

Nicholas Waglechner[1], Erin Choi[1], Manija Rahimi[1], Patryk Aftanas[1], Robert A Kozak[1,2,3], Xena Li[1,2,4], Kevin Katz[1,2,3,4], Christie Vermeiren[1,3]

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OBJECTIVE: We report a marked increase in vancomycin-resistant *Enterococcus faecalis* (VREfa) identified from routine clinical surveillance specimens in our microbiology laboratory serving multiple hospital networks. *E. faecalis* isolates carrying *vanA* or *vanB* genes were analyzed using whole-genome sequencing (WGS) to investigate the observed increase and its potential significance.

METHOD: Clinical isolates from routine surveillance swabs (nasal/rectal) were confirmed as VREfa by standard laboratory protocol and underwent WGS on the Illumina MiniSeq platform. Sequence data were analyzed with Bactopia for multi-locus sequence typing, antimicrobial resistance detection, and pangenome analysis, including recombination-corrected core-genome alignment and phylogenetic tree construction.

RESULTS: Between 2022 and 2024, 222,826 VRE surveillance screens were performed. VRE-positive screens increased from 378 (0.75%) to 767 (0.86%), while VREfa cases rose from 2 to 34 (0.53% to 4.27%), representing an eight-fold increase. WGS was performed on 32 isolates, along with 2 reference ATCC strains, resulting in 34 sequences. The most frequent sequence type (ST) was ST6 (21 isolates), followed by ST1928 (6 isolates). Other STs included ST881 (two isolates), ST227 (two isolates), and one isolate each of ST776, ST25, ST30, and ST19. One isolate was unassigned. Among these, 18 isolates carried *vanB* and 15 carried *vanA*. Two closely related ST6 clusters (<35 SNPs) were identified: one *vanA* (6 isolates) and one *vanB* (15 isolates). ST227 and ST25 isolates also carried *vanB* but were unrelated to ST6.

CONCLUSION: This significant rise in VREfa, particularly *vanB*-type isolates, highlights emerging resistance patterns. Genomic analysis revealed closely related clusters with no clear epidemiological links, raising concerns about potential undetected transmission pathways. These findings underscore the importance of ongoing enhanced surveillance and infection control measures to mitigate VREfa spread.

RAPID FIRE POSTER PRESENTATIONS

Session A
Wednesday, April 30

RFA001
Epidemiology of cystic echinococcosis in the Canadian Pacific Northwest: a 12-year retrospective review

Calvin K F Lo[1], Suefay H Liu[1,2], Mohammed Al-Abri[3], Martin Cheung[4], Jonathan Laley[4], Muhammad G Morshed[1,4], Maja Segedi[3], Catherine Hogan[1,4], Katherine Plewes[5]

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OBJECTIVE: Human cystic echinococcosis (CE), caused by *Echinococcus granulosus sensu lato*, is a complex neglected parasitic infection. Despite being endemic in Canada, its burden remains unknown because it is not a nationally notifiable disease. This study examined the epidemiology of CE between 2010 and 2022 in the Canadian Pacific Northwest region.

METHOD: A retrospective chart review was conducted on individuals identified through the provincial reference laboratory who were diagnosed with either confirmed, probable, or possible CE (per WHO-IWGE criteria) between January 1, 2010 and December 31, 2022. Demographic characteristics, risk factors, clinical presentation, diagnostics, interventions, and outcome data were collected for analysis.

RESULTS: A total of 41 CE cases (21 confirmed, 1 probable, and 19 possible) were reported during the study period. History of residence outside Canada was documented in 59% of cases. No travel history was reported in 7%, although these individuals resided rurally with close animal contact. The most common cyst location was liver (73%), followed by lung (12%), both liver and lung (7%), and other organs (spleen, muscle, spine; 7%). All individuals in our cohort had diagnostic imaging performed, most commonly CT. Most individuals (95%) also underwent echinococcus serology testing (59% positive, $n = 39$). Additional diagnostics included histopathology (81% positive, $n = 16$), microscopy (77% positive, $n = 13$), and PCR testing (73% positive, $n = 11$). A combination of surgical intervention with antiparasitic treatment was pursued in 51% of cases. Management was unknown in 24% of cases. No deaths were recorded at 12 months post-treatment.

CONCLUSION: Human CE disease is uncommonly acquired and diagnosed in the Canadian Pacific Northwest region, with only 7% of cases acquired locally. However, the diagnosis remains challenging given the asymptomatic

disease course and lack of standardized diagnostic tools. Further efforts are required to optimize diagnostic algorithms and integrate multidisciplinary management to enhance surveillance and care delivery for individuals with CE.

RFA002

Characterizing missed opportunities for definitive oral antimicrobials in prosthetic joint infections: A 1-year review

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OBJECTIVE: Oral antimicrobials are increasingly used as definitive therapy for prosthetic joint infections (PJIs) given evidence of non-inferiority and fewer adverse effects compared to IV antimicrobials. We aimed to evaluate the definitive antimicrobial regimens used in PJI management at two teaching hospitals over a 1-year period, and to assess factors that influenced clinicians' choice of oral versus IV antimicrobials.

METHOD: Admissions for infected hip or knee prostheses meeting the 2011 Musculoskeletal Infection Society (MSIS) definition of PJI were identified over a 1-year period via retrospective chart review. Medical and surgical strategies used were documented, and a web-based survey was sent to Infectious Disease and Orthopedics physicians at our institution. A case was adjudicated as an opportunity for definitive oral antimicrobial therapy if the following criteria were met: no concurrent infection requiring IV therapy, identifiable pathogen susceptible to at least one highly bioavailable oral antimicrobial, no history of impaired gastrointestinal absorption, and weight <100 kg.

RESULTS: Forty-eight hip or knee PJIs were identified. Two-stage revision arthroplasty was the most common surgical strategy employed (22/48, 45.8%), followed by debridement and implant retention (15/48, 31.3%). Infectious Diseases was consulted in all cases. Definitive IV antimicrobial therapy was used in 83% of cases compared to definitive oral therapy in 17%. Of the 25 cases adjudicated to be opportunities for definitive oral antimicrobial therapy, oral antimicrobials were only used in 5 (20%). All physicians surveyed felt culture-negative infection was a significant consideration favouring use of IV antimicrobials (>70% agreement among respondents).

CONCLUSION: Eighty percent of opportunities to use definitive oral antimicrobials for PJI were missed at our institution, representing a significant opportunity for quality improvement. An institutional consensus guideline for PJI antimicrobial therapy was created based on feedback from stakeholders. Follow-up data will be collected for comparison.

RFA003

Linking two worlds: Harnessing metabolomics and lipidomics to elucidate the mechanisms of the *mleN*ΔA467 compensatory mutation of ceftriaxone-resistant *Neisseria gonorrhoeae*

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OBJECTIVE: *Neisseria gonorrhoeae* caused an estimated 82.4 million infections globally in 2020 and has become a global concern due to its rapid development of antimicrobial resistance. Ceftriaxone-resistant strains with the *penA41* resistance mutation exhibit impaired growth compared to susceptible strains. However, resistant bacteria can acquire compensatory mutations to restore growth, such as a *mleN* gene codon deletion (*mleN*ΔA467), which encodes a putative malate/lactate antiporter. This combination will increase infection morbidity worldwide, highlighting the need for comprehensive biochemical maps of *N. gonorrhoeae* to combat this superbug. The overarching goal of this project is to investigate how the unfit ceftriaxone-resistant strain (*penA41*) and its compensatory mutation, *mleN*ΔA467, influence bacterial metabolism to confer resistance and increase fitness. Since these mutated genes encode membrane proteins involved in cell wall synthesis and metabolite transport, we hypothesize this will alter lipid metabolic pathways.

METHOD: We analyzed the metabolome and lipidome of a ceftriaxone-susceptible strain (FA19), a modified ceftriaxone-resistant FA19 strain (FA19 *penA41*), and two strains with the *mleN*ΔA467 compensatory mutation (FA19 *mleN*ΔA467 and FA19 *penA41 mleN*ΔA467). Bacteria were cultured in Graver-Wade medium. Metabolites were analyzed by liquid chromatography-mass spectrometry (LC-MS) semi-targeted metabolomics. Lipids were extracted using a modified Folch method and analyzed using LC-MS/MS.

RESULTS: Extracellular metabolomics revealed alterations in tricarboxylic acid intermediates and increased lysine production in compensatory mutants, suggesting that metabolic alterations and energy pathways are associated with restoring biological fitness in FA19 *penA41 mleN*ΔA467. Preliminary untargeted lipidomics emphasized phospholipid composition changes in compensatory mutants. Intracellular triacylglycerols and phosphatidylglycerols were particularly affected in ceftriaxone-resistant strain with *mleN*Δ*A467*.

CONCLUSION: The results highlight the critical role of the *mleN*ΔA467 compensatory mutation in enhancing the fitness of ceftriaxone-resistant *N. gonorrhoeae* through metabolic alterations. Future work will refine metabolomics and lipidomics protocols to further investigate antimicrobial resistance and compensatory mechanisms.

RFA004

A retrospective comparison study of samples collected intraoperatively for the diagnosis of bacterial infection

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OBJECTIVE: Swabs are not considered the optimal specimen choice in many clinical scenarios. Choosing Wisely Canada recommends that swabs should not be routinely obtained during surgical procedures. The aim of this quality improvement initiative was to compare the diagnostic quality of swabs versus fluid or tissue for the intraoperative diagnosis of bacterial infection.

METHOD: All patients who had intraoperative specimens—swabs, tissue, or fluid—collected at a large tertiary hospital between November 2022 to March 2023 were included in this study. A retrospective chart review was performed to determine clinical outcomes.

RESULTS: A total of 821 operation room (OR) visits occurred during the specified time period. In 179 cases we received swabs only and in 489 cases we received fluid or tissue only. A total of 144 patients (153 procedures) submitted both a swab and fluid or tissue for bacterial culture. In patients with both swabs and fluid or tissue, the total number of samples collected included 208 aerobic swabs, 204 anaerobic swabs, 27 fluids, and 387 tissues. The average number of samples submitted per OR visit was 5.4. An organism was deemed a likely contaminant if this was stated in the clinical notes or if antibiotics administered did not provide coverage for the organism. Otherwise, it was considered a probable pathogen. The proportion of cases where fluid/tissue samples identified a probable pathogen and swabs did not was 20.2%. The proportion of cases where swabs identified a probable pathogen and fluid/tissue samples did not was 12.0%. The proportion of OR visits in which swabs, fluids, and tissues yielded a clinically determined contaminant was 27%, 0%, and 16%, respectively.

CONCLUSION: Intraoperative swabs are more likely to miss probable pathogens relative to optimal specimen types. Swabs also display a significantly higher proportion of contaminants identified, which can lead to unnecessary antibiotic treatment.

RFA005

Beyond the matrix: Rethinking antibiotic tolerance in CF biofilms using 3D models

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OBJECTIVE: While antimicrobial therapies have been intensively developed, no clear explanation exists for the extreme tolerance of cystic fibrosis (CF) biofilms to antibiotics. We address how and why these biofilms are impossible to eradicate by studying the influence of the biofilm matrix and developing a platform to simplify and speed up such studies.

METHOD: Commercial alginate was chemically modified to mimic the degree of acetylation of *in vivo* bacterial alginate, mixed with eDNA and *P. aeruginosa* and used as bioink to print 3D biofilms. Minimum inhibitory and bactericidal concentrations of Tobramycin, Ciprofloxacin, Meropenem, Colistin, and Aztreonam were determined for the PAO1 strain, followed by kill-curve assays to evaluate antibiotic efficacy. Live-dead fluorescence microscopy and (cryo)-scanning electron microscopy assessed the impact of antibiotics on bacterial viability and biofilm structure. A penetration model explored interactions between alginate (±eDNA) and antibiotics.

RESULTS: *P. aeruginosa* thrived in the printed bacterial alginate, forming microcolonies similar in appearance to *in vivo* biofilms. We demonstrated that modified alginate and eDNA act as barriers to antibiotic penetration. However, penetration rates improve over time, reaching almost 100% for most antibiotics by 8–20 hours, regardless of the matrix type (with or without eDNA). Overnight antibiotic assays further indicate that acetylation reduces antibiotic effectiveness when compared to non-acetylated alginate. However, eDNA appears to counteract this reduction in efficacy, possibly by stabilizing biofilm structure. The addition of eDNA enhances antibiotic efficacy by reducing CFU/mL to lower levels compared to non-acetylated and acetylated alginate conditions.

CONCLUSION: These results challenge the conventional understanding of biofilm tolerance mechanisms focused on biofilm matrix barrier properties. These findings will open the door to new therapeutic strategies that target beyond the matrix barrier by concentrating on disrupting bacterial stress responses, quorum sensing, and metabolic adaptations within the biofilm environment as the likely mechanisms for CF biofilm antibiotics tolerance.

RFA006

Trends in antimicrobial resistance among Gram-negative organisms in an academic tertiary care laboratory between January 2013 and December 2024: A continued rise in MDRO and XDRO *Klebsiella pneumoniae*

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OBJECTIVE: The emergence of multidrug-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 in a tertiary care academic clinical laboratory serving four acute care hospitals.

METHOD: Susceptibility testing results from January 2013 through December 2024 were collected for *Enterobacterales* spp. (avg. n = 6,188/yr), *Pseudomonas aeruginosa*

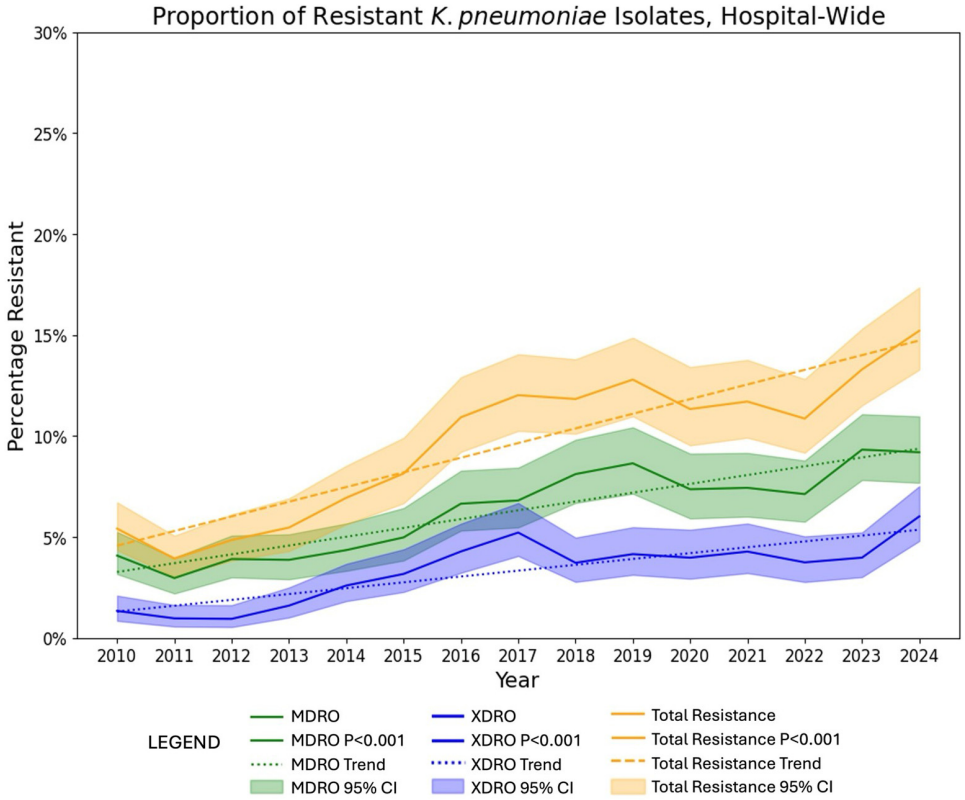

Figure RFA006-01: Proportion of MDRO, XDRO, and total resistance among *K. pneumoniae isolates* hospital-wide between 2010 and 2024. Data from 2010–2012 included to demonstrate the relative stability in resistance prior to 2013.

(avg. n = 1,219/yr), and *Acinetobacter* spp. (avg. n = 66/yr) isolated from all specimen types. Among *Enterobacterales* spp., *E. coli* (avg. n = 4,257/yr) and *K. pneumoniae* (avg. n = 1,198/yr) were predominant. For each category of organisms, each patient was represented only once per year. Using CPHLN and CACMID definitions, *Enterobacterales* isolates were classified as either multidrug-resistant (MDRO) or extensively drug resistant (XDRO), while *P. aeruginosa* and *Acinetobacter* spp. isolates were classified as XDRO. The modified Wald method was used to calculate 95% confidence interval, and Chi-square was used to calculate test for trends.

RESULTS: From 2013 to 2024, resistance among *K. pneumoniae* increased steadily, from 5.5% to 15.2% ($p < .001$). This was driven primarily by MDRO organisms, which increased from 3.9% to 9.2% ($p < .001$). XDRO resistance also increased significantly, from 1.6% to 6.0% ($p = .014$). Resistance among *E. coli* also increased, from 14.6% to ss20.4% ($p = .002$). This trend was also driven by MDRO organisms, which increased from 10.9% to 17.8% ($p < .001$). XDRO resistance decreased slightly, from 3.7% to 2.6% ($p < .001$). By contrast, the proportion of XDRO *P. aeruginosa* decreased significantly hospital-wide, from 4.2% to 0.5% ($p < .001$). XDRO *Acinetobacter* spp. displayed no significant trends, owing to insufficient data.

CONCLUSION: Over the time period under study, *K. pneumoniae* has emerged as an organism of concern for multidrug resistance. MDRO and XDRO rates have increased dramatically, highlighting a need for increased surveillance and stewardship for this overlooked organism (Figure RFA006-01). By contrast, XDRO rates among *E. coli* and *P. aeruginosa* have decreased.

RFA007

Antimicrobial stewardship audit and feedback to reduce unnecessary oral antibiotic prescribing: a single-centre, quasi-experiment pilot study

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OBJECTIVE: The rising prevalence of antibiotic-resistant organisms restricts available treatment options, with greater risk to patient morbidity. Hospital discharges represent key transitional care points for intervention, with 65% of patients reportedly prescribed inappropriate antibiotics. Despite existing guidelines for routinely encountered infections (eg, urinary tract infections [UTI], pneumonia), inappropriate discharge prescriptions are commonly observed. Our study evaluated a novel approach of audit and feedback over 3 months, intervening on oral antibiotic prescriptions of patients discharged from Internal Medicine Clinical Teaching Units (CTU).

METHOD: A single-centre study was conducted at a tertiary care teaching hospital from July through September 2024. Patients discharged on oral antibiotics for acute infection from CTU were included. The Antimicrobial Stewardship Program team conducted a real-time audit and provided feedback on antibiotic appropriateness based on duration or spectrum of coverage. The number of appropriate discharge antibiotics during the 3-month intervention period was compared to the number of appropriate CTU discharge prescriptions in the pre-intervention period (ie, October 2023–March 2024).

RESULTS: One hundred twenty-one patients were prescribed antibiotics upon discharge during the intervention periods (total of 133 antibiotics). Compared to the pre-intervention period, appropriate antibiotic prescription significantly increased from 50% to 83% post-intervention ($p < .001$). Median discharge days decreased from 5 days to 4 days ($p < .001$) and total therapy decreased from 9 days to 7 days ($p = .012$). In the sub-analysis for patients with uncomplicated pneumonia, UTIs, and skin and soft tissue infections, there was a statistically significant increase in appropriate discharge prescriptions between pre-intervention and post-intervention periods (41% versus 81%, $p < .001$).

CONCLUSION: This study demonstrated the effectiveness of implementing structured antimicrobial stewardship review at the time of patient discharge. Our findings support the value of incorporating communication of AMS interventions amidst usual patient discharge workflow to

improve appropriate antibiotic prescribing at transitional points in patient care.

RFA008

Utility of cytomegalovirus (CMV) qualitative polymerase chain reaction from gastrointestinal biopsies in predicting the diagnosis of CMV gastrointestinal disease: a 10-year retrospective study

Cole Schonhofer[1], Calvin K F Lo[1], Daniel R Owen[1], Khuloud Aldhaheri[2,3], Nancy Matic[1,4], Christopher F Lowe[1,4], David F Schaeffer[1], Sarah Belga[2], Alissa Wright[2]

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OBJECTIVE: The gold standard for cytomegalovirus (CMV) gastrointestinal (GI) disease diagnosis is histopathological examination of tissue biopsies. However, histopathology is time consuming and can produce equivocal results. Although less invasive, plasma CMV viral load (CVL) is thought to have limited accuracy in diagnosis of CMV GI disease. The utility of tissue PCR for diagnosis of CMV GI disease is still debated. We conducted a retrospective study comparing tissue PCR to histopathology for diagnosis of CMV GI disease.

METHOD: We included patients who had endoscopic tissue biopsies with histopathology and CMV tissue PCR results between February 2014 and January 2024. Sensitivity, specificity, and receiver operating characteristic (ROC) curves were calculated to assess tissue PCR accuracy compared to histopathology (gold standard). Multivariable logistic regression was used to evaluate potential predictors of CMV GI disease, including age, sex, plasma CVL, lymphocyte count, and underlying diagnosis (solid organ transplant, bone marrow transplant [BMT], and autoimmune conditions).

RESULTS: Five hundred thirty-four patients underwent 637 total endoscopies, with 84/534 (15.7%) undergoing 2 or more procedures. Histopathologic evidence of CMV disease was found in 41/637 biopsies (6.4%) and in 37/534 patients (6.9%). Compared to histopathology, CMV tissue PCR had 100% sensitivity (100% negative predictive value) and 72% specificity (19% positive predictive value). Area under ROC curve (AUC) was 0.86 (95% CI 0.84–0.88). Multivariable analysis demonstrated CVL > 1,000 IU/ml was significantly associated with histopathologically proven CMV GI disease (adjusted odds ratio = 32.3, 95% CI 10.3–101.0), while BMT diagnosis was negatively associated (adjusted odds ratio = 0.05, 95% CI 0.01–0.35).

CONCLUSION: CMV tissue PCR correctly identified CMV GI disease in 100% of histopathologically proven cases. Specificity was poor, potentially reflecting detection of viral shedding. Overall, our study suggests that use of tissue PCR should be limited to ruling out rather than diagnosing CMV GI disease. Further studies could assess correlations between plasma CVL, tissue PCR, and underlying diagnoses.

RFA009

The prevalence of candidemia in patients with candiduria

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OBJECTIVE: Candiduria is common among hospitalized patients in large part due to excessive and unnecessary sampling of urine. While typically asymptomatic and benign, many patients receive antifungals unnecessarily. Furthermore, the rate of invasive fungal infection related to candiduria is cited as low. We aimed to review the local prevalence of candiduria and the associated rates of candidemia among inpatients.

METHOD: This was a retrospective cohort study conducted in an academic hospital from January 1, 2023 to July 31, 2024. Adult inpatients with a urine culture positive for *Candida* species were reviewed. Duplicates were removed, and a randomized sample was used for chart review including demographics, comorbidities, antibiotic use, urine culture results, blood culture results within 90 days of candiduria, and antifungal therapy.

RESULTS: During the study period there were 611 unique inpatients with candiduria. Of them, 377 (61.7%) urine samples were from catheters, 189 (30.9%) from midstream, 30 (4.9%) from cystoscopy, and 14 (2.2%) from nephrostomy tubes. Of the randomized sample of 199 patients, candidemia was only identified in 10 (5%) Most of the blood cultures (8/10) were positive within 48 hours of the urine culture. The remaining two were candidemic after 48 hours. All patients with candidemia had received antibiotics within 30 days prior to the onset of candiduria and candidemia. *Candida albicans* was identified in five patients, non-*albicans* in five patients, and mixed species (*albicans* and non-*albicans*) in one patient.

CONCLUSION: This study underscores the low rate of candidemia in the setting of candiduria. In most cases, candidemia and candiduria were detected at the same time. Therefore, candiduria did not lead to invasive fungal infection within 90 days. Future analysis will review all candiduria patients for assessment of symptoms and antifungal use.

RFA010

Monkeypox virus shedding despite tecovirimat treatment in a Canadian cohort

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OBJECTIVE: During the 2022 mpox outbreak, tecovirimat (TPOXX™), a smallpox antiviral, was used to treat mpox infections in Canada. We examined the shedding of infectious mpox virus (MPXV) in skin lesion swabs from tecovirimat-treated and untreated individuals and investigated potential resistance mutations.

METHOD: Participants with laboratory-confirmed mpox infection were prescribed tecovirimat between June 20 and August 12, 2022, and provided up to three weekly skin lesion swabs. Viable MPXV was quantified using $TCID_{50}$ assays on VeroE6 cells and observing cytopathic effects over time, and the tecovirimat target protein VP37 was sequenced to detect resistance mutations.

RESULTS: Viable MPXV was detected in 31% (17/55) of lesions from tecovirimat-treated individuals ($n = 9$) and 34% (21/62) from untreated individuals ($n = 8$) with no significant difference in duration of shedding between groups. All untreated individuals shed infectious MPXV in at least one lesion for up to 9 days post-symptom onset, with five out of eight shedding beyond 2 weeks. Among tecovirimat-treated participants, three out of nine still had viable MPXV after 7 days of treatment, including up to 15 days after starting tecovirimat (44 days following symptom onset). While some lesions did not yield viable virus, low infectious levels of MPXV were inferred from Ct values in 4/55 and 5/62 lesions to date from treated and untreated participants, respectively. Sequencing of 24 lesion swabs identified no novel mutations in the *VP37* gene from either treated and untreated individuals, including pre- and post-treatment samples, suggesting that tecovirimat resistance mutations were not widely circulating in this cohort during the 2022 outbreak.

CONCLUSION: Tecovirimat treatment did not appear to significantly alter the duration of viable MPXV shedding in this cohort, offering insights into recent negative clinical trial findings. While no resistance mutations were identified in this cohort, this study highlights the need for further research to evaluate the clinical utility of tecovirimat in treating mpox infections.

RFA011

A 5-year retrospective review of antimicrobial susceptibility trends for AmpC-producing *Enterobacterales* in Western Canada

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OBJECTIVE: Current Infectious Diseases Society of America guidelines and literature support the use of cefepime as a carbapenem-sparing agent to treat infections due to inducible AmpC-producing organisms. To better understand local susceptibility trends for AmpC-producing *Enterobacterales*, we conducted a 5-year retrospective review of minimum inhibitory concentration (MIC) distributions for ceftriaxone, cefepime, piperacillin-tazobactam (PTZ), and

meropenem across a geographic health authority in western Canada.

METHOD: MIC data were retrieved from the BD Epicentre™ system for isolates collected between November 2019 and October 2024. We included isolates obtained from blood cultures, invasive specimens, or urine/miscellaneous samples that identified moderate-risk inducible AmpC (MRAC; eg, *Citrobacter freundii* complex, *Enterobacter cloacae* complex [*E. cloacae*], *Klebsiella aerogenes*) or low-risk inducible AmpC (LRAC; eg, *Serratia marcescens*, *Providencia rettgeri*, *Morganella morganii*) producing organisms. Surveillance and screening samples were excluded. MIC values were compared for ceftriaxone, cefepime, PTZ, and meropenem using CLSI M100-E34 breakpoints for *Enterobacterales*. Descriptive statistics were computed for each antimicrobial and bacterial species.

RESULTS: A total of 5,809 isolates were analyzed, with 3,646 (62.8%) identified as MRAC. The most common MRAC and LRAC species were *E. cloacae* (45.7%) and *M. morganii* (43.8%), respectively. Across all organisms, susceptibility rates for ceftriaxone (MIC $\leq$ 1 µg/ml), PTZ (MIC $\leq$ 8 µg/ml), cefepime (MIC $\leq$ 2 µg/ml), and meropenem (MIC $\leq$ 1 µg/ml) were 81.6%, 87.4%, 95.5%, and 98.7%, respectively. MRAC organisms demonstrated lower susceptibility to ceftriaxone (76%) and PTZ (81.5%) compared to LRAC (91.1% and 97.3%, respectively). Cefepime and meropenem demonstrated similar susceptibility rates for MRAC (93.6% versus 99.0%) and LRAC (99% for both). MIC_{50} and MIC_{90} for cefepime were 1 µg/ml for all species except *E. cloacae*, for which MIC_{90} was 4 µg/ml.

CONCLUSION: Over the past 5 years, 95.5% of AmpC isolates demonstrated susceptibility to cefepime. Further research is necessary to correlate these findings with patient outcomes and establish MIC thresholds to guide routine testing and clinical use of cefepime.

RFA012
Review of poliovirus serology requests in a Canadian province (2023–2024)

Charlotte Rosen[1], Nathan Zelyas[2,3], Hong Yuan Zhou[1,4], Byron Berenger[1,4], Karla Gustafson[1], Jamil N Kanji[1,4]

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OBJECTIVE: The National Advisory Committee on Immunization (NACI) advises against routine poliovirus serology (POLV-S) testing for poliovirus (POLV) immunity, recommending age-appropriate re-vaccination when vaccination history is unknown. POLV-S tests strain laboratory resources, often result in unnecessary phlebotomy, and are frequently canceled due to a lack of test availability. This study assessed 1 year of provincial POLV-S requests to assess for gaps in adherence to national guidelines.

METHOD: Data on POLV-S requests from July 1, 2023 to December 31, 2024 were obtained from the laboratory information system and provincial physician registry (provincial population of 4.9 million). Patient demographics, physician specialty, years of experience, provided history, reasons for testing, availability of vaccine records, and additional serologies ordered were analyzed.

RESULTS: Of 108 POLV-S requests (requested by 77 physicians), the median patient age was 34.5 years (71.3% female). All ordering physicians were general practitioners (median 10 years of experience, range 1–40). Only 3 (2.8%) requests were for POLV-S alone; 105 (97.2%) included a median of 7 additional serology tests, most commonly measles, rubella, and mumps IgG (89.8–90.7%). Patient history was absent in 86 (79.6%) requests. Testing was primarily for employment (45.5%), occupational health forms (27.3%), immigration (13.6%), and immunity verification (13.6%). Vaccine records were available for 39 (36.1%) patients, of which 28 (72.0%) lacked documentation of a POLV vaccine date. POLV vaccine dates were recorded for 11 (10.2%) patients, with a median interval of 5,792 days (range 8–8,410) since vaccination.

CONCLUSION: Our findings highlight the need to educate clinicians on NACI guidelines to reduce unnecessary POLV-S testing. While the number of requests was low compared to the provincial population, it was felt to be high given the national guidance. Promoting re-vaccination when vaccination history is unknown can minimize unnecessary phlebotomy, improve laboratory efficiency, and enhance immunity in individuals with uncertain POLV status.

RAPID FIRE PRESENTATIONS

Session B
Wednesday, April 30

RFB001
Evaluation of a syphilis point-of-care test at a high-volume urban sexually transmitted infection clinic in Canada

Kathleen Whyte[1], Katrina Yuen[2], Maya Tharp[2], Ramin Azmin[2], Ian Hunter[2], Brody Lyons[2], Eri Flores[2], Muhammad G Morshed[3], Raymond Tsang[1], Troy Grennan[2,4]

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OBJECTIVE: Determine the performance characteristics of a *Treponema pallidum* (syphilis) antibody point-of-care test (POCT) used in a population seeking sexually transmitted infection (STI) care at a high-volume clinic in urban Canada, compared to standard syphilis serology (enzyme immunoassay [EIA]). Additionally, to determine feasibility of POCT use by assessing participant and health care provider (HCP) acceptability of the POCT.

METHOD: Reveal Rapid TP Antibody Test was offered to patients aged 19 years and older attending the clinic and requiring conventional syphilis serology as part of routine STI screening. Those consenting to participate provided a fingerstick blood specimen for use with the POCT and completed a brief survey. POCT performance was compared with the results of conventional serology. HCPs also completed an acceptability survey.

RESULTS: In total, there were 525 POCT completed and available for analysis. Median age was 32, and 66.9% were male. For detection of antibodies to treponemal antigens, the performance characteristics of the POCT when compared to EIA were as follows: sensitivity 71.3% (95% confidence interval [CI] 63.0–78.7); specificity 97.9% (95% CI 96.0–99.1). The POCT was reactive for 8/13 (61.5%) cases of newly diagnosed syphilis infections; however, it was nonreactive in 5/6 (83.3%) primary infections diagnosed. A majority of participants (81.6%) were satisfied with the overall POCT experience, and all HCPs felt the POCT to be acceptable.

CONCLUSION: When used in conjunction with clinical assessment and patient history, the Reveal Rapid TP Antibody Test POCT performed very well for identifying both new and previous syphilis at an urban Canadian STI clinic. It may not be reliable for very early (ie, primary) infections, though this would need replication with a larger sample size. Both participants and providers found the test to be acceptable, suggesting that this assay is a feasible option in select populations seeking STI screening.

RFB002

Diagnostic yield of clinical metagenomics for sterile site infections: A 5-year prospective study

Mohammad Rubayet Hasan[1,2,3], Anju Sharma[4], Sathyavathi Sundararaju[4], Mohammed Suleiman[4], Clement Kin-Ming Tsui[5,6], Andres Perez-Lopez[4,7], Patrick Tang[6,8]

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OBJECTIVE: Infections of normally sterile sites cause significant morbidity and mortality, but the etiology often remains unknown. Metagenomic next-generation sequencing (mNGS) is an emerging diagnostic approach that has the potential to detect all potential pathogens. This prospective study assessed the diagnostic yield of mNGS in sterile site infections over 5 years.

METHOD: mNGS was evaluated using both simulated sterile site (SS) specimens (including blood and cerebrospinal fluid) and retrospective SS specimens previously tested using conventional methods. Additionally, specimens that were negative by culture and PCR were prospectively tested using mNGS and Sanger sequencing for bacterial 16S rDNA, fungal ITS rDNA, and mycobacterial *hsp65* (16S/ITS/*hsp65*). Sanger sequencing was performed on the ABI3500 while mNGS shotgun DNA libraries were prepared with Nextera XT and sequenced on an Illumina MiSeq. Metagenomic data were analyzed using CZ ID pipeline (https://czid.org/).

RESULTS: In 15 simulated SS specimens spiked with bacterial and viral pathogens, mNGS results showed 67%–90% agreement with qPCR for the respective pathogens. For 17 retrospective culture-positive/negative specimens, the agreement with mNGS was 82.4%. A total of 179 specimens (negative by culture and PCR) from cases of central nervous system infections, endocarditis, and other infections were tested prospectively using 16S/ITS/*hsp65*, of which 93 were also tested by mNGS. The overall positivity rates for 16S/ITS/*hsp65* sequencing and mNGS were 27.9% and 21.5%, respectively ($\chi^2 = 1.3$, $p = .25$). Compared to 16S/ITS/*hsp65* sequencing, mNGS demonstrated a sensitivity of 70% (95% CI 45.7–88.1), a specificity of 91%

(95% CI 84.7–97.7), and an overall accuracy of 86% (95% CI 77.7–92.5).

CONCLUSION: Although mNGS shows promise as a diagnostic tool, its cost effectiveness compared to traditional methods needs further evaluation. Targeted sequencing for specific group of pathogens might be a more practical approach for most cases of SS infections. An assessment of the clinical impact of these results is ongoing.

RFB003

Assessing the burden of nosocomial antimicrobial resistance by comparing the wastewater resistome of tertiary care hospitals in Calgary to the overall community

Nicole Acosta[1], Jangwoo Lee[1], Emily Au[1], Barbara J Waddell[1], Kristine Du[1], Matthew J Penney[1], Bruce Dalton[2], Maria A Bautista[1], Rhonda Clark[1], Benson Weyant[1,2], Johann D Pitout[1], Joseph Kim[1,2], Bayan Missaghi[1,2], Oscar Larios[1,2], Jenine Leal[1], Elissa Rennert-May[1,2], Jamil N Kanji[1,2], Paul Westlund[3], Christine O'Grady[1], John Conly[1,2], Casey R J Hubert[1], Michael D Parkins[1,2]

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OBJECTIVE: Hospitalized patients are susceptible to acquiring infections from antimicrobial-resistant organisms (AMROs), highlighting the importance of creating adaptable tools to understand, predict, and prevent them. Wastewater-based surveillance (WBS) can comprehensively and inclusively monitor for AMR in near real time. We sought to compare the abundance of antimicrobial resistance genes (ARG) in sewage from three tertiary care hospitals (one paediatric/two adult hospitals) with a municipal wastewater treatment plant (WWTP).

METHOD: Composite wastewater was collected from March 2022 through December 2023. DNA extraction was performed from wastewater pellets followed by Illumina sequencing and DeepARG-SL analysis. ARG burden is presented as copies of each ARG/16S-rRNA gene. Alpha and beta diversity was analyzed by calculating richness and Bray-Curtis dissimilarity. Dunn, Mann-Whitney, and ANOSIM tests were conducted using R.

RESULTS: From 114 samples, ARG sequences were categorized into 28 ARG types and 1,342 ARG subtypes. The most dominant ARG types included multidrug resistance genes (23.2%), MLS (18.1%), and beta-lactam resistance genes (15.3%), where beta-lactams were the most diverse. Key high-priority ARGs (ie, bla_{KPC}, bla_{NDM}, bla_{OXA}, *vanA*, and *qnrS*) were significantly more abundant in hospitals compared to WWTP ($p < .0001$, Dunn's Test). ARG abundance in hospitals fluctuated more over time than in the community. There were differences in the alpha diversity among hospital and WWTP samples when Richness ($p = .003$, Mann-Whitney) was analyzed. To test whether there was a significant difference between groups, ANOSIM test was performed and showed that the resistomes were found to be distinguishable by location ($R = 0.419$, $p = .0001$).

CONCLUSION: The resistome of hospital wastewater differs markedly from that of the community. Clinically relevant ARGs were found at higher abundance in hospitals, and their burden was highly dynamic, consistent with a rapidly changing hospital population. WBS has the potential to augment infection prevention and control and antimicrobial stewardship programs, providing near real-time data on the hospital resistome.

RFB004

Integrated safety analysis of fecal microbiota, live-jslm (RBL) in preventing recurrent *Clostridioides difficile* infection from 3 prospective clinical studies and efficacy outcomes from a phase 3 open-label study: Subgroup analyses of Canadian participants

Thomas Louie[1], Theodore S Steiner[2], Dina Kao[3], Dan Smyth[4], Beth Guthmueller[5], Tracey Jason[6], Susan N Elliott[6], Shivam Srivastava[7], Christine Lee[8]

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OBJECTIVE: Fecal microbiota, live-jslm (RBL) was approved by the US Food and Drug Administration for preventing recurrent *Clostridioides difficile* infection (rCDI) in adults following standard-of-care (SOC) antibiotic treatment. A prospective phase 3, open-label study (PUNCH CD3-OLS; NCT03931941) recruited a wider patient population with diverse comorbidities and reported RBL was safe and efficacious for preventing rCDI. Prior integrated safety analyses demonstrated good tolerability. This analysis evaluated the safety of RBL in Canadian participants from

three prospective clinical studies and efficacy of RBL from PUNCH CD3-OLS.

METHOD: Participants were aged ≥18 years with documented rCDI and completed SOC antibiotics. One dose of RBL was administered 24–72 hours after SOC antibiotic completion. Safety data were combined from one phase 2 (PUNCH CD2 [NCT02299570]) and two phase 3 studies of RBL (PUNCH CD3 [NCT03244644], PUNCH CD3-OLS). Treatment-emergent adverse events (TEAEs) were recorded for a minimum of 6 months and up to 24 months. Treatment success was evaluated at 8 weeks and sustained clinical response at 6 months after RBL administration.

RESULTS: Participants in Canada and the United States were mostly White and female; the median age was 63 years. Seven hundred forty-four participants (Canada, $N = 141$; US, $N = 603$) received one dose of RBL. TEAEs were reported in 76.6% of Canadian participants (108/141); most were gastrointestinal and of mild-to-moderate severity. Serious TEAEs occurred in 11.3% of Canadian participants (16/141) with no clustering; most were related to CDI recurrence and/or preexisting conditions. In PUNCH CD3-OLS, 75.2% of Canadian participants (88/117) achieved treatment success at 8 weeks; 90.9% (80/88) had a sustained clinical response at 6 months. Safety and efficacy outcomes were similar between Canadian and US participants.

CONCLUSION: RBL was well tolerated in Canadian adults with rCDI across three clinical studies and efficacious in preventing rCDI among Canadian participants from PUNCH CD3-OLS.

RFB005

Preparedness for *Candida auris* in Canadian Nosocomial Infection Surveillance Program hospitals, 2024

Charlie Tan[1], Amrita Bharat[2], Erin McGill[3], Robyn Mitchell[3], Olivia Varsaneux[3], Kristine Cannon[4], Marthe K Charles[5], Jeannette L Comeau[6], Ian Davis[7], Johan Delport[8], Tanis Dingle[9], Janine Domingos[10], Philippe J Dufresne[11], Chelsey Ellis[12], Jennifer Ellison[4], Amna Faheem[13], Charles Frenette[14], Linda Hoang[15], Susy Hota[16], Kevin C Katz[17], Pamela Kibsey[18], Julianne V Kus[19], Bonita Lee[20], Xena Li[21,22], Yves Longtin[23], Kathy Malejczyk[24], Shazia Masud[25], Dominik Mertz[26], Sonja Musto[27], Kishori Naik[28], Senthuri Paramalingam[29], Susan M Poutanen[30], Dale Purych[25], Stephanie W Smith[31], Jocelyn A Srigley[32], Reena Titoria[33], Jen Tomlinson[27], Kathleen (Xuetao) Wang[34], Titus Wong[35], Deborah Yamamura[36], Allison McGeer[37]

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OBJECTIVE: To assess the state of *Candida auris* preparedness in Canadian hospitals.

METHOD: A cross-sectional survey of Canadian Nosocomial Infection Surveillance Program (CNISP) hospitals was conducted. In June 2024, surveys were e-mailed to infection prevention and control (IPAC) departments at CNISP hospitals and their microbiology laboratories, assessing policies for patient screening, managing colonized/infected and exposed patients, laboratory methods for *Candida* identification and susceptibility testing, and processing screening specimens. Results were compared to a previous survey from 2018.

RESULTS: All 109 hospitals and 32/33 laboratories completed the surveys. Most hospitals had policies for admission (78%, 85/109) and post-exposure (82%, 89/109) screening. In the 56 hospitals completing both 2018 and 2024 surveys, screening policies increased from 18% to 73% ($p < .001$). Admission screening included patients with recent (<12 months) out-of-country hospitalization in 55% (60/109) of hospitals. Overall, 99% (108/109) of hospitals implemented transmission-based precautions for cases (private room, donning gowns/gloves, enhanced cleaning/disinfection); 90% (98/109) required dedicated equipment. Most hospitals (70%, 76/109) continued precautions indefinitely for cases. Overall, 82% (89/109) screened and implemented precautions for exposed roommates; 50% (54/109) screened exposed wardmates. Frequency and timing of screening for exposed patients, and policies for discontinuation of precautions for exposed roommates varied. All hospitals used axilla and groin swabs (pooled or separate), at minimum, for screening. The majority (81%, 26/32) of laboratories identified all clinically significant *Candida* isolates to species level; this increased from 48% to 85% ($p < .001$) in the 27 laboratories completing both 2018 and 2024 surveys. Twenty-four laboratories (75%) processed screening specimens in-house and had standard operating procedures. Most (96%, 23/24) plated directly onto chromogenic agar. A variety of incubation temperatures and times were used.

CONCLUSION: Hospitals and laboratories have made progress in *C. auris* preparedness, but areas for improvement remain. This study identified variability in practices, possibly relating to evidence gaps and resource constraints.

RFB006

Wastewater-based and clinical surveillance of *Mycoplasma pneumoniae* prevalence and macrolide resistance

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OBJECTIVE: *Mycoplasma pneumoniae* occurs endemically across the globe, with outbreaks typically occurring every 3–7 years. Widespread surveillance and clinical testing of *M. pneumoniae* is often sparse in between outbreaks. Here, our goal was to develop and optimize a method for the surveillance of *M. pneumoniae* in wastewater from a large city centre. We tracked the prevalence of *M. pneumoniae*, compared the wastewater levels to local clinical testing data, and determined the proportion of *M. pneumoniae* mutations associated with resistance to macrolides.

METHOD: Wastewater samples were collected as 24-hour composite samples three times per week from raw influent at a large catchment wastewater treatment plant. *M. pneumoniae* was tracked using a quantitative polymerase chain reaction (qPCR) assay with a quantitative standard. Mutations conferring macrolide resistance were detected using next-generation sequencing of targeted amplicons. Clinical lab data were aggregated on a weekly basis for positive tests in the community, and clinical testing for macrolide resistance was determined using mutation-specific qPCR probes.

RESULTS: A novel qPCR assay was successfully developed and optimized to specifically detect *M. pneumoniae* and not closely related species present in wastewater. The prevalence of *M. pneumoniae* in wastewater was detected and quantified during a recent increase in cases, and this quantitative wastewater data correlated with local positive tests from the clinical data. Moreover, the proportion of wild-type and mutant forms of the ribosomal RNA *23S* gene in *M. pneumoniae* were quantified following sequencing and alignment to the *M. pneumoniae* genome and compared to local clinical data.

CONCLUSION: Here, we have developed an assay that quantitatively tracks the prevalence of *M. pneumoniae* and the presence of mutations conferring macrolide resistance in wastewater that correlates with local clinical testing data during a recent peak in *M. pneumoniae* cases.

RFB007

Building capacity for confirmatory point-of-care testing for STBBIs in underserved populations across Canada

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OBJECTIVE: To address health inequities by increasing accessibility to confirmatory testing for sexually transmitted and bloodborne infections (STBBIs). This is achieved through building capacity and providing quality oversight for molecular-based point-of-care testing (POCT) in community-based institutions serving underserved and undiagnosed populations in Canada.

METHOD: During the COVID-19 pandemic, the Public Health Agency of Canada's (PHAC) National Microbiology Laboratory Branch (NMLB) established a POCT network for SARS-CoV-2. Post-pandemic, this infrastructure was leveraged by the NMLB's National STBBI Laboratories to build capacity for STBBI POCT using the Cepheid GeneXpert®. The Xpert® HCV Viral Load (VL) Fingerstick assay, a diagnostic and quantitative tool suitable for POCT, was selected for initial implementation. A small-scale verification using residual clinical and contrived specimens evaluated the assay's sensitivity and specificity against the gold-standard Aptima® HCV Quant DX assay. Commercial material (AcroMetrix) was assessed for use as proficiency testing material. Participants included communities with prior testing experience and new community-based organizations.

RESULTS: The Xpert® HCV VL Fingerstick assay demonstrated concordance with the gold standard, with an RNA viral load difference of <0.5 log10 for most samples. Sensitivity and specificity were also in agreement. AcroMetrix proved stable and reproducible when diluted into donor blood, supporting onboarding and proficiency testing with noninfectious materials that mimic patient specimens. Three organizations were successfully onboarded, achieving "Proficient" results in a pilot external quality assessment.

CONCLUSION: Communities and community-based organizations in Canada have demonstrated their ability to successfully implement POCT. Leveraging this technology, they have expanded testing to include respiratory viruses (SARS-CoV-2, influenza, and RSV), tuberculosis, and STBBIs (HCV, HIV, Chlamydia, and Gonorrhea). Community-led POCT improves STBBI detection and linkage-to-care by reducing stigma and facilitating earlier treatment initiation. On-site monitoring and counselling minimize travel barriers and reduces loss to follow-up. This initiative underscores the feasibility of integrating POCT into community settings to address health inequities and improve health outcomes.

RFB008

Influenza treatment team: Virtual care pathway to antiviral treatment

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OBJECTIVE: Canadian guidelines recommend oseltamivir as soon as possible for influenza treatment in outpatients with risk factors for complications. Heavy workload in emergency departments and a lack of primary care providers are barriers to timely therapy initiation. The Influenza Treatment Team, a pilot virtual care team staffed by pharmacists and an on-call physician, aimed to promptly connect eligible outpatients with oseltamivir therapy.

METHOD: Positive influenza PCR results were referred from provincial microbiology laboratories to the Influenza Treatment Team. Outpatients aged ≥1 year, not already prescribed oseltamivir, who either self-referred for PCR testing without a documented primary care provider or were tested and discharged from an emergency department, were phoned to undergo assessment and receive education. Those with risk factors, ongoing symptoms, and within 7 days of symptom onset were offered oseltamivir, prescribed by the Influenza Treatment Team pharmacist. If requested, symptomatic household contacts of influenza-confirmed patients were also assessed.

RESULTS: Between January 23 and July 27, 2024, the Influenza Treatment Team completed initial assessments for 1,823 referrals, identifying 1,133 patients for phone assessment. Full assessments after connecting with the patient or caregiver by phone were completed for 82% (924/1,133). Those fully assessed had a mean age of 34 years, and 14% (130/924) were ≥65 years. Oseltamivir was initiated for 17% (160/924). The median time from referral to full assessment completion was 8.0 hours (IQR 4.4–23.0). For those prescribed oseltamivir, the median time from referral to prescription was 5.5 hours (IQR 3.0–17.7).

CONCLUSION: This provincial pilot initiative successfully reached a high proportion of outpatients living in rural and urban areas alike soon after positive influenza PCR reporting. Prioritizing targeted phone assessments for high-risk outpatients in any jurisdiction and future expansion

into long-term care and inpatient settings have significant potential to increase access to oseltamivir and improve influenza-related outcomes.

RFB009

Simultaneous detection of *Mycoplasma pneumoniae* and genotyping for macrolide susceptibility in nasopharyngeal specimens using a multiplex TaqMan qPCR

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OBJECTIVE: *M. pneumoniae* (MP) causes upper respiratory tract infections and pneumonia, especially in children. Macrolide resistance in MP is due to the acquisition of point mutations in the *23S* rRNA gene. The objective of the present study was to assess the prevalence of MP and its macrolide susceptibility in nasopharyngeal (NPS) specimens based on a newly developed multiplex qPCR assay.

METHOD: All NPS specimens ($n = 3{,}140$) sent to Hamilton Regional Laboratory in 2024 for MP detection were tested using a multiplex PCR with primers and probes targeting specific regions of 16s rDNA and 23S rDNA for detection of MP, and its macrolide susceptibility, respectively. Non-susceptible genotypes were tested using three TaqMan probes for resistant SNPs to detect resistant genotypes. PCR results were confirmed by Nanopore sequencing of a 928bp region of *23S* rDNA that harbors SNPs associated with macrolide resistance.

RESULTS: In 2024, 12.2% (383 of 3,140) specimens tested positive for MP, compared with 0.3% (2 of 576) in 2022 and 0.4% (2 of 555) in 2023. Among the positives, 90.1% were from patients ≤18 years old, and 92.2% were collected from August to December 2024 with positivity rates of 19.2% in August, 24.2% in September, 22.2% in October, 13.2% in November, and 6.6% in December. Of 383 positives, 336 (87.7%) were positive with *23S* rDNA wild-type probe and were interpreted as macrolide-susceptible genotype. The remaining 47 (12.3%) specimens were positive with A2063G SNP probe and interpreted as macrolide-resistant genotype. No other resistant genotypes were detected.

CONCLUSION: The present study shows an unprecedented increase of MP, especially in children ≤18 years of age, in 2024 compared with the previous 2 years. However, the genotypic resistance to macrolides remains relatively low. Continued surveillance of macrolide resistance is crucial for informing appropriate antimicrobial management of MP infections.

RFB010

Recurrent invasive pneumococcal disease in Calgary and Toronto, 2004–2022

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OBJECTIVE: Our objective was to describe features of adults with recurrent invasive pneumococcal disease (rIPD) in Calgary and Toronto.

METHOD: The Toronto Invasive Bacterial Disease Network (TIBDN) and the Calgary Area *Streptococcus pneumoniae* Epidemiological Research (CASPER) group perform population-based surveillance for IPD in Toronto/Peel and Calgary and surrounding areas, respectively. rIPD is defined as subsequent episode of IPD ≥ 30 days after a previous IPD episode. We included cases from 2004–2022 to describe clinical and demographic features and outcomes in those with and without rIPD. Fatal first cases were excluded.

RESULTS: There were 5,300 and 1,903 IPD episodes in 5,108 and 1,784 persons in Toronto and Calgary, respectively; 166 (3.2%) and 102 (5.7%) patients had ≥1 rIPD episode in Toronto and Calgary, respectively. Cases in Calgary had a lower median age for all groups than in Toronto (54.7 versus 62.2 years for first episodes). Median age was lower in recurrent versus single cases for both sites. Being unhoused was more common in those with rIPD than single episodes in both sites but higher in the IPD cohort from Calgary (22% of single; 48% of rIPD) than from Toronto (5.8% single; 13.3% rIPD). Alcoholism was higher in Calgary (30% of single, 70% of rIPD versus 11% and 12% in Toronto). In both sites illicit/IV drug use was higher in those with rIPD. Hematologic malignancy and stem cell transplant were more common in rIPD in Toronto; HIV was more prevalent in rIPD at both sites. Serotype distributions, particularly in rIPD, differ between the two sites.

CONCLUSION: Factors associated with recurrent IPD have both similarities and differences between Calgary and Toronto. In Calgary, rIPD is most associated with being unhoused, alcoholism, and drug use; in Toronto, these factors are less prominent, and severely immunocompromising conditions comprise a greater proportion of cases.

RFB011

Accuracy of plasma cell-free DNA PCR for non-invasive diagnosis of mucormycosis

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OBJECTIVE: The diagnosis of invasive mucormycosis is particularly challenging because conventional non-invasive testing methods are ineffective. The diagnosis relies heavily on invasive specimens, which suffer from poor sensitivity and slow turnaround time. The study aimed to evaluate the performance of Mucorales plasma cell-free DNA (cfDNA) PCR in immunosuppressed and non-immunosuppressed patients with pulmonary, disseminated, or localized mucormycosis.

METHOD: A retrospective cohort study was conducted between September 2020 and May 2024 and included patients who underwent Mucorales plasma cfDNA PCR for suspected invasive fungal disease (IFD). According to the European Organization for Research and Treatment of Cancer and the Mycoses Study Group Education and Research Consortium (EORTC/MSGERC) definition for IFD, test results were categorized as proven or probable mucormycosis for sensitivity and no Mucorales infection for specificity analysis. Mucorales plasma cfDNA PCR is a laboratory-developed singleplex real-time PCR assay designed to detect *Mucor*, *Rhizopus*, and *Rhizomucor* species.

RESULTS: The study included 85 positive and 212 negative Mucorales plasma cfDNA test results from unique patients. Per EORTC/MSGERC definitions, 48 patients had proven or probable mucormycosis while 170 did not have mucormycosis. The overall sensitivity of the assay was 83.3% (40/48, 95% CI 69.8–92.5), and specificity was 92.9% (158/170, 95% CI 88.0–96.3). The sensitivity was 89.7% (35/39, 95% CI 75.8–97.1) in immunocompromised patients and 55.6% (5/9, 95% CI 21.2–86.3) in immunocompetent patients. Sensitivity also varied by infection site: disseminated 100% (14/14, CI 95% 76.8–100), pulmonary 85.0% (17/20, 95% CI 62.1–96.8), and localized disease 64.3% (9/14, 95% CI 35.1-87.2).

CONCLUSION: Mucorales plasma cfDNA PCR has demonstrated high sensitivity as a non-invasive diagnosis of mucormycosis, particularly in immunosuppressed patients and those with pulmonary and disseminated infection. Future studies are needed to confirm its performance for different populations and clinical presentation.

RFB012

Antimicrobial susceptibility in Canada: Initial results from AMRNet surveillance, 2020–2022

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OBJECTIVE: Summarize Canadian antimicrobial susceptibility trends by specimen type, setting, and patient demographics.

METHOD: Antimicrobial susceptibility data for bacteria and fungi from inpatient and outpatient/community clinical specimens were submitted from Canadian public and private laboratories. Screening specimens were excluded. Duplicate specimens were removed as per Clinical and Laboratory Standards Institute recommendations where feasible. To be included in percent susceptibilities, bacteria-antimicrobial combinations had to meet the following criteria: three or more jurisdictions submitted data for the antimicrobial representing ≥85% of isolates of

the respective bacteria (submissions with <85% coverage excluded). As part of program development, in some jurisdictions, only certain specimen types, organisms, or regions were submitted. Not all jurisdictions participated in all years.

RESULTS: Overall, 12,704,435 susceptibility test results between 2020 and 2022 were analyzed, representing 1,041,456 isolates. Data were submitted from seven jurisdictions (BC/NB/NL/NT/ON/PEI/SK). Overall, 873,631 (84%) isolates originated from urine, 44,869 (4%) from blood, and 22,331 (2%) from respiratory specimens. The most frequently identified organisms were *Escherichia coli* (35%), *Staphylococcus aureus* (8%), *Klebsiella pneumoniae* complex (6%), *Enterococcus faecalis* (4%), and *Pseudomonas aeruginosa* (2%). In 2022, percent susceptibilities among *E. coli* urine specimens were 99.9% meropenem, 98.5% piperacillin-tazobactam, 95.4% ceftazidime, 93.6% gentamicin, 82.3% trimethoprim-sulfamethoxazole, and 74.1% ciprofloxacin. Percent susceptibilities among *S. aureus* blood specimens were 99.3% vancomycin, 97.0% trimethoprim-sulfamethoxazole, and 83.2% oxacillin. Antimicrobial susceptibilities differed between inpatients and community/outpatients. In 2022, 0.2% of *E. coli* isolated from inpatients were resistant to carbapenems compared to 0.02% among community/outpatients ($p < .0001$). Percent susceptibilities differed among demographic groups. In 2022, methicillin resistance was identified in 23% of *S. aureus* isolates from individuals aged 0–59 years compared to 14% among individuals aged 60+ ($p < .001$).

CONCLUSION: AMRNet surveillance data can monitor trends in organisms, susceptibility patterns, and differences among patient groups. These data can inform stewardship efforts.

RAPID FIRE PRESENTATIONS

Session C
Thursday, May 1

RFC001
Reducing unnecessary microbiologic tests through the use of rules in an electronic health system

Benson Weyant[1], Nathan Zelyas[2,3], Carmen L Charlton[2,3], William Stokes[2,3], Hong Yuan Zhou[2,4], Sean Jiang[5], Maria Falsetti[2], Byron Berenger[2,4]

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OBJECTIVE: Diagnostic stewardship improves patient care and reduces health system costs by promoting appropriate test use. Ordering serological and nucleic acid tests (NATs) for infectious diseases can be challenging with differing indications based on the clinical picture, previous results, or pathogen. We aimed to use our electronic health system (EHS) to enable real-time, patient-specific education on infectious disease test appropriateness.

METHOD: From October 2023–2024 we assessed two diagnostic stewardship measures within our provincial EHS (Epic Systems™) for 35 orders (27 serology, 8 NATs): Best Practice Advisories (BPAs) triggered at the point of ordering serology tests; and auto-cancelation rules upon receipt of the sample at the testing lab (acute care and community generated orders). BPAs flagged duplicate orders (within 3 days for IgM and 7 days for IgG), previously positive IgG or missing prerequisite tests (eg, positive IgG for NAT). Providers could override the BPA if necessary. Effectiveness was assessed by counting test cancellations post-implementation.

RESULTS: Over 12 months, BPAs led to 23,524 cancelled tests, representing 2.3% of the total targeted tests ordered, with 69,706 (4.4%) additional tests auto-cancelled by laboratory rules. BPAs were activated for a previous positive result (19,030 or 80.4%) or repeat testing within 1 week (1,812 or 14.5%). Providers overrode BPAs on only 146 occasions (0.4%). The most effective BPAs were for HTLV NAT (87.5% decrease), HIV1 NAT (47.5%), and toxoplasmosis NAT (17.9%). For auto-cancellation rules, the most effective were prenatal panels (54.9%), rubella IgG (19.2%), and VZV IgG (13.2%). BPAs prevented 20,859 phlebotomies and saved $49,208 in laboratory reagents alone. Utilization rules saved an additional $199,149.

CONCLUSION: Integrating BPAs into EHS effectively supports diagnostic stewardship at the point of ordering, reducing unnecessary phlebotomies, improving test selection, and saving resources. When electronic ordering is

available, auto-cancellations by the laboratory information system are an effective alternative.

RFC002

Clinical outcomes of patients experiencing methicillin-sensitive *Staphylococcus aureus* bacteremia as a function of the cefazolin high inoculum effect: A population-based multi-year study

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OBJECTIVE: The high inoculum effect (HIE) associated with beta-lactams, particularly cefazolin, has been recognized as a phenotype that may adversely impact clinical outcomes of methicillin-susceptible *Staphylococcus aureus* (MSSA) infections. We aimed to investigate if HIE influenced outcomes in a non-selected, general population of MSSA bacteremia.

METHOD: All MSSA bacteremia episodes occurring in residents of Calgary, Canada between 2012–2014 and 2019 were identified. Isolates were assessed for the cefazolin HIE phenotype using CLSI 2009 criteria defined as a fourfold or higher change in MIC between broth microdilution with standard inoculum (5×10^5 CFU/mL) versus high inoculum (5×10^7 CFU/mL). Patient outcomes were assessed via a retrospective chart review that included primary outcomes of mortality, recurrence of bacteremia, and metastatic complications. Demographics and clinical data were assessed first using univariate analysis and associated factors with a $p \leq .10$ underwent multivariate logistic regression (GraphPad Prism 10.4.1).

RESULTS: Demographic and clinical characteristics between patients with MSSA bacteremia did not differ based on presence of HIE phenotype. HIE phenotype did not associate with duration of BSI (3.41 IQR 1.68-4.42 versus 3.54 IQR 1.54-4.22, $p = .457$) or with status as complicated versus not (83.7% versus 83.6%, $p = .999$), irrespective of treatment. When investigating HIE as a function of cefazolin- versus cloxacillin-based therapy, there was no difference in treatment duration for complicated bacteremia (44.72 days IQR 32.31–53.14 versus 44.10 IQR 34.86–51.10, $p = .675$), and there was no difference in recurrence risk ($p > .05$), but any recurrences within 90 and 180 days only occurred with cefazolin. Thirty-day survival did not differ (79.4 versus 78.4%, $p = .780$), although Kaplan-Meier survival curves demonstrated a modest divergence after 30 days, but remained non-significant (HR = 1.127, $p = .056$).

CONCLUSION: In our population-based cohort, the cefazolin HIE did not affect MSSA bacteremia outcomes, as 30-day and 1 year mortality were not different. Recurrence risk as a function of HIE requires further exploration.

RFC003

Epidemiology of *Mycoplasma pneumoniae* pneumonia in children: A retrospective chart review

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OBJECTIVE: Community-acquired pneumonia (CAP) is commonly diagnosed in Canadian children. History-taking, physical examination, and imaging cannot reliably discriminate between viral, typical (eg pneumococcal), and atypical pneumonia. Unfortunately, optimal treatment strategies for each of these types of CAP differ, and so their relative incidence drives management algorithms. The primary objective of our study was to compare the incidence of *Mycoplasma pneumoniae* test positivity in children at McMaster Children's Hospital (MCH) between June and October 2024 compared to this time period in the two prior years.

METHOD: All respiratory specimens (nasopharyngeal swab, throat swab, bronchoalveolar lavage, pleural fluid) sent for PCR detection of *M. pneumoniae* from paediatric patients at MCH from June to October in 2024, 2023, and 2022 were eligible for inclusion. Testing was accomplished using a lab-developed assay.

RESULTS: In total, there was 1 positive *M. pneumoniae* test in the 2022 study period, 1 in the 2023 study period, and 187 in the 2024 study period. In 2024, there were 3 positives in June, 5 in July, 39 in August, 55 in September, and 85 in October. The proportion of positive *M. pneumoniae* tests was 1.8% in the 2022 study period, 1.6% in the 2023 study period, and 20.2% in the 2024 study period. Percent positivity was 12.0% in June 2024, 11.6% in July 2024, 21.4% in August 2024, 22.9% in September 2024, and 19.7% in October 2024.

CONCLUSION: There was a clear increase in the incidence of *M. pneumoniae* test positivity in children in 2024 as compared to the two previous years. It is important to ensure that front-line clinicians are aware of the timing and magnitude of seasonal flare-ups of this pathogen, since the incidence impacts the development of both diagnostic testing and antimicrobial treatment algorithms.

RFC004

A novel approach to leadership of antimicrobial stewardship programs: A provincial 'Operational Triad' in Alberta

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OBJECTIVE: Antimicrobial stewardship programs (ASPs) are traditionally a partnership between infectious disease specialists and pharmacists. Though effective for containing antimicrobial use and costs, quality and safety oversight can enhance patient-centric outcomes with additional health system benefits. In 2024, Alberta transitioned to a new leadership system for ASP, emphasizing quality improvement and patient safety. We describe the merits of this provincial ASP framework.

METHOD: We reviewed the historical leadership model of Alberta Health Services' (AHS) ASP and its evolution from a decentralized to provincial model under a novel leadership framework emphasizing quality improvement and patient safety.

RESULTS: Previously, AHS ASP reported under Pharmacy, focusing on policy and formulary development. The five zones developed individual ASPs, with varied reporting structures, no direct physician reporting, and little inter-zone collaboration, leading to inefficiencies and inequities. In 2024, AHS introduced a new governance structure, placing ASP under Quality and Health Care Improvement while continuing to leverage expertise from Medical, Pharmacy, and Quality and Safety leads through an 'Operational Triad' at the provincial level. The medical director leads the program, providing medical expertise, program direction, and oversight. Quality ensures optimal design and evaluation of ASP quality improvement (QI) initiatives. Pharmacy provides linkages to ASP and front-line pharmacists, formulary reviews, and utilization data. The triad supports zonal implementation of stewardship interventions, ensuring shared resources and provincial oversight. Benefits included allocating an ASP pharmacist and a physician leads to each zone and centralizing communications, data analysis, reporting, and QI initiative development. The integrated ASP enhanced resource sharing, facilitated community key partner engagement, and permitted tele-stewardship, increasing program effectiveness, particularly in remote sites.

CONCLUSION: A novel operational triad of Medical, Pharmacy, and Quality and Safety leadership can enhance ASP effectiveness by aligning stewardship with patient care priorities. This approach improves resource utilization, supports evidence-based interventions, and provides a scalable framework for other health systems.

RFC005

Detection of parvovirus B19 in pooled nasopharyngeal specimens (NPS) from paediatric patients with upper respiratory tract infections

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OBJECTIVE: Parvovirus B19 is known to be transmitted via respiratory droplets, causing both symptomatic and asymptomatic infections in children. However, routine respiratory virus testing does not include testing for this virus. Recently, an unusually high level of parvovirus B19 activity has been reported in many countries, including the USA and Europe, but data from Canada remain limited. In this study, we screened paediatric nasopharyngeal swab (NPS) specimens, which were negative for eight common respiratory viruses, for parvovirus B19 using PCR.

METHOD: Pooled sampling was employed as an efficient and cost-effective surveillance strategy. From April to December 2024, residual NPS specimens submitted to the Hamilton Regional Laboratory Medicine Program (HRLMP) virology laboratory for respiratory virus testing and found to be negative for common respiratory viruses

were collected. Pools of four NPS specimens were extracted (NUCLISENS® easyMAG®, bioMérieux) and tested by a laboratory-developed, validated parvovirus B19 PCR assay.

RESULTS: A total of 522 pools, comprising 1,950 individual NPS specimens, were assessed, of which 31 were positive. The inferred overall prevalence of parvovirus is 1.6% (95% CI 1.1–2.3), assuming one positive specimen per pool. We observed the highest prevalence in May 2024 (4.0%) followed by a gradual decline toward the end of the year, with a prevalence of 0.8% in December 2024. The average monthly prevalence rate was 1.8%. Further analysis of individual specimens from all positive pools to determine the actual prevalence of parvovirus B19, and its clinical relevance is currently underway.

CONCLUSION: This study highlights the utility of pooled sampling and PCR-based surveillance in identifying undiagnosed viral pathogens, such as parvovirus B19, in paediatric populations. The findings contribute to a better understanding of the seasonal dynamics of parvovirus B19 and propose a scalable model for efficient public health monitoring of this virus.

RFC006

Impact of revision in Aminoglycosides breakpoints against *Enterobacterales* in the 33rd edition of the Clinical and Laboratory Standards Institute (CLSI) M100 document on clinical reporting at a tertiary care hospital

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OBJECTIVE: Aminoglycosides (AG) have a broad spectrum of activity but are associated with significant toxicity and have a narrow therapeutic window. Clinical and Laboratory Standards Institute (CLSI) revised their long-standing AG breakpoints in the M100 33rd edition in 2023, after 43 years based on the pharmacokinetic/ pharmacodynamics (PK/PD) and clinical outcome data for *Enterobacterales*. Our study enumerated the impact of these revised breakpoints on the categorical agreement (CA) by analyzing the percentage of isolates that had a change in their susceptibility interpretation. We evaluated the performance of VITEK 2 our reference antimicrobial susceptibility test (AST) method against disk diffusion (DD).

METHOD: For the study, we included 35 clinical isolates and 3 isolates from American Type Culture Collections (ATCC) representing *Enterobacterales*. Using standard inoculum obtained from a young culture plate, we tested susceptibility to amikacin, gentamicin, and tobramycin by VITEK 2 and DD methods in parallel. The breakpoint results were compared using now obsolete and updated breakpoints to monitor for changes in CA via both VITEK2 MIC and DD study results.

RESULTS: *Enterobacterales* isolates exhibited an overall 21.5% change in breakpoint interpretation when applying the revised AG breakpoints from CLSI M100 33rd edition. There was a 10.5%, 8%, and 3% change observed for tobramycin, gentamicin, and amikacin, respectively. Comparative analysis of the verification study between VITEK2 and DD results were within the acceptable CA of 97% and without major or very major discrepancies.

CONCLUSION: The changes in breakpoint interpretation indicate a shift toward increased resistance and intermediate susceptibility to AGs, emphasizing the need for laboratories to prioritize validation and implementation to ensure appropriate and effective AG utilization. Implementing the revised CLSI breakpoints is important not only for antimicrobial stewardship but ultimately for optimal patient outcomes and reduced toxicity.

RFC007

Clostridioides difficile colonization: A pilot study evaluating prediction of infection in paediatric oncology patients

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OBJECTIVE: *Clostridioides difficile* (CD) is an important cause of morbidity in paediatric oncology patients with CD infection (CDI) leading to gastrointestinal pathology in addition to cancer treatment delay. Targeted prevention strategies may reduce CDI if at-risk patients can be detected. This study aims to determine if CD colonization at the time of oncologic diagnosis is associated with an increased likelihood of CDI during cancer treatment.

METHOD: Nested retrospective study evaluating paediatric oncology patients diagnosed and treated at a tertiary children's health centre between July 1, 2016 and June 30, 2024. Stool samples previously procured early in the malignancy treatment course were analyzed for CD colonization using lateral flow and PCR identifying patients as CD colonized or non-CD colonized. Charts were reviewed for all patients; development of CDI during their oncologic treatment course and its clinical course, in addition to demographics and potential confounders were collected. Odds ratio (OR) for CDI with 95% confidence interval (CI) and *p* were calculated.

RESULTS: Forty-six patients aged 1–17 years were identified. Seven patients (15%) patients were CD colonized at diagnosis. Overall, 22% ($n = 10$) developed CDI; 43% ($n = 3$) in the CD-colonized group developed CDI compared to 18% ($n = 7$) in the non-CD–colonized group. OR for development of CDI if CD-colonized was 3.43 (95% CI 0.64–18.30, $p = .12$) when compared to non-CD colonized. For patients who developed CDI, average days to onset in the CD-colonized group was 161 (range 71–259) compared to 374 (range 72–1335) days in the non-CD–colonized group.

CONCLUSION: This pilot study suggests a potential association between CD colonization and an increased risk of CDI during the treatment course in paediatric oncologic patients. Although limited by sample size, this study provides important novel preliminary findings. Further research through prospective study design may help identify risk factors for CDI development and allow for study of potential targeted prevention interventions.

RFC008

Efficacy and safety of doxycycline in the treatment of community acquired pneumonia: A systematic review and meta-analysis

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OBJECTIVE: Doxycycline has been recommended in guidelines as one of the antibiotic options for the treatment of community-acquired pneumonia (CAP); however, the strength of the recommendation is generally graded as weak, and the level of evidence is graded as low. The objective of this meta-analysis is to summarize the literature on the relative efficacy and safety of doxycycline compared to other antibiotics for the treatment of CAP.

METHOD: A systematic review of MEDLINE, EMBASE, Web of Science, Scopus, Cochrane Library, and medRxiv.org was conducted. Eligible studies included randomized controlled trials (RCTs) and observational studies assessing persons with CAP, both inpatients and outpatients. The interventions compared doxycycline (alone or in combination) to other antibiotics (alone or in combination). The primary outcome was clinical improvement, with secondary outcomes including mortality, time to resolution, length of hospital stay, clinical failure, and adverse effects (including *Clostridioides difficile* infection). Risk of bias was assessed using the ROBINS-I tool for non-randomized studies and the Cochrane RoB 2 tool for RCTs. A random-effects model was used for meta-analysis.

RESULTS: Twenty-six studies (9 RCTs and 17 cohort studies; $N = 203{,}295$) met inclusion criteria, published between 1974 and 2024. There was no significant difference between doxycycline and comparators for clinical improvement (odds ratio 1.07; 95% CI 0.66–1.71). Doxycycline was associated with reduced mortality (OR 0.66; 95% CI 0.45–0.96) and adverse effects including *C. difficile* infection (OR 0.45; 95% CI 0.25–0.82). There was no significant difference between doxycycline and comparators for clinical failure, time to resolution, and hospital length of stay.

CONCLUSION: Doxycycline is a safe and effective first-line treatment for CAP. A large randomized controlled trial is recommended to confirm these findings.

RFC009

Verification of fluconazole disc diffusion susceptibility testing for *Candida* species using two disc manufacturers

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OBJECTIVE: Increased fluconazole non-susceptibility has made empiric treatment of candidemia challenging. Accurate timely susceptibility testing is essential. This study veri-

fied fluconazole disc diffusion, which can provide accessible and rapid results.

METHOD: Two-hundred and twenty-eight archived Candida bloodstream isolates (*Candida albicans* [$n = 56$], *Candida glabrata* [$n = 60$], *Candida parapsilosis* [$n = 63$], and *Candida tropicalis* [$n = 50$]) with historic fluconazole broth microdilution data (BMD) from 2013–2024 were tested. Fluconazole disc diffusion using two discs (Liofilchem and Oxoid) on Mueller-Hinton agar with 2% glucose and methylene blue dye (Micronostyx) incubated for 24 hours following CLSI M44-3E was completed. Results were compared to BMD data. Discrepant isolates were repeated with incubation extended to 48 hours following CLSI M27M44S. VMEs were adjudicated with YO9 Sensititre™. Reproducibility, categorical agreement (CA), very major errors (VME), major errors (ME), and minor errors (MiE) were compared against CLSI-M52 thresholds.

RESULTS: For all species combined, at 24 hours' incubation for the Oxoid and Liofilchem fluconazole discs, respectively, CA was 94%/93%, VME was 3%/9%, ME was 0%/0%, and MiEs were 5% (50% overcalling increased susceptibility) and 7% (64% overcalling increased susceptibility). VME were noted in *C. albicans* ($n = 1$) and *C. parapsilosis* ($n = 2$) and MiE in all four species. Incubating isolates with discrepant results for 48 hours corrected VME and MiE for most isolates with non-confluent growth and had no impact on those with confluent growth resulting in CA of 96%/93%, VME 0%/3%, ME 0%/0%, and MiEs 6% (35% overcalling increased susceptibility) versus 6% (29% overcalling increased susceptibility) for the Oxoid and Liofilchem fluconazole discs, respectively. Reproducibility was 100% for both disc manufacturers.

CONCLUSION: Fluconazole Oxoid and Liofilchem disc diffusion meets the CLSI M52 acceptance criteria for reproducibility, VME, ME, and MiE after 24 hour' incubation as long as isolates with non-confluent growth are re-incubated for 48 hours. The different incubation instructions in CLSI M44-3E and CLSI M27M44S affect interpretation and should be addressed.

RFC010

Breaking barriers: Exploring sexually transmitted infection screening needs in homeless shelter clients in an urban city centre

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OBJECTIVE: Individuals experiencing homelessness are at increased risk of contracting infections such as sexually transmitted infections (STIs) due to higher-risk behaviours and barriers to accessing testing. This study aimed to explore STI testing needs for shelter clients in an urban city and assess barriers to sexual health care.

METHOD: Participants were recruited from nine shelter sites. Each participant completed an anonymous survey evaluating their behaviour, perceptions, and knowledge relating to STIs. Participants provided urine (males) or urine and self-collected vaginal swabs (females) tested for *Chlamydia trachomatis* (CT), *Neisseria gonorrheae* (NG), *Mycoplasma genitalium* (Mgen), *Trichomonas vaginalis* (TV), and human papillomavirus (HPV).

RESULTS: A total of 285 participants (37.5% female, 58.9% male, 1.4% transgender, 1.1% non-binary, 1.1% unspecified) completed the questionnaire, and 265 self-collected specimens were obtained. Testing revealed that 25% of participants had at least one infection. The overall prevalences of CT, NG, MG, TV, and HPV were 1.6%, 1.2%, 5.5%, 3.6%, and 4.4%, respectively, with higher rates among females: 4.3%, 4.3%, 10.9%, 9.1%, and 18.7%, respectively. Approximately 48.4% of respondents reported having one or more partners in the past 6 months, and 5.3% reported 10 or more. However, only 29.5% reported being tested for an STI in the last 12 months. Women were more likely to be tested: 38.3% of females had been tested in the last 12 months versus 24.2% of males ($p < .001$). Only 8.4% reported testing positive for an STI in the past year, with females disproportionately affected ($p = .006$). Roughly 22% found STI testing accessible but required some assistance, while 7.7%% found it difficult or very difficult to access, with more males reporting difficulties.

CONCLUSION: While most respondents found STI testing accessible, testing rates were low, especially among males. More females reported accessing testing services but experienced higher rates of STIs. These results suggest that site-specific STI screening strategies may be necessary.

RFC011

Vaccination rates and incidence of vaccine-preventable diseases among people living with HIV in Manitoba, Canada, from 2018 to 2022: A retrospective cohort study

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OBJECTIVE: The objectives of this study were to describe the rates of vaccination among people living with HIV that were enrolled in the Manitoba HIV Program between 2018 and 2022, disaggregated by age, sex, gender, race/ethnicity, sexual orientation, drug use, and houselessness; and to correlate vaccination rates with the incidence of vaccine-preventable diseases.

METHOD: This retrospective cohort study included all adults newly diagnosed with HIV in Manitoba from January 1, 2018 to December 31, 2022. Data was collected from clinical charts after at least 1 year follow-up, then analyzed and disaggregated by age, sex, gender, sexual orientation, race/ethnicity, drug use, and houselessness. Outcomes included vaccination rate, incidence of vaccine-preventable diseases, and mortality.

RESULTS: Six hundred and three adults were newly diagnosed with HIV from 2018 to 2022. Of them 56.2% were male and 43.8% female; 62.0% heterosexual and 21.8% gay, bisexual, and men who have sex with men; 54.4% reported injection drug use; and 33.2% experienced houselessness. The percentage of those who received one or more doses of pneumococcal vaccine was 70.2%; influenza: 56.7%; meningococcal: 20.7%; hepatitis A: 27.2%; hepatitis B: 46.8%; HPV: 17.1%; and COVID-19: 73.5. Only 4.4% of pneumococcal vaccine recipients were given all scheduled doses, and 20.5–48.6% of people completed the other vaccines schedules.

CONCLUSION: People living with HIV in Manitoba have a low proportion of vaccines recommended by national and international guidelines among this population. It is important to perform future research to understand the reasons behind opting out of vaccination and for not completing vaccinations for those who have received initial doses.

RFC012

Factors associated with differential vaccine uptake among people with HIV in a geographically defined HIV clinic population

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OBJECTIVE: People with HIV (PWH) are at an increased risk for many vaccine-preventable diseases. Despite the importance of vaccination, low acceptance and uptake of routine, COVID-19, and influenza vaccines in PWH has been reported. We aimed to characterize the uptake of pneumococcal, COVID-19, and influenza vaccines among PWH at a geographically defined HIV clinic.

METHOD: Demographic and clinical characteristics were ascertained from PWH $\geq$ 18 years old receiving care at a geographically defined HIV clinic population as of July 1, 2022. Vaccine uptake was categorized as any versus none for each pneumococcal, COVID-19, and influenza vaccine from the latest date of entry into the SAC cohort or from January 1, 2000 until July 1, 2022. Log-binomial models estimated crude and adjusted prevalence ratios (aPR) and associated 95% confidence intervals for factors associated with each type of vaccine uptake. Multivariable models were adjusted for demographics, social determinants of health, and clinical factors.

RESULTS: Among 1,892 PWH, 1,549 (85%) received at least one pneumococcal vaccine, 1,677 (92%) received a COVID-19 vaccine, and 1,175 (64%) received an influenza vaccine. The median age at baseline was 50 years (IQR:

42–58 years), and 72% of the study participants were male. After adjustment, non-Hispanic white PWH had reduced COVID-19 uptake. Race/ethnicity was not associated with influenza or pneumococcal vaccine uptake. Heterosexual HIV acquisition risk was associated with reduced uptake of all included vaccines, whereas injection drug use risk was only associated with reduced COVID-19 vaccine uptake. Higher educational attainment was only associated with greater COVID-19 vaccine uptake. Duration of HIV was positively associated with increased vaccine uptake across all three vaccines. Unsuppressed viral load was associated with reduced uptake of both COVID-19 and pneumococcal vaccines.

CONCLUSION: Factors associated with reduced vaccine uptake may vary by vaccine type, and differences should be considered when designing targeted strategies to improve vaccine uptake among PWH.

RAPID FIRE PRESENTATIONS

Session D
Thursday, May 1

RFD001
Development of a Canadian consensus protocol to evaluate appropriateness of antimicrobial prescribing in hospitals for local quality improvement and national benchmarking: Getting the best of both worlds through an implementation science framework

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OBJECTIVE: Hospital antimicrobial stewardship (AMS) programs promote and measure appropriate use of antimicrobials, including adherence to guideline for quality improvement (QI). There is no consensus among Canadian hospitals on a standardized approach to evaluate and report appropriate use while accounting for hospital characteristics or regional epidemiology. We sought recommendations from Canadian AMS/infectious diseases (ID) experts for a standardized protocol that supports hospital QI while informing Canada's national AMS strategies.

METHOD: We applied the Consolidated Framework for Implementation Research (CFIR) to delineate actors, barriers, and facilitators in standardizing protocol for appropriate use evaluation. We surveyed hospital AMS/ID experts to determine the current state, then conducted semi-structured interviews for their recommendations on the assessment framework, workflow, information technology, reporting, and resources for standardized evaluation. Findings underwent thematic analyses using the constant comparison method and mapping to CFIR domains.

RESULTS: We received 58 survey responses from pharmacists (67%; corresponding response rate 18%) and physicians (19%) from 10 provinces and 1 territory. Multisite, single-site, and regional/provincially governed AMS programs were similarly represented. The majority of respondents (98%) use a Canadian-specific evaluation protocol if available. The two main goals were AMS program planning (53%) and guideline development (21%). The two most important facilitators were compatibility with electronic medical record system (47%) and an informative report (41%). The most preferred frameworks were locally developed guidelines (39%), AMS principles (25%), and national guidelines (19%). Key barriers were lack of human resources (53%), lack of time (17%), and lack of expertise (14%). Interviews with 28 AMS/ID experts from six provinces identified data collection efficiency and flexibility to accommodate hospital/regional characteristics as the most impactful features of a standardized evaluation tool.

CONCLUSION: We developed a preliminary protocol to evaluate and report appropriate antimicrobial use, accommodating local AMS QI needs plus regional and national benchmarking goals. The next steps involve validation before national implementation.

RFD002
Health care resource utilization and cost burden of COVID-19 cases in Ontario, Canada

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OBJECTIVE: This study aims to describe the real-world health care resource utilization (HCRU) and cost burden associated with COVID-19 cases in Ontario, Canada, as well as assessing variation in these metrics by vaccination status.

METHOD: We conducted a population-based retrospective cohort study using administrative health data from Ontario, focusing on COVID-19 cases from January 1, 2021 to May 31, 2023. Cases were identified by their first positive PCR test, and their health care interactions were followed for up to 12 months post-infection. HCRU and direct health care cost were compared before and after infection using generalized linear models.

RESULTS: Data from a total of 1,321,174 COVID-19 cases were analyzed, with 87% of cases having at least one health care interaction in the year preceding their infection. Mean HCRU increased post-infection, with the greatest rise observed in the first month, primarily driven by hospitalizations (Month 1: 1.1 ± 0.3 hospitalizations versus Look-back: 0.1 ± 0.1 hospitalizations per person per month [PPPM], $p < .0001$) and ICU admissions (Month 1: 1.0 ± 0.1 admissions versus Look-back 0.1 ± 0.0 admissions PPPM, $p < .0001$). The mean health care cost per person rose from CAD $4,278.6 \pm 15,670.9$ to CAD $5,872.9 \pm 20,630.6$ ($p < .0001$) in the 6 months pre- versus post-infection, primarily driven by ICU admission, hospitalization, and mechanical ventilation costs. On average, vaccinated individuals exhibited smaller increases in ICU costs (vaccinated: +CAD 5,838 to CAD 18,730 versus unvaccinated: +CAD 24,597) and hospitalization costs (vaccinated: +CAD 623 to CAD 5,201 versus unvaccinated: +CAD 9,072) post-infection compared to unvaccinated cases.

CONCLUSION: Data from this study cohort suggest that COVID-19 increases HCRU as a result of hospitalization, ICU admission, and mechanical ventilation. These findings underscore the importance of vaccination in reducing severe outcomes and health care costs, supporting the need to improve uptake through public health strategies and individual patient counseling.

RFD003

Detection of viral and bacterial pathogens in suspected ocular infections using untargeted metagenomics sequencing

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OBJECTIVE: Ocular infections can result in irreversible vision loss and are caused by a variety of infectious agents including viruses, bacteria, parasites, and fungi. Conventional diagnostic testing of ocular specimens is limited in how many targets can be detected simultaneously, cultivation bias, and the irreplaceable nature of the specimens. Here we evaluated pathogen detection in specimens collected from cases of inner ocular infection with untargeted metagenomics using the Oxford Nanopore platform.

METHOD: In patients with ocular infection, we retrospectively compared the accuracy of pathogen identification between conventional diagnostics methods—qPCR and bacterial culture—and nanopore metagenomics. Nucleic acid from patient specimens was used as input for library preparation and then sequenced on a minION flowcell. The WIMP workflow on the EPI2ME platform was used to determine taxonomy and abundance of the detected targets.

RESULTS: Of 22 known patient positive specimens, 20 were positive for viral targets (HSV, CMV, VZV) using reference qPCR tests and 2 were positive for bacteria using traditional culture-based methods. Nanopore metagenomics sequencing identified 20/20 viral positives (100%) and 2/2 bacterial culture-based positives. The positive agreement (PPA) between nanopore and the reference methods was 100%. However, the number of aligned reads to the suspected viral target was dependent on the quantity of input nucleic acid and the abundance of the target as determined by qPCR with Cq values of >33.0, resulting in <10 aligned reads.

CONCLUSION: Metagenomic sequencing using nanopore technology was able to correctly identify human herpesviruses as well as bacterial pathogens in cases of ocular infection. Untargeted metagenomics shows promise for the rapid and accurate detection of a variety of pathogens from ocular specimens. Setting thresholds for detection in specimens with low target abundance and achieving sufficient sequencing depth remain challenges to the application of this method for clinical diagnostics.

RFD004

Development of a HSV1/2, VZV, and syphilis lesion assay in Manitoba, Canada

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OBJECTIVE: To evaluate a multiplex lesion panel for the detection of *Treponema pallidum* (TPA), herpes simplex virus (HSV), and varicella zoster virus (VZV) and to improve diagnostic turnaround times (TAT) for syphilis in Manitoba.

METHOD: From June 2021 to March 2023, a quality assurance study screened over 5,000 mucocutaneous lesion swabs initially submitted for HSV and VZV testing. These samples were subsequently tested for TPA. The study assessed positivity rates, TAT for TPA testing, and the presence of follow-up testing, including TPA PCR and serology.

RESULTS: Positivity rates were 13% for HSV-1, 13% for HSV-2, 6.7% for VZV, and 6.6% for TPA. The average TAT for TPA testing sent to a reference laboratory was 17.8 days. Among TPA-positive specimens, 36% lacked a corresponding TPA PCR test, and 19% did not have syphilis serology within 30 days. The multiplex lesion panel, including TPA, showed high sensitivity and specificity for HSV-1, HSV-2, VZV, and TPA, with reproducibility across multiple runs. Adding TPA to the panel reduced the TAT to 4 days.

CONCLUSION: Incorporating TPA testing into a multiplex lesion panel significantly improved diagnostic efficiency and reduced TAT. This strategy is critical for addressing the rising incidence of syphilis in Manitoba and improving public health outcomes by ensuring timely and accurate diagnoses.

RFD005

A real-time PCR for hypervirulent *Streptococcus pyogenes* strain M1UK in isolates and throat swabs

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OBJECTIVE: Significant morbidity and mortality are associated with invasive group A streptococci (iGAS) infections caused by *Streptococcus pyogenes*. In 2019, a hypervirulent strain M1UK was associated with increased iGAS activity in the UK (2014–2016). M1UK spread to other countries, including Canada. Compared to ancestral M1global strains, M1UK harbours 27 distinct mutations, one linked to hypervirulence through overexpression of the superantigen SpeA. In this study, two other M1UK-specific adjacent mutations in *rofA* were used for a Taqman real-time PCR aimed to facilitate M1UK surveillance using isolates or throat swabs.

METHOD: PCR specificity was assessed using *S. pyogenes* isolates from all 535 non-duplicated iGAS cases from 2012 to 2024 in Nova Scotia. These had previously been characterized by *emm* (M) typing using Sanger or next-generation sequencing. Isolates from iGAS cases included 142 *emm1* types (37 M1global, 17 M1intermediate, and 88 M1UK) as well as various other *emm* types that previously circulated in Canada. Non-GAS streptococci or closely related bacteria ($n = 32$) were also evaluated. Next, the M1UK PCR was tested on throat swabs in liquid Amies collected in 2024 and compared to the 514 paired *S. pyogenes* cultures obtained that were characterized by *emm* sequencing. The sensitivity of PCR was compared to culture with triplicate 10-fold serial dilutions of M1UK in liquid Amies media.

RESULTS: The PCR detected all M1UK strains, without cross-reactions with other *emm1* types (M1global or M1intermediate), non-*emm1* types, or closely related streptococci. All 88 M1UK strains were detected, with the first identified in 2015 and large expansions in years 2018/2019 and 2023/2024. The use of the M1UK PCR on throat swabs showed similar performance as culture, and the proportion of M1UK and overall *emm* type distribution in throat swabs mirrored those of iGAS cases.

CONCLUSION: Overall, the M1UK-specific PCR was a reliable surveillance tool for isolates and throat swabs.

RFD006

Review of diphtheria anti-toxin serology utilization in a Canadian province (2023–2024)

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OBJECTIVE: Pre-vaccine or routine serologic testing using diphtheria anti-toxin serology (DATS) is not routinely recommended to guide administration of diphtheria toxoid–containing vaccines (DTCVs). DATS titres are generally reserved for investigating humoral immunodeficiency (H-ID) in select patient groups or post-injection site reaction to a DTCV. The National Advisory Committee on Immunisation (NACI) advises individuals with incomplete/inadequate vaccine records be considered unimmunized and administered age-appropriate primary vaccine series unless circumstances dictate otherwise. We reviewed 1 year of DAT serology requests in our province to assess alignment with current guidance.

METHOD: A line listing of DATS requests was extracted from our laboratory information system (LIS) from May 1, 2023 to April 30, 2024. We evaluated testing volumes and the specialty area of practice of each ordering clinician as per the provincial College of Physicians and Surgeons or their department in the LIS.

RESULTS: During the 1-year period, 2,661 requests for DATS-serology testing were received. The five most common ordering clinician types were physicians in general practice (1,554, 58.4%), immunology (523, 19.7%), nephrology (303, 11.4%), paediatrics (183, 6.9%), and pharmacists (52, 2.0%). With a laboratory cost of $25 per test (base cost plus supplies/technologist time), testing costs for each group were $38,850 (general practice), $13,075 (immunology), $7,575 (nephrology), $4,575 (paediatrics), and $1,300 (pharmacy).

CONCLUSION: Assuming the majority of DATS ordered by general practice and pharmacy groups were likely immunity checks rather than testing for H-ID or post rare adverse event to a DTCV, up to 60% ($40,150) of test requests during the review period may not align with guidance. This volume of non-concordant testing can lead to increased health system (especially laboratory) costs. An important limitation is that individual requisitions were not reviewed to assess test indication. These findings highlight the need for ongoing education regarding appropriate indications for DTCV-related serology testing.

RFD007
Creutzfeldt-Jakob disease testing at the National Microbiology Laboratory, 2016–2024

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OBJECTIVE: Prion disease is caused by misfolding of the host Prion protein (PrP) into an infectious, disease-causing conformation that accumulates in the brain of affected individuals, leading to rapid neurodegeneration and invariably death. The most common human prion disease, sporadic Creutzfeldt-Jakob disease (sCJD), develops spontaneously at a rate of roughly 2 per 1,000,000 population per year. The Prion Disease Section operates out of the National Microbiology Laboratory and provides Canada-wide diagnostic testing services to clinicians confronted with suspected cases of CJD. Surrogate biomarkers for human prion disease, including 14-3-3 and hTau, are routinely measured in patient cerebrospinal fluid (CSF). Importantly, PDS supports CJD diagnosis using the end-point quaking-induced conversion (EP-QuIC) test, which operates with a specificity/sensitivity approaching 100% and directly detects prion seeding activity in patient CSF. Positive CSF tests can be corroborated through postmortem analysis of autopsied tissue, which directly detects the accumulation of specific prion glycoforms in the brain. This information, when interpreted alongside genetic test results describing the patient's genetic status at codon 129 of the prion protein, helps identify the specific prion strain present in individual cases.

METHOD: Results from CSF test panels, genetic testing, and postmortem tissue analysis performed between 2016 and 2024 were retrieved from the NML Laboratory Information Management System. Where possible, prion subtypes were assigned to cases based on codon 129 genotype results, (MM, MV, or VV) and the specific prion glycoform profile detected during postmortem analysis.

RESULTS: Analysis of retrieved data is ongoing. Results will highlight the distribution of prion subtypes detected in Canada between 2016 and 2024 and national trends in CSF test results over the indicated time period.

CONCLUSION: Together, analysis of clinical specimens collected pre- and postmortem capture the landscape

of human prion diseases circulating in the Canadian population.

RFD008

Rapid patient contact tracing following a large measles exposure event using an electronic medical record system

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OBJECTIVE: A travel-related measles case was identified at a paediatric hospital 3 days after admission. This was a significant exposure event impacting the emergency department (ED) and a medical inpatient unit. Timely identification of susceptible contacts is critical to limit further spread of measles by offering post-exposure prophylaxis and initiating appropriate isolation for admitted patients. An investigation was undertaken with the goal of using an electronic medical record system (EMR) to efficiently identify all exposed, susceptible patients in the ED, including the waiting room, and on the inpatient unit.

METHOD: An EMR was used to map the dates and times of the index patient's movements in hospital, as well as the time when appropriate isolation was implemented. Reports were built to extract exposed patient line lists and to facilitate inpatient follow-up by the hospital Infection Control team. Electronic vaccination records were reviewed to determine which exposed patients were susceptible to developing measles.

RESULTS: A total of 315 patients were identified as exposed to the index measles case, including 281 patients in ED and 40 patients on an inpatient unit. One-hundred and eleven of the exposed patient contacts were considered susceptible. Seventeen of the exposed susceptible patient contacts remained in hospital, and of these, 10 were eligible for intramuscular immunoglobulin and 8 received immunoglobulin. None of the 17 admitted patients were eligible for vaccination as post-exposure prophylaxis based on the time from initial exposure. Exposed susceptible patient contacts were identified using the EMR the same day the measles case was identified.

CONCLUSION: Use of an EMR facilitated contact tracing of measles-exposed susceptible patient contacts. This approach enabled efficient, timely contact tracing compared to manual review of patient lists and paper charts to identify patients who required follow-up.

RFD009

A comparative evaluation of the IR Biotyper as a tool for determining relatedness of clinical isolates

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OBJECTIVE: Relatedness between organisms is traditionally determined by genetic comparison methods with often long turnaround times. Processes that can provide faster results may enhance surveillance and outbreak detection. The Bruker IR Biotyper (IRBT) uses for your Fourier-transform infrared spectroscopy to generate "spectroscopic fingerprints" of microbial isolates by measuring infrared absorption at a range of wavelengths. We aimed to evaluate the instrument's suitability as a screening tool in identifying related isolates.

METHOD: Clinical isolates of *Streptococcus pyogenes* ($N =$ 121), *Candida parapsilosis* ($N = 59$), *Salmonella enterica* ($N = 50$), and *Staphylococcus argenteus* ($N = 15$) were analyzed. Frozen isolates were subcultured up to three times to Columbia blood agar, Sabouraud dextrose agar, or tryptic soy agar. Analysis was performed using the instrument's default settings, with linear discriminant analysis applied. Results were compared to "gold standard" genetic data (emm type, whole-genome sequencing [WGS] clusters, O:H typing, sequence type [ST]). A subset of *S. pyogenes* isolates ($N = 14$) was compared to data from previously characterized outbreaks.

RESULTS: The IRBT results were in 58.6% agreement with emm types for *S. pyogenes*; the highest agreement was in *emm* type 1 ($N = 30$) at 74.8%. Outbreak isolates showed 81.5% agreement with their respective WGS outbreak numbers. *C. parapsilosis* isolates were in 78.0% agreement with clusters identified previously by WGS, with one cluster ($N = 5$) at 100% agreement. *S. enterica* isolates clustered at 94.0% agreement with O-serogroups but did not cluster well (36.0%) according to O:H serovars. Agreement of *S. argenteus* isolates with ST was 73.3%, with the highest agreement in ST 2250 ($N = 9$) at 88.9%.

CONCLUSION: The results demonstrate that the IRBT's performance in determining species type and relatedness

varies among organisms evaluated and appears to perform best for *S. enterica* based on O-serogroup. Further investigation is required to determine whether the IRBT can function as a screening tool in an acute care clinical microbiology laboratory.

RFD010

Antibiotic therapy for diabetic foot infections: A systematic review and network meta-analysis

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OBJECTIVE: Optimizing antibiotic regimens for diabetic foot infections (DFI) may reduce morbidity and mortality. Existing meta-analyses of randomized controlled trials (RCTs) are limited to head-to-head antibiotic comparisons. Our recent systematic review and network meta-analysis (NMA) compared both directly (within-trial) and indirectly (across trials) antibiotic regimens for uncomplicated skin and soft tissue infections. Here we present the preliminary results on therapies for DFI (full results available at the conference).

METHOD: A search using Ovid MEDLINE, EMBASE, and Cochrane CENTRAL up to April 15, 2023 was conducted. Eligible RCTs and quasi-RCTs of participants with DFI treated with antibiotics (oral or parenteral) were screened independently and in duplicate, followed by data extraction, risk of bias, and GRADE assessment. Outcomes included clinical improvement at test-of-cure visit (TOC), all-cause mortality, and serious adverse effects (SAE). Absolute network effect estimates (ie, odds ratio) with 95% credible intervals (CrIs) were generated against a standardized comparator.

RESULTS: Twenty-two RCTs ($n = 9{,}292$ participants) met the inclusion criteria, with 16/20 (80%) trials focused on hospitalized patients. To date, an NMA was performed on mortality and SAE for ampicillin-sulbactam, ertapenem, and piperacillin-tazobactam. Participants on ampicillin-sulbactam had a lower mortality when compared to participants on ertapenem (−16.3 per 1,000, 95%CrI −16.3 to −5.8) and piperacillin-tazobactam (−16.3 per 1,000, 95% CrI −16.3 to −9.7). No mortality differences were observed between ertapenem and piperacillin-tazobactam. Estimates for SAEs were similar. Preliminary analysis for TOC suggested similar outcomes across antibiotics studied (analysis pending finalization). Overall risk of bias was high in 19/22 (87%) trials, with most studies at risk of bias for their randomization process (15/22, 68%) and limited allocation concealment (19/22, 87%).

CONCLUSION: To our knowledge, this is the first comprehensive network meta-analysis to address specifically antibiotic-related outcomes for DFI. Final analysis and GRADE assessment are forthcoming.

RFD011

Estimates and projections of susceptibility to polio among the childhood population in British Columbia, Alberta, and Ontario

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OBJECTIVE: Despite decades of progress towards polio eradication, wild and vaccine-derived polioviruses still circulate in numerous regions, posing ongoing risk for countries that have eliminated polio. Recent environmental detections of circulating Vaccine-Derived Poliovirus 2 (cVDPV) in North America and Europe raise concerns regarding the potential for poliovirus transmission in settings with historically high levels of immunization with inactivated polio vaccine (IPV), including Canada. In this study, we estimated the number of potentially polio-susceptible children in three Canadian provinces.

METHOD: We combined publicly available data on subprovincial IPV coverage in successive birth cohorts and age-specific population projections to estimate the number and percentage of children aged <18 years (British Columbia and Alberta) or 7–17 years (Ontario) susceptible to polio in 2024. We projected the expected number of polio-susceptible children in 2035 if vaccination coverage patterns remain at current levels.

RESULTS: In 2024, an estimated 146,000 (14%) children <18 years in Alberta and 237,000 (26%) in BC were polio susceptible. In Ontario, 331,000 (18%) children 7–17 years were polio susceptible. Assuming current vaccination coverage patterns remain constant, by 2035 corresponding numbers of susceptible children are projected to rise

to 207,000 in Alberta (18%), 270,000 (28%) in BC, and 335,000 (18%) in Ontario. In Alberta this corresponds to a 43% increase in susceptible children, driven by suboptimal coverage in certain areas and higher projected population growth in this province; projected increases in BC and Ontario are 14% and 2%, respectively.

CONCLUSION: Understanding geographic differences in population susceptibility to vaccine-preventable diseases, considering both vaccination coverage and demographic changes, is important for informing immunization activities. Such data can also be used in combination with modelling approaches to assess domestic risk. Important caveats include challenges in data comparability across provinces and uncertainties regarding the durability of IPV-induced immunity and impact of in- and out-migration on susceptibility estimates.

RFD012

Examination of remdesivir utilization and appropriateness in COVID-19 patients in acute care: A multi-centre, interrupted time series analysis of standard of care versus drug conservation efforts versus drug conservation efforts plus antimicrobial stewardship intervention

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OBJECTIVE: There are no published data reporting remdesivir (RDV) appropriateness in COVID-19 patients. Given a RDV shortage declared on January 24, 2024, our objectives were to examine RDV utilization, appropriateness, and the effectiveness of two drug conservation interventions.

METHOD: An interrupted time series (ITS) study at two Canadian tertiary care hospitals examined three periods in 2024: Period 1 (January 1–23): standard of care [SOC]; Period 2 (January 24–February 9): drug shortage conservation efforts (CONS); and Period 3 (February 10–March 8): CONS plus prospective audit and feedback (PAF). Hospitalized and emergency department patients age ≥18 years administered RDV were included. The primary outcome was RDV appropriateness assessed against institutional guidelines. Secondary outcomes included utilization (defined daily dose per incident COVID-19 case) and clinical outcomes.

RESULTS: There were 226 RDV prescriptions. The mean patient age was 71 ± 16 years, and 54.7% were men. Most prescriptions were written by Medicine (150, 66%). Overall, 100 (44.2%) RDV prescriptions were for severe COVID-19; 84 (84.0%) were guideline concordant. Another 120 (53.1%) were to reduce the risk of progression to severe disease; 46 (38.3%) were guideline concordant. Of these guideline discordant RDV prescriptions, 37/74 (50%) were for asymptomatic patients and 16/74 (21.6%) lacked risk factors for disease progression. Of the 46 guideline concordant prescriptions, 30 (65.2%) qualified for nirmatrelvir-ritonavir (NMVr) given no contraindications. There were insufficient data in six prescriptions. RDV appropriateness was similar in all three periods (55.1% versus 58.7% versus 61.5%, $p =$ NS) with no utilization difference between periods, or when compared to non-study hospitals in Period 3. NMVr use was minimal. The median LOS was 11 days, 30-day ICU admission rate 5.5%, 30-day mortality rate 9.8%, and 30-day readmission rate 20% with no differences between the periods.

CONCLUSION: RDV use was commonly guideline discordant. CONS and CONS + PAF were not effective strategies to increase appropriateness or decrease utilization.

CASE REPORT SYMPOSIUM

Friday, May 2

CR01

Malaria testing: The importance of LAMP for detecting low-level parasitemia

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OBJECTIVE: This case highlights the utility of loop mediated isothermal amplification (LAMP) in diagnosing chronic low-level parasitemia in malaria infections.

CASE SUMMARY: A 24-year-old male presented to the emergency department with a 48-hour history of headaches. There were no red flags, and he was found to be

afebrile. He immigrated from Uganda 2 weeks prior and had no previous history of malaria prophylaxis or treatment. His physical exam and baseline investigations, including complete blood count, were normal. He was diagnosed with tension headache and was discharged home. He re-presented to the Refugee clinic 48 hours later with worsening headache. The team completed testing for malaria, and his loop mediated isothermal amplification assay (LAMP) came back positive. He was referred to the emergency department for further investigations and review. His rapid detection test (RDT) and thick and thin smears came back negative. (Of note, multiple individuals reviewed the thick and thin smears.) Malaria PCR was completed and confirmed a diagnosis of *Plasmodium falciparum*. He was treated as an outpatient for malaria with resolution of his headache.

DISCUSSION: This case highlights a patient from a malaria-endemic region with low levels of parasitemia leading to a semi-immune state and minor symptom presentation. The case illustrates the increased sensitivity with LAMP (97%–99%, can detect >2 parasites/microlitre) compared to thick and thin smears and RDT (both can detect >100 parasites/microlitre). The diagnosis was confirmed with PCR testing. LAMP is now prioritized in our laboratory for malaria diagnosis due to its high sensitivity. Only positive LAMP results will prompt a smear review. This approach enhances diagnostic accuracy, particularly in low parasitemia cases, underscoring the importance of advanced diagnostic tools in non-classic malaria presentations.

CR02

When common meets rare: Neonatal group B streptococcal sepsis presenting as acute parotitis

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OBJECTIVE: This report highlights an uncommon presentation of a common disease. We describe a 6-week-old infant presenting with acute parotitis and group B *Streptococcus* (GBS) bacteremia. Our aim is to highlight the importance of prompt recognition and management of this rare presentation of late-onset GBS infection.

CASE SUMMARY: We report a case of a 6-week-old infant, born at 36 weeks' gestation via spontaneous vaginal delivery to a GBS-negative mother. He presented to the hospital with fever, irritability, and poor feeding. Clinical examination revealed left-sided facial swelling with erythema and tenderness extending to the neck. Ultrasound confirmed non-suppurative parotitis, and blood cultures yielded GBS within 7 hours of collection. Due to a failed lumbar puncture, the infant was treated empirically for presumed GBS meningitis with a 14-day course of ampicillin. By the third day of treatment, the facial swelling had significantly resolved.

DISCUSSION: Acute suppurative parotitis in neonates is an uncommon infection, most frequently caused by *Staphylococcus aureus*. However, GBS can also be a causative agent, often associated with concurrent bacteremia. GBS case reports typically describe parotitis as a unilateral swelling and fever, often accompanied by positive blood cultures, as seen in our case. While some infants may develop severe complications such as respiratory failure and septic shock, timely diagnosis and treatment generally lead to favorable outcomes. The median age of presentation is approximately 30 days, though cases have been reported in infants up to 12 weeks old. Recurrence of parotitis following treatment has been documented, underscoring the importance of educating parents about potential risks and ensuring close follow-up after discharge.

CR03

First described case of endogenous infection of *Blastomyces dermatitidis/gilchristii* in Newfoundland and Labrador diagnosed on autopsy: A case report

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OBJECTIVE: Blastomycosis is a fungal infection that can be localized to the lungs or disseminated to different body parts. Blastomycosis is endemic to parts of the United States and has been reported to be prevalent in soil near the Great Lakes but is classically not thought to be clinically relevant outside of these areas. This case report describes the first presumed endemic case of blastomycosis in Newfoundland and Labrador.

CASE SUMMARY: An adult immunocompetent male with no lifetime travel history outside of Newfoundland presented to a community center with hypoxia and lesions of the skin and oropharynx. CT scan showed numerous ground-glass opacities with interlobular septal thickening bilaterally. Blood cultures, urine cultures, and viral respi-

ratory panel were negative. He was initially treated with empiric antibiotic therapy with piperacillin-tazobactam and vancomycin. Due to our local microbiology and presence of endemic symptoms, he was also empirically treated for tuberculosis; however, testing was also negative. Six days after the initial presentation, the cytology report from his bronchial washings noted large broad-based budding yeast forms; however, by that time, his family had elected to withdraw care given worsening of his acute respiratory distress syndrome (ARDS). An autopsy was performed, and microbiology histopathological analysis of lung tissue were consistent with *Blastomyces dermatitidis/gilchristii* infection.

DISCUSSION: This case represents a probable increase in the Canadian epidemiology pattern of blastomycosis. With no travel history, it is possible this case represents the first reported probable endogenous case in our province. His cutaneous findings likely represent advanced, diffuse disease. Given this, clinicians should consider blastomycosis in their differential, even in immunocompetent patients with no travel history, especially in those being treated for ARDS with classic cutaneous findings when no other etiology has been found despite ample sample acquisition.

CR04
A case of fatal rabies encephalitis in an 11-year-old child

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OBJECTIVE: To review the diagnostic process for rabies in Canada, critically appraise the Milwaukee Protocol, and explore novel rabies therapeutics such as adenovirus vector–based vaccines and intrathecal rabies immunoglobulin.

CASE SUMMARY: An 11-year-old boy presented with acute right-sided facial droop after 10 days of progressive right eye discharge, facial paresthesias, and numbness. A bat exposure 1 month prior in a Northern Ontario cottage community was recalled: the patient had awoken to a bat on his face covering his nose and mouth. The bat did not appear diseased to the parents and was not observed to scratch or bite the child. The parents had not sought care immediately after this and no post-exposure prophylaxis was administered. Within 24 hours of presentation he was noted to have brainstem dysfunction with impaired gag, nystagmus, and severe dysarthria, as well as hypersalivation. He was not yet encephalopathic, with Glasgow Coma Scale (GCS) of 15. Neuroimaging revealed multifocal lesions involving the brainstem, caudate nucleus, cerebral gray matter, and cervical spinal cord. Over the next 48 hours he had progressive neurological decline to GCS 3. Rabies diagnosis was confirmed on saliva PCR. Intraventricular rabies immunoglobulin was offered but declined by the family. He was managed supportively, and one-way extubation was performed after 2 weeks.

DISCUSSION: Rabies is exceedingly rare and near universally fatal, with the last reported case in Ontario in 1967. The diagnostic process in Canada involves sending nuchal skin biopsy, saliva, and spinal fluid to Canadian Food Inspection Agency for PCR and serum and spinal fluid to National Microbiology Laboratory for serum neutralization testing. Once symptoms appear, there is no role for rabies vaccine or immunoglobulin. The Milwaukee Protocol is an experimental management approach involving therapeutic coma induction introduced in 2004. However, subsequent evidence has not demonstrated reproducible efficacy. Novel therapeutic approaches include intraventricular immunoglobulin and adenovirus vector–based vaccines.

CASE REPORT POSTERS

CRP001
A diagnostic vortex: Orbital vertex syndrome secondary to *Pseudomonas aeruginosa*

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OBJECTIVE: Orbital apex syndrome (OAS) is characterized by vision loss from optic neuropathy and ophthalmoplegias due to the involvement of oculomotor nerves in the orbital apex, namely cranial nerve (CN) II through VI. It can have infectious, inflammatory, neoplastic, endocrine, and vascular etiologies. Our purpose is to highlight factors leading to delayed diagnosis of *Pseudomonas aeruginosa* in causing OAS.

CASE SUMMARY: A 79M with history of pituitary macroadenoma with debulking surgery in 2000 and 2013, bilateral glaucoma, cataracts, and secondary adrenal insufficiency presenting presented with 6-month history of left facial weakness, headache, and left CN VI palsy. His initial diagnosis was giant cell arteritis (GCA) that led to empirical corticosteroids treatment. However, two temporal biopsies

were negative. He progressed to complete bilateral ptosis with vision loss. Lumbar puncture showed mildly elevated protein, no pleocytosis, and negative bacterial and fungal studies. Contrast-enhanced MRI of the brain showed dural thickening ("pachy-meningeal") along the sphenoid bones and extending bilaterally into the orbital apices. A dural biopsy demonstrated acute on chronic inflammation, foci of necrosis. Sterile site cultures grew numerous *Pseudomonas aeruginosa*. Antibiotic therapy resulted in resolution of headaches but not of vision loss or CN palsies.

DISCUSSION: GCA and OAS share clinical features: headache and cranial neuropathies. In this case, a delayed diagnosis resulted from (1) corticosteroid treatment possibly masking clinical and radiologic signs, (2) CSF pleocytosis or peripheral leukocytosis being absent, and (3) dural enhancement being visible only on MRI with gadolinium contrast. This case highlights that patients with a history of trans-sphenoidal surgery presenting with headache and CN palsies should undergo prompt brain imaging (contrast-enhanced MRI) prior to corticosteroids (if GCA suspected) to assess the orbital apices. The absence of documented sinusitis/osteomyelitis does not preclude the possibility that *Pseudomonas aeruginosa* reaches the dural space. Conceivably, inoculation into the dural space occurred at the time of pituitary surgery.

CRP002 – WITHDRAWN

CRP003

A case of pulmonary tularemia from a rural Canadian mink farm

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OBJECTIVE: To describe a challenging-to-diagnose case of pulmonary tularemia acquired through exposure to a mink farm, and to discuss the epidemiology, clinical considerations, and management of *Francisella tularensis* infection.

CASE SUMMARY: This report presents the case of an otherwise healthy 24-year-old man of Jamaican origin who recently immigrated to Canada for employment on a mink farm. He presented to care with fevers, chest pain, and truncal ataxia and proximal muscle weakness. Initial investigations showed a consolidation on chest X-ray and markedly elevated CK and liver enzymes. His CSF was unremarkable. Gram stain from blood cultures revealed Gram-negative coccobacilli, ultimately speciating to *Francisella tularensis*. A diagnosis of pulmonary tularemia causing empyema was made, and he was managed with a pigtail catheter and several weeks of doxycycline.

DISCUSSION: This case presented diagnostic and management challenges for clinicians given the patient's constellation of non-specific symptoms and abnormal bloodwork. *Francisella tularensis* is a slow-growing organism, and an out-of-province referral was required for confirmatory testing, which further delayed diagnosis. The initial differential diagnosis and management decisions made for this patient are discussed, along with the importance of maintaining a high degree of suspicion for this disease when assessing a patient with zoonotic exposure. The discussion also highlights variations among tularemia presentations, including uncommon features such as neuroinvasive disease and rhabdomyolysis, as well as considerations in unwell patients. It cautions against the restrictive misnomer "rabbit fever," describes Canadian epidemiology, and underscores laboratory considerations for safe and efficient identification of the pathogen. Finally, it presents a discussion of pathogen-directed management for pulmonary tularemia.

CRP004

Drug resistant tuberculous meningitis (DR-TBM) in low incidence setting: Two cases and evidence review highlighting key advances and knowledge gaps in clinical management

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OBJECTIVES: 1. Highlight the unique diagnostic and management challenges of DR-TBM, a TB syndrome with high mortality and no evidence-based treatment guidance.

2. Review the role of molecular testing for early diagnosis and treatment decisions in DR-TBM in a low-incidence setting.

3. Present emerging evidence informing decisions around use of novel anti-tuberculous medications for DR-TBM.

CASE SUMMARY: Between 2022 and 2024, two patients with DR-TBM were encountered in a centralized provincial TB program: pre-XDR TBM with disseminated disease (Patient 1) and MDR-TBM (Patient 2). Rapid diagnosis and early treatment decisions utilized molecular diagnostics. Both cases were treated with regimens including novel agents. Drug selection was informed by susceptibility testing and limited clinical and pharmacokinetic data. Patient 1 was treated with Meropenem/Amoxicillin-Clavulanate, Bedaquiline*, Cycloserine*, Linezolid*, Clofazimine*, and Delamanid*. Adverse events included neutropenia, peripheral neuropathy, and ototoxicity. Patient 2 was treated with Moxifloxacin*, Linezolid*, Clofazimine, Cycloserine, Bedaquiline*, and Pretomanid*. Adverse events included suicidal ideation and associated self-harm. There was discordance between phenotypic (susceptible) and genotypic (resistant) drug susceptibility testing for Rifampin, and based on a review of the WHO Catalogue of Mutations, it was decided to treat the case as resistant (Patient 2). In both cases, therapeutic drug monitoring was used. Following 18 (Patient 1) and 12 (Patient 2) months of treatment, both had excellent clinical outcomes up to last follow-up.

*Definitive continuation phase regimen (>9 month)

DISCUSSION: Management of DR-TBM poses unique challenges. Herein we present two cases and review the emerging evidence that can inform management, particularly relating to key decision points including (1) the role of molecular diagnostics in diagnosis; (2) selection of antituberculous regimens (drug and duration) for DR-TBM in the era of novel oral regimens for DR-TB; (3) implications of pharmacokinetics and therapeutic drug monitoring; and (4) clinical decision-making in the setting of discordance between genotypic and phenotypic DST.

CRP005

A rare presentation of *Listeria monocytogenes*: Wrist septic arthritis leading to meningoencephalitis

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OBJECTIVE: Septic arthritis caused by *Listeria monocytogenes* is a rare condition that typically affects large joints, with wrist involvement being exceptionally uncommon and diagnostically challenging. This report describes a unique presentation of *Listeria monocytogenes*–induced septic arthritis in the wrist of a 79-year-old immunocompromised woman, which was then complicated by meningoencephalitis.

CASE SUMMARY: The patient, known for rheumatoid arthritis on methotrexate, presented with progressive wrist pain and edema. Initial treatment for a presumed arthritis flare was ineffective, and her condition worsened with the onset of fever. Imaging revealed a significant abscess in the right wrist, prompting surgical drainage and debridement. Postoperatively, the patient developed seizures and meningoencephalitis, requiring intensive care management. Blood cultures and intraoperative pus cultures confirmed *Listeria monocytogenes* as the causative organism. A lumbar puncture could not be performed, but a brain MRI revealed findings consistent with meningoencephalitis. She received a 6-week course of intravenous ampicillin, which led to clinical improvement.

DISCUSSION: This case adds to the limited literature on *Listeria* arthritis, particularly its atypical presentation involving smaller joints and progression to central nervous system complications. *Listeria monocytogenes* should be considered a potential cause of infectious arthritis in immunocompromised patients presenting with systemic symptoms. This case illustrates the diagnostic challenge of differentiating infectious arthritis from a rheumatoid arthritis flare. Prompt synovial fluid analysis is crucial to avoid diagnostic delays and initiate appropriate treatment.

CRP006

Forward transmission of a *Brucella melitensis* laboratory acquired infection within a large Canadian hospital system

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OBJECTIVE: Highlight difficulties identifying *Brucella* spp. in a non-endemic setting and explain ramifications of misidentification for clinical laboratory personnel through an illustrative case.

CASE SUMMARY: A blood culture from a patient admitted to a peripheral hospital within our hospital system

became positive at approximately 69 hours and was worked up according to standard procedures. The peripheral laboratory identified Gram-positive cocci by microscopy and forwarded the microscopy slides and positive blood culture bottles to our central laboratory for further workup. A corrected report of Gram-positive bacilli was issued. Pinpoint colonies grew on blood and chocolate agars; no identification could be made by automated mass spectrometry. Further testing was performed on the open bench. The isolate was then forwarded to the jurisdictional reference laboratory where it was identified as *Brucella melitensis*. A risk assessment was conducted identifying 14 high-risk exposure events. A staff member who subsequently became febrile presented to two separate emergency departments where blood cultures were obtained. Patient specimens were submitted without information regarding exposure history and grew out *Brucella melitensis*, resulting in exposures at both laboratory sites. Surveillance for additional laboratory-acquired infections is ongoing.

DISCUSSION: Review of 25 years of data from our hospital system identified a total of 10 additional cases of *Brucella* spp., of which 9 did not report Gram-negative coccobacilli from initial Gram stain. A review of the literature found multiple instances of *Brucella* spp. from blood culture with significant morphology and stain variation. Additionally, mass spectrometry libraries for clinical use may not contain extensions for RG3/4 organisms. Root cause analysis of this index event identified several contributing factors for intervention, including education on limitations of Gram stain interpretation, revision of protocols for unidentifiable isolates, and promoting communication between clinical teams and the laboratory.

CRP007

Case series of autochthonous ascariasis in Manitoba, Canada

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OBJECTIVE: This case series serves to alert Canadian medical practitioners of the presence of *Ascaris suum* causing autochthonous ascariasis. We emphasize that ascariasis should be considered in the workup of growth retardation, especially with a history of pig exposure. Using genomic sequencing, we demonstrate that pigs serve as important reservoirs of *Ascaris suum* in Canada. We propose that prevention and control measures should be focused not only on humans but also on infected pigs.

CASE SUMMARY: *Ascaris* is a genus of parasitic nematodes known to cause infections in humans and pigs. From January to December 2024, we identified four cases of autochthonous ascariasis in Manitoba, Canada. All cases were asymptomatic except for an 18-month-old infant who had been failing to gain weight in the prior 6 months. Three of the four cases had contact with pigs on small-scale hobby farms. Given that *Ascaris lumbricoides* and *Ascaris suum* are morphologically identical, we pursued sequencing of the mitochondrial DNA. Phylogenetic analysis using the whole mitochondrial sequence and the *cox1* gene matched *Ascaris suum*. All cases were treated with mebendazole, with good result.

DISCUSSION: To our knowledge, this is the first report of *Ascaris suum* as a zoonotic pathogen in Canada. There are increasing reports of ascariasis in the United States with epidemiologic links to organic pig farms; however, we are the first to provide genomic analysis. Our case highlights the need for Canadian paediatric medical practitioners to inquire about pig exposure and send investigations to rule out ascariasis in cases of growth retardation. From a One Health perspective, future prevention and control measures should focus not only on humans but also on infected pigs.

CRP008

Mycoplasma hominis meningitis in a neonate: Managing in the dark

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OBJECTIVE: We describe a rare case of neonatal *Mycoplasma hominis* meningitis, highlighting diagnostic challenges, surveillance of treatment response, and therapeutic considerations.

CASE SUMMARY: A term female infant presented on the fourth day of life with fever and was started on empiric antibiotics for meningitis. Cerebrospinal fluid (CSF) analysis revealed neutrophilic pleocytosis. *M. hominis* grew on

routine culture media from CSF on the fourth day of incubation. Based on limited published data, the patient was treated with IV moxifloxacin. Magnetic resonance imaging (MRI) showed diffuse leptomeningeal enhancement with empyemas, prompting addition of IV doxycycline. As moxifloxacin is rarely used in children, drug level testing was arranged at an international laboratory and confirmed to be within therapeutic range. Serial MRIs showed mixed responses with resolution of empyemas by 10 weeks, but new enhancements despite clinical stability prompted extension of therapy. After 3 months of moxifloxacin and 10 weeks of doxycycline, neuroimaging again showed fluctuating enhancements. A repeat LP confirmed resolution of pleocytosis with negative cultures. The patient was asymptomatic and thus transitioned to oral moxifloxacin monotherapy. MRI after an additional month of therapy showed mixed resolving/recurring enhancements with normal clinical examination, thus moxifloxacin was discontinued.

DISCUSSION: *M. hominis* meningitis is associated with high morbidity attributable to delayed diagnosis using molecular methods such as 16S PCR, since the organism typically fails to grow in conventional culture. Early detection with growth on routine media is very uncommon and likely accounts for our patient's favourable clinical response without neurological sequelae. Optimal treatment for *Mycoplasma* meningitis remains unclear, though moxifloxacin, combined with doxycycline, has precedent in the literature. Monitoring moxifloxacin drug levels in our patient allowed for confirmation of therapeutic levels. Unique in our case was the use of serial MRIs documenting new leptomeningeal enhancements despite biochemical improvement and normal clinical examination, potentially representing a post-infectious immunologic/neuroinflammatory process.

CRP009

First published use of bacteriophage therapy for a prosthetic joint infection in Canada

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OBJECTIVE: Document the first published use of bacteriophage therapy for a prosthetic joint infection (PJI) in Canada, demonstrating its potential as a safe and effective option for difficult-to-treat infections.

CASE SUMMARY: A 74-year-old male with a total hip arthroplasty in 1973 and multiple revisions developed a methicillin-susceptible *Staphylococcus aureus* (MSSA) PJI in 2013. Hardware removal was not viable, and repeated attempts at suppressive antibiotic therapy, often with dual agents, failed to prevent relapse. The patient underwent seven incision-and-debridements (I&Ds) over the course of his infection. In May 2023, we began to explore bacteriophage therapy. Qeen Biotechnologies identified phages effective against the MSSA isolate, and a two-phage cocktail was selected. Following approval by Health Canada and the University of Calgary (REB23-1733), phages were administered during a planned I&D. Locally, phage was injected into the hip, followed by 2 weeks of twice-daily intravenous therapy with standard-of-care antibiotics. Except from initial mild rigors, therapy was well tolerated and resulted in decreased pain, normalization of inflammatory markers, and improvement in quality of life.

DISCUSSION: PJIs represent a therapeutic challenge, owing in part to biofilm-associated resistance. Bacteriophages, naturally occurring viruses that specifically infect and lyse bacteria, can enzymatically degrade biofilms, enhancing antibiotic efficacy. Emerging evidence for phage therapy in PJIs is promising, with an eightfold reduction in relapse rates (4.5% versus 36.4%) reported in a 2023 trial (PMID: 36851713) and an 88% success rate in a systematic review of bone and joint infections (PMID: 37932115).

Phage therapy is safe, with transient transaminitis as the most common adverse effect. However, regulatory hurdles, cost, and the lack of standardized protocols currently limit its use. Classified as experimental therapy in Canada, phage use is restricted to clinical trials. This case underscores the potential for broader adoption of phage therapy in managing PJIs across Canada.

CRP010

Fuming at a complex finding: A case report of *Aspergillus fumigatus* complex brain abscess in a previously healthy patient admitted with acute liver failure

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OBJECTIVE: Invasive aspergillosis (IA) is a well-known entity in patients with immune compromise, including those with neutropenia, hematologic malignancy, HIV, organ transplantation, or iatrogenic immune suppression. IA has also been described in patients with end-stage cirrhosis or acute liver failure, usually manifesting as a fatal complication in the context of underlying comorbidities and/or steroid use. Our purpose in presenting this case report is to highlight acute liver failure as a risk factor for IA, as well as the importance of close follow-up and tissue biopsy.

CASE SUMMARY: We present a case of a 60M with a history of bipolar disease admitted with acute liver failure secondary to acetaminophen overdose. He was admitted to ICU with altered mentation with initial CT brain findings of vasogenic edema. On repeat imaging 4 days later, there was interval development of a small focus of cortical hyperdensity with surrounding hypodensity in the right precentral gyrus suggestive of microhemorrhage with vasogenic edema. Notably, this microhemorrhage coincided with INR normalization. Over the next 13 days, this evolved into a ring-enhancing pattern with necrotic centre surrounded by a halo of vasogenic edema, causing mass effect. The lesion was biopsied and grew *Aspergillus fumigatus* complex. He was started on voriconazole and was seen 2 months later doing well with no progression of infection.

DISCUSSION: Several factors contributed to this patient's excellent clinical outcome: (1) brain imaging was obtained early due to the patient's altered mental status; (2) the appearance of a focus of microhemorrhage and vasogenic edema coinciding with the normalization of the coagulation profile raised suspicion for angioinvasive infection; (3) timed repeat imaging reinforced this suspicion; and (4) prompt tissue biopsy confirmed the diagnosis. This case adds to published evidence that liver failure, acute or chronic, should be considered a risk factor for invasive aspergillus infection.

CRP011

Two cases of acquired hepatitis B infection without hepatitis B core antibody seropositivity: A driver for change in local laboratory processes

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OBJECTIVE: The diagnosis of hepatitis B virus (HBV) infection is confirmed through the detection of specific serological and molecular markers. In Alberta, positive hepatitis B surface antigen (HBsAg) is automatically reported as "indeterminate" when combined IgM/IgG antibodies to the HBV core antigen (HBcAb total) are not detected, even when HBSAg is a very strong positive with positive confirmatory antibody neutralization testing. We report two cases of chronic HBV infection that were initially missed because of this reporting mechanism, leading us to implement measures to prevent these rare cases.

CASE SUMMARY: Case 1 involves a patient admitted with opportunistic infection from advanced HIV/AIDS. Case 2 involves a patient with chronic lymphocytic lymphoma on rituximab and venetoxclax. In both cases, each patient was screened for hepatitis B with the following results: HBsAg indeterminate, HBcAb total negative. In response to the indeterminate HBsAg result, the HBsAg and HBcAb total were repeated serially with the same result. Due to rising liver enzymes of unclear etiology, both cases eventually underwent HBV DNA molecular testing, which came back strongly positive, indicating a high viral load.

DISCUSSION: These cases highlight the opportunity for quality improvement in reporting HBV serological markers. The use of "indeterminate" for positive HBsAg and negative HBcAb total was misleading and led to a delayed diagnosis of chronic hepatitis B in both cases. In response, our laboratory plans to flag these unusual results (strong HBsAg positive, negative HBcAb total) for further review by the microbiologist on call. In addition, our laboratory has plans for reflex HBV DNA PCR on serum samples with positive HBsAg, regardless of the HBcAb result.

CRP012

Emergence of fluconazole resistance in an isolate of *Candida lusitaniae* causing bloodstream infection in a paediatric oncology patient assessed by whole-genome sequencing: A case report

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OBJECTIVE: To use whole-genome sequencing (WGS) to assess a *Candida lusitaniae* strain causing recurrent bloodstream infection (BSI) with acquisition of fluconazole resistance.

CASE SUMMARY: A male in his mid-teens was admitted to a tertiary care hospital for oncology care and developed a micafungin breakthrough *Candida lusitaniae* BSI on day 28 of hospitalization. Antifungal susceptibility testing performed with the Sensititre™ YeastOne™ panel revealed susceptibility to fluconazole (MIC $\leq$ 0.12 µg/mL). Follow-up blood cultures were negative by day 2 with fluconazole treatment. The patient was treated with fluconazole for 52 days, with a total hospital stay of 83 days. The patient was subsequently discharged on daily fluconazole prophylaxis and readmitted 7 months later for graft failure. At day 8, fluconazole-resistant *Candida lusitaniae* BSI was identified (fluconazole MIC = 128 µg/mL). WGS using Illumina technology (paired-end, 150 bp inserts, Nextera600) was performed on both the susceptible and resistant isolates. We focused on analyzing orthologous genes to those involved in antifungal resistance in other *Candida* species. A unique mutation in *msh2* and a partial deletion of the *mlt1* gene were identified in the resistant isolate. We also demonstrated two aneuploidies on chromosomes CH408081 and GG70277. CH408081 duplication resulted in an increased copy number of *erg3* and *erg11* genes. ERG3 and ERG11 are enzymes involved in ergosterol synthesis, and ERG11 is the direct target of fluconazole action.

DISCUSSION: *C. lusitaniae* candidemia with acquired fluconazole resistance through upregulation of *MFS7* multidrug transporter expression driven by *mrr1* V668G substitution was previously reported in a case series. However, the results in this case show a novel molecular signature and an alternative mechanism, suggesting a wide array of adaptability for azole resistance in *C. lusitaniae*.

CRP013

Microbiologic diagnosis of a cystic soft tissue lesion caused by *Actinomadura madurae*

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OBJECTIVE: To describe the diagnostic process of a rare case of actinomycetoma caused by *Actinomadura madurae*, diagnosed by 16S rRNA sequencing after misidentification as *Nocardia* species by MALDI-ToF.

CASE SUMMARY: A 22-year-old Sudanese female presented with a 3-year history of painless swelling of her left posterior foot with intermittent drainage. Blood work was normal and HIV serology was negative. MRI revealed multilobulated soft tissue mass lesions in the left calf extending to the ankle. Open biopsy tissue pathology showed a cluster of filamentous organisms, while Gram stain identified long, beaded, branching Gram-positive bacilli that were Ziehl-Neelsen negative and modified Kinyoun positive. The organism did not grow on routine culture media but grew tiny white colonies on BCYE at 13 days and in Bactec MGIT tubes. MALDI-ToF (VITEK MS) identified the organism as *Nocardia farcinica* (99.9% match), but the Bruker MALDI Biotyper failed to provide an identification. Subsequent 16S rRNA sequencing of both the isolate and specimen identified *Actinomadura madurae*.

DISCUSSION: Actinomycetoma is a chronic granulomatous disease caused by branching, filamentous Gram-positive bacteria, including *Nocardia*, *Streptomyces*, and *Actinomadura*. It forms small nodules that progress to large, painless lesions and is common in tropical and subtropical regions. *Actinomadura madurae* is a rare causative agent of actinomycetoma. Diagnosis relies on identifying aggregated colonies resembling "grains" on histopathology and often requires molecular confirmation. Treatment is typically

non-surgical and consists of a prolonged course of antimicrobials. This patient has been started on co-trimoxazole with a plan to treat for 1 to 2 years. Our VITEK MS database (v3.2) does not include *Actinomadura* species, leading to the misidentification as *Nocardia*. *Actinomadura* species are also not listed on the Bruker Biotyper 2023 database. The final identification was confirmed by sequencing and morphological examination. This case describes a rare infection and emphasizes the importance of correlating MALDI-ToF results with morphology and other microbiological tests.

CRP014

Difficult-to-treat dermatophyte infection caused by emerging pathogen *Trichophyton mentagrophytes* subtype *indotineae*

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OBJECTIVE: To report a challenging case of dermatophyte infection due to the emerging pathogen *Trichophyton mentagrophytes* subtype *indotineae* in an immunocompromised patient with multiple comorbidities. This case highlights the diagnostic and therapeutic complexities involved and the essential role of molecular testing for accurate pathogen identification and management.

CASE SUMMARY: A 63-year-old woman from Kosovo with severe rheumatoid arthritis (RA) was on immunosuppressive therapy, including tocilizumab, methotrexate, and prednisone, when she presented with a chronic, treatment-resistant dermatophyte infection. Her rash began 6 years prior, initially under her breasts, and later spread to her trunk and upper limbs, forming large, itchy erythematous patches with raised, annular borders. Initial fungal cultures identified *Trichophyton mentagrophytes*. Fluconazole was initially effective but was withheld due to drowsiness from interactions with her seizure medication, clobazam. After tapering clobazam, fluconazole was reintroduced; however, when the dose was tapered, the infection relapsed. By that time, a second culture had been collected, confirming *T. indotineae*. Fluconazole was subsequently stopped, and treatment was switched to itraconazole 200 mg twice daily, resulting in complete resolution of her rash with only mild residual itching managed by antihistamines. Continued itraconazole treatment was planned for 12 months to prevent relapse, alongside ongoing monitoring of her condition and RA management.

DISCUSSION: This case highlights the complexities of managing *T. mentagrophytes* subtype *indotineae* infections in an immunocompromised patient with severe rheumatoid arthritis. Persistent infection, despite multiple antifungal therapies, required adaptive treatment due to antifungal resistance and drug interactions. Switching to itraconazole ultimately led to improvement, underscoring the importance of flexible strategies in resistant cases. It emphasizes the need for molecular identification of *T. indotineae* in non-responsive dermatophytosis, even in non-endemic regions such as Canada. Key takeaways include the importance of antifungal stewardship, susceptibility testing, high index of suspicion, and interdisciplinary collaboration in managing treatment-resistant infections in immunocompromised patients.

CRP015

Ruptured fungal mycotic aneurysm resulting in catastrophic intraabdominal hemorrhage: Rare infectious complication of sarcoidosis

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OBJECTIVE: This case report has two primary purposes: (1) to highlight the increased risk for severe infectious complications in patients with advanced sarcoidosis owing both to inherent adaptive immunodeficiency and to use of immunosuppressive therapy; and (2) to report a ruptured fungal mycotic aneurysm, a rare infectious complication with few cases reported in peer-reviewed literature.

CASE SUMMARY: Mycotic (infectious) aneurysm is a rare and life-threatening complication of systemic infection, frequently associated with infective endocarditis. We report the case of an early-50s male with pulmonary sarcoidosis prescribed corticosteroids, who presented to hospital following abrupt cessation of therapy. He was found to have bacteremia and experienced a precipitous drop in hemoglobin, dying in hospital before the source of bleeding could be identified. A postmortem examination revealed a massive intraabdominal hemorrhage from a distal superior mesenteric artery mycotic aneurysm in the context of IE. Aortic valve vegetations were found at autopsy, and bacteria and fungi were observed on microscopy. Several distant body sites, including the site of aneurysm rupture as well as the brain and spleen, showed septic emboli on histology. In consultation with an expert pulmonary pathologist, autopsy findings confirmed advanced sarcoidosis with multiple extrapulmonary sites of involvement.

DISCUSSION

Key Points:

- Mycotic aneurysms are rarely caused by fungal pathogens; this case represents the first SMA fungal aneurysm reported in literature.
- Patients with sarcoidosis are at high risk of developing severe opportunistic infections, owing both to inherent adaptive immunodeficiency associated with sarcoidosis and to the use of systemic immunosuppressive agents in the treatment of sarcoidosis. The case aims to highlight the importance of monitoring for infectious complications in patients with sarcoidosis. The patient presented in this case report showed features of advanced pulmonary and extrapulmonary sarcoidosis on autopsy.
- Visceral mycotic aneurysms are a catastrophic complication of IE and should be considered in septic patients with mutable and non-specific gastrointestinal symptoms.

CRP016

Lymphomatoid granulomatosis involving the central nervous system in an immunocompromised patient

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OBJECTIVE: To describe a rare cause of rim-enhancing central nervous system (CNS) lesions in immunocompromised hosts.

CASE SUMMARY: We present a 38-year-old man with recent diagnosis of Epstein-Barr virus (EBV)-positive diffuse large B-cell lymphoma and hemophagocytic lymphohistiocytosis. He completed five cycles of R-CHOEP (Rituximab-Cyclophosphamide-Doxorubicin-Vincristine-Etoposide-Prednisone), with positive treatment response. Screening MRI head performed 8 months after diagnosis revealed multifocal rim-enhancing lesions involving the right basal ganglia and bilateral temporal lobes. He was referred to our centre for diagnostic resection. Histopathology revealed dense polymorphic infiltrates comprised of histiocytes, lymphocytes, and sparse, highly atypical, and often multinucleated giant cells, with an angiocentric and angiodestructive distribution. Epstein-Barr encoding region (EBER) in situ hybridization was positive in numerous cells; this was consistent with grade 3 lymphomatoid granulomatosis (LYG). The patient was resumed on chemotherapy with second-line MATRix (Methotrexate-Cytarabine-Thiotepa-Rituximab) and is currently awaiting autologous stem cell transplantation.

DISCUSSION: LYG is a rare EBV-associated lymphoproliferative disorder, hypothesized to arise from defective immune surveillance of EBV-infected B cells, notably a functional defect in $CD8^+$ cytotoxic T cells, leading to sustained lytic replication. LYG most commonly affects the lungs, followed by CNS, skin, kidney, and liver. CNS involvement is observed in approximately one-third of patients; neuroimaging typically demonstrates focal intraparenchymal lesions, which can develop rim enhancement. Unlike other EBV-associated lymphoproliferative disorders, LYG rarely involves lymph nodes and bone marrow. Diagnosis is typically made pathologically; LYG is characterized by a unique polymorphous angiocentric and angiodestructive infiltrate with coagulative necrosis. EBV (via EBER in situ hybridization) is typically present. LYG is graded histologically as low-grade (grades 1 and 2) and high-grade (grade 3) based on the number and density of EBV-positive atypical B cells. Treatment of LYG depends on disease grade and underlying disease biology, and includes immunomodulation via reducing existing immunosuppression, combination immunochemotherapy, and hematopoietic stem cell transplant.

CRP017

Tuberculosis of the left wrist presenting as chronic monoarthritis with sinus tract formation

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OBJECTIVE: To describe an unusual presentation of osteoarticular tuberculosis.

CASE SUMMARY: We present an 85-year-old Mauritian-born man of Chinese descent admitted to hospital for chronic progressive left wrist deformity. He developed left wrist pain and swelling 1 year before presentation. Nodular lesions subsequently formed, which would open with seropurulent discharge and reveal underlying fascia and tendon. X-ray demonstrated diffuse destruction of the

carpal bones, metacarpals, and distal radial/ulnar metadiaphyses. He ultimately underwent surgical management, with irrigation/debridement and instrumented fusion of the left wrist. Intraoperatively, extensive erosion of the wrist structures was appreciated. Histopathology demonstrated abundant necrotizing granulomatous inflammation. Few acid-fast bacilli were identified on smear. *Mycobacterium tuberculosis* complex was detected via polymerase chain reaction (BD MAX™ MDR-TB assay), and *M. tuberculosis* was subsequently confirmed on culture. Phenotypic drug susceptibility testing demonstrated susceptibility to first-line agents. The patient was started on rifampin, isoniazid, ethambutol, and levofloxacin, with pyrazinamide avoided due to age and comorbid gout. At 6-month follow-up, there has been significant improvement in his left wrist. He remains on maintenance therapy with rifampin and isoniazid, with planned duration of therapy of at least 9 months.

DISCUSSION: Osteoarticular disease comprises approximately 10% of extrapulmonary tuberculosis in Canada, most commonly involving the spine/vertebrae and large, weight-bearing joints. Tuberculosis of the wrist, defined as involvement of the carpal bones, metacarpals, and distal radius and ulna, accounts for less than 1% of osteoarticular tuberculosis. The clinical presentation is often insidious, with progressive swelling, pain, and digital numbness from nerve compression. In advanced cases, joint stiffness and draining sinus tracts can form, as was seen in our case. Diagnosis is typically made via tissue sampling for mycobacterial culture and histopathology. Treatment is with standard anti-tuberculosis therapy for at least 6 months, with extension up to 12 months based on clinical and microbiologic factors.

CRP018

Massive chest wall and flank tuberculous abscess with associated Pott's disease: A case report

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OBJECTIVE: Tuberculosis (TB) with vertebral involvement (Pott's disease) is a morbid condition that is rare in regions with low TB incidence. We present a case of large tuberculous chest wall and flank abscess with associated Pott's disease, highlighting this disease's insidious presentation and the extent of disease burden that may develop if time to diagnosis is delayed.

CASE SUMMARY: An immunocompetent 22-year-old male who immigrated to Canada from India presented to the emergency department with a bulging mass on the right side of his back that had been slowly enlarging over the past year. There were no associated back pain, systemic symptoms, or respiratory complaints, and he was neurologically intact. CT scan and MRI demonstrated a 46 × 26 × 8-cm collection extending from the right chest wall just posterior to the first rib down to the flank at the L4–L5 level. There was an associated communicating phlegmon involving the T8–T10 vertebral bodies, as well as involvement of the 7th–9th ribs. Interventional Radiology performed a partial drainage procedure, removing 1.7 L of purulent fluid that was positive for *Mycobacterium tuberculosis* complex (MTBC) by GeneXpert MTB/RIF testing with subsequent confirmation of MTBC by culture. There was no evidence of active pulmonary involvement. Anti-tuberculous medications were initiated, with planned treatment duration of 12 months.

DISCUSSION: This case highlights that musculoskeletal TB including Pott's disease may present with subtle nonspecific symptoms that develop over the course of months to years, which can result in substantial delay to diagnosis. Systemic features may be absent even in the setting of high disease burden. While this is an unusual disease in Canada, high index of suspicion is important to prevent disease complications especially in the setting of changing local TB epidemiology and immigration patterns.

CRP019

Detection of *Plasmodium falciparum* by 16S rDNA sequencing from pericardial fluid in a patient with negative blood antigen and microscopy

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OBJECTIVE: This case describes a clinically complex scenario where *Plasmodium falciparum* was discovered in an unlikely clinical specimen via 16S rDNA sequencing by detection of apicoplast organelle genetic material—a finding not previously reported in the literature.

CASE SUMMARY: A 73-year-old Nigerian visiting Canada with chronic hypertension on daily Aspirin and antihypertensives was admitted 2 weeks after arrival with acute exertional dyspnea and tachycardia. Imaging showed a large pericardial effusion and multifocal ground-glass opacities, while blood work showed microcytic anemia. Initial malaria whole-blood antigen and microscopy tests were negative. Pericardiocentesis revealed serosanguineous fluid with negative microscopy and cultures (bacterial, mycobacterial, fungal). The patient left against medical advice within 72 hours of admission but returned shortly after in respiratory distress with evidence of pulmonary edema. He was intubated and given meropenem for presumed sepsis and doxycycline based on a low-positive rickettsial serology result. The initial pericardial fluid underwent 16S rDNA testing, with a sequence matching *P. falciparum* apicoplast DNA. Malaria antigen testing and *P. falciparum* qPCR on the fluid confirmed the 16S rDNA finding, although repeat blood samples collected a month after doxycycline were negative by microscopy and antigen testing. The patient received a 3-day course of atovaquone-proguanil and improved clinically after an extended hospital stay complicated by delirium and deconditioning. He remains well at follow-up post-discharge.

DISCUSSION: This case highlights a rare presentation of *P. falciparum* infection diagnosed from a pericardial effusion. It demonstrates the value of 16S rDNA PCR sequencing in infectious disease diagnoses, even though it is not recommended as a diagnostic method for malaria. It also underscores the importance of maintaining malaria as a differential diagnosis in patients from endemic regions despite initially negative microscopy or antigen tests, and the potential of increasingly prevalent molecular methods to unravel similar atypical cases.

CRP020

A case of multidrug-resistant *Bacteroides fragilis* in a newly arrived Canadian

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OBJECTIVE: *Bacteroides fragilis* is not typically considered a challenging pathogen to treat in North America. However, rare cases of imported multidrug-resistant (MDR) *B. fragilis* have been reported. We present an MDR strain isolated in a newly arrived Canadian carrying genes linked to metronidazole and carbapenem resistance.

CASE SUMMARY: A 28-year-old female born in Afghanistan, recently immigrated to Canada from Pakistan, presented with abdominal abscesses secondary to a perforated bowel. Bacterial culture from abscess drainage identified *B. fragilis*, alongside *E. coli* (AmpC-producing), *K. oxytoca*, and *E. faecium*. The *B. fragilis* isolate was resistant to piperacillin-tazobactam, carbapenems, clindamycin, metronidazole, and tetracycline but susceptible to moxifloxacin, imipenem-relebactam, and tigecycline. Carbapenemase production was positive via anaerobic mCIM. MALDI-TOF (Bruker) presumptively identified the isolate as a CfiA carbapenemase producer. PCR at the National Microbiology Laboratory (NML) confirmed the presence of the *cfiA* gene. Whole-genome sequencing identified antimicrobial resistance genes (*nimE*, *tet(Q)*, *cfiA*, *erm(F)*, *cfxA3*, *sul2*), correlating with phenotypic resistance.

DISCUSSION: MDR *B. fragilis* is rarely reported in North America, with only 50 *cfiA*-positive isolates documented in Canada by NML since 2011. Data on resistance to other antimicrobials in these isolates remain unavailable. Most North American cases involve travel history. MDR *B. fragilis* prevalence varies globally: 4%–40% reported in China, Japan, Slovenia, Belgium, and the UK. Although published data from Pakistan or Afghanistan are lacking, cases in travellers from Afghanistan have been reported in the United States. This case highlights the need to consider travel or immigration from regions with high MDR pathogen prevalence when selecting empiric therapy prior to susceptibility results.

CRP021

Echoes of the past: *Haemophilus influenzae* type b resurfaces in a rare non-facial cellulitis case

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OBJECTIVE: This case report aims to expand the understanding of *Haemophilus influenzae* type B (HiB)-associated skin and soft tissue infections, specifically non-facial presentations. It highlights the need for continued vigilance in underimmunized populations and provides a review of the literature on this rare manifestation. Additionally, the report explores the role of vaccination and herd immunity in reducing the prevalence of what was once a common infection.

CASE SUMMARY: An 11-month-old unimmunized girl presented with a 2-day history of a red-purplish spot on her right leg that progressed to erythema, tenderness, and fever. Clinical examination revealed an indurated erythematous lesion on the right leg. Lab results showed elevated WBC and CRP, and blood cultures identified *Haemophilus influenzae* type B. Treatment was initially started with intramuscular ceftriaxone, followed by IV ampicillin once antibiotic susceptibility results were available. The patient completed 10 days of antibiotic therapy with full resolution of symptoms.

DISCUSSION: Hib was historically a major cause of morbidity and mortality in children under 5, particularly due to its association with bacterial meningitis and pneumonia. Skin and soft tissue infections caused by Hib were primarily observed as facial cellulitis, resulting from its nasopharyngeal colonization. However, non-facial cellulitis remains an exceptionally rare manifestation, even prior to widespread vaccination, with only three documented cases of lower limb cellulitis between 2000 and 2017. A 1965 study by Murray Feingold and Sydney S. Gellis identified a distinctive clinical sign of Hib cellulitis: a characteristic red-purple discoloration, which was also noted in our case. The implementation of routine Hib vaccination programs has led to a dramatic reduction in Hib infections, with incidence rates decreasing by over 90% and near elimination in regions with high vaccine coverage. This case underscores the importance of vigilance in diagnosing and managing Hib infections in underimmunized populations to prevent the resurgence of this once-prevalent pathogen.

CRP022

A case of chronic intestinal schistosomiasis diagnosed through colonoscopy

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OBJECTIVE: The symptoms of chronic intestinal schistosomiasis (CIS) can be non-specific and easily dismissed or misdiagnosed as other bowel pathologies. In this case report we discuss a diagnosis of CIS by colonoscopy and discuss how awareness of such presentations, coupled with a thorough travel and exposure history, may provide initial clues to alert one to the diagnosis.

CASE SUMMARY: We report a 42-year-old man with an over 5-year history of fluctuating left lower quadrant pain, intermittent diarrhea, and occasional hematochezia. He had emigrated to Canada 17 years previously after living in Uganda and South Sudan. He reported no current health issues but in childhood had been hospitalized for 6 months with schistosomiasis, which was treated using traditional medicine. Physical examination revealed a soft abdomen with some mild tenderness in the left lower quadrant with deep palpation.

The patient underwent colonoscopy when an abnormal vascular pattern was noted, described as star-shaped vasculature in the distal colon with uninflamed, non-friable mucosa. In addition, five sessile polyps were resected from the rectosigmoid and the rectum. Histology found viable schistosoma eggs surrounded by granulomatous histiocytic and mixed inflammation in the lamina propria and submucosa. Serology for schistosomiasis was positive; however, stool testing for ova and parasites was negative ×3. Review of the histology identified ova consistent with *S. mansoni*. Based on the positive serology and colonoscopy

findings, the patient was treated with 600 mg praziquantel TID for 2 days and reported a complete recovery 2 weeks post-treatment.

DISCUSSION: This case demonstrates how CIS may present in non-endemic settings, demonstrating the diagnostic challenges due to its non-specific symptoms, ambiguous lab work, and unclear infection history. Ultimately, for our patient, it was the unique vascular pattern on colonoscopy that signalled something atypical, and biopsy helped confirm the diagnosis.

CRP023

Prosthetic valve infective endocarditis secondary to *Rothia dentocariosa* associated with the formation of multiple mycotic pseudoaneurysms

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OBJECTIVE: *Rothia dentocariosa* is a rare cause of infective endocarditis that is associated with a high incidence of mycotic aneurysms. We describe a rare case of prosthetic valve infective endocarditis secondary to *Rothia dentocariosa*, complicated by multiple tibioperoneal and hepatic mycotic aneurysms.

CASE SUMMARY: A 77-year-old woman with prior transcatheter aortic valve implantation (TAVI) presented with 10 days of myalgia, diarrhea, fever, and lethargy. Blood cultures drawn 12 hours after initiation of ceftriaxone for possible urinary tract infection were negative for growth. Computer tomography (CT) imaging of the abdomen showed focal splenic infarcts. She later developed right calf pain, and imaging revealed a pseudoaneurysm arising from a blowout of the distal tibioperoneal trunk, requiring surgical repair. While off antibiotics, two sets of blood cultures were sent, and one of four bottles was positive for the growth of *Rothia dentocariosa*, susceptible to penicillin. Piperacillin-tazobactam and vancomycin were initiated, later switched to ceftriaxone monotherapy. Transthoracic echocardiography (TTE) showed no obvious vegetations. CT angiography revealed a subacute infarct of the corpus callosum, suspected vegetations within the aortic valve implant, splenic infarcts, and mycotic aneurysm of the right hepatic artery. Transesophageal echocardiography (TEE) showed significant aortic prosthetic valve dysfunction, two vegetations, and an aortic perivalvular abscess. She subsequently developed worsening calf pain with a new left tibioperoneal trunk pseudoaneurysm, again requiring surgical repair. Seven weeks later, she underwent aortic valve replacement and aortic root abscess repair. Intraoperative valvular tissue culture was negative for growth, but 16S PCR amplified bacterial DNA from the explanted valve tissue was consistent with *Rothia dentocariosa*. She completed additional 2 weeks of ceftriaxone following aortic valve replacement.

DISCUSSION: This case highlights the unique propensity for *Rothia dentocarisoa* endocarditis to form mycotic aneurysms, and the importance of obtaining blood cultures prior to initiating antibiotics in patients with suspected infective endocarditis.

CRP024

When the bugs go viral: A case of West Nile virus encephalitis

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OBJECTIVE: West Nile encephalitis is a rare but notable condition in Canada. It can mimic other, more common neurologic and infectious diseases, and recognizing classic signs is crucial for a prompt diagnosis. This case highlights pertinent clinical and biochemical findings of West Nile virus (WNV) encephalitis that may be missed due to the unique presentation of the infection.

CASE SUMMARY: After working at his cabin at a lake in Western Manitoba in the summer, a man in his 70s from Western Manitoba presented to a local hospital with proximal limb weakness and gastrointestinal symptoms. His subsequent transfer to an academic hospital was triggered by the new development of chest pain, and he was diagnosed with myocarditis. Over the course of his hospitalization, he developed worsening neurologic symptoms, including bulbar weakness leading to aspiration and hypoxia. After intubation, a lumbar puncture was performed, revealing elevated white blood cells including lymphocytes and plasma cells. Eventually, WNV IgM positivity in the cerebrospinal fluid led to a final diagnosis of WNV encephalitis.

DISCUSSION: This case underscores the importance of maintaining a broad differential diagnosis in encephalitis, as well as in myocarditis, and obtaining confirmatory testing early. This patient demonstrated some of the classic clinical findings of WNV encephalitis including rash and neurologic findings similar to that of poliomyelitis. Imaging studies, including MRI, CT, and EEG, show no specific

findings indicative of the virus. Similarly, without directed testing for WNV IgM, there is no classic biochemical profile for diagnosis, although the presence of lymphocytic pleocytosis and plasma cells on lumbar puncture can be suggestive of WNV encephalitis. Finally, it serves as a reminder of the importance of preventive measures against WNV, which does not have a treatment beyond supportive care and can be devastating.

CRP025

Severe community-acquired pneumonia with acute respiratory distress syndrome due to *Blastomyces gilchristii*

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OBJECTIVE: Consider empiric treatment for pulmonary blastomycosis in critically ill patients with community-acquired pneumonia (CAP) who fail to respond to antibiotic therapy. Without accessible urinary antigen testing, microscopy of respiratory specimens can rapidly identify blastomycosis.

CASE SUMMARY: A 41-year-old man was transferred to our intensive care unit from a community hospital with severe CAP and acute respiratory distress syndrome requiring intubation and venovenous extracorporeal membrane oxygenation. He deteriorated despite outpatient amoxicillin and levofloxacin followed by inpatient piperacillin-tazobactam and azithromycin. He was otherwise healthy aside from locally resected bladder cancer 5 years prior. Travel history was notable for outdoor excursions to the Sudbury and Barrie areas in the few months preceding.

He was empirically started on liposomal amphotericin B (LAmB) to cover endemic fungi pending bronchoscopic workup. Microscopy of bronchoalveolar lavage fluid (BAL) revealed abundant yeast resembling *Blastomyces* spp., and BAL galactomannan was elevated. Culture ultimately grew *Blastomyces gilchristii*. He was continued on LAmB for a 4-week course, by which time he was extubated to supplemental oxygen. He did not tolerate transition to itraconazole due to hepatotoxicity and was switched to 1 year of isavuconazole.

DISCUSSION: *Blastomyces gilchristii* is a recently defined member of the *Blastomyces dermatitidis* species complex endemic to Northern Ontario. Although clinical data on *B. gilchristii* are sparse, it is usually limited to pulmonary disease that can be severe**.** Empiric therapy with LAmB should be considered in critically ill patients with CAP who fail empiric antibiotics and have had exposure to endemic areas. Canadian access to non-invasive urinary antigen testing is limited, so early diagnosis relies on microscopic recognition of typical yeast forms in respiratory specimens. BAL galactomannan can be a useful adjunctive test due to antigenic cross-reactivity. Clinical experience with oral agents other than itraconazole is limited, but our case suggests isavuconazole is reasonable in patients who experience itraconazole-related toxicities.

CRP026

Helicobacter cinaedi bacteremia in a 2-month-old well-appearing febrile infant

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OBJECTIVE: Highlight the clinical presentation, diagnostic challenges, treatment, and outcome of *Helicobacter cinaedi* bacteremia in a healthy infant.

CASE SUMMARY: A 2-month-old full-term boy presented with a fever (39°C) without focal symptoms. The initial workup showed leukocytosis and elevated CRP. He received IV ampicillin and cefotaxime for 48 hours. Later, the blood culture grew Gram-negative bacilli (GNB) after 4 days. Despite being afebrile and doing well, he was recalled for clinical evaluation and prescribed 5 days of oral azithromycin given the suspicion of possible Campylobacter on Gram stain. A repeat culture (GNB) grew after 4 days, so he was readmitted and started on IV ampicillin and gentamicin. 16s PCR identified the GNB as *Helicobacter cinaedi*. Exposure history revealed contact with a deceased hamster and family dog. Further workup, including CSF, echocardiogram, abdominal ultrasound, and immunology evaluation, was normal. He completed 6 days of IV therapy and was discharged on oral amoxicillin and trimethoprim-sulfamethoxazole for a total antibiotic duration of 2 weeks.

DISCUSSION: *Helicobacter cinaedi* is a Gram-negative spiral bacterium belonging to the family Helicobacteriaceae of the order Campylobacterales. It is difficult to grow on culture and usually takes 4 to 10 days, requires microaerobic conditions and high humidity. The identification is made

by MALDI-TOF or 16s PCR. It has multiple reservoirs, including hamsters, dogs, cats, and humans. It can infect both immunocompetent and immunosuppressed individuals. Clinical manifestations vary from bacteremia, common in all age groups, to gastrointestinal symptoms, cellulitis, and, rarely, arthritis or meningitis. Paediatric cases are rare, ranging from mild to severe presentations. *H. cinaedi* resists macrolides and quinolones but responds to carbapenems, aminoglycosides, tetracyclines, penicillin, and cephalosporins. Long-term antibiotic therapy (2–6 weeks) is advised, even for asymptomatic patients. The prognosis is generally favourable, but recurrent bacteremia may occur, likely due to gastrointestinal translocation.

CRP027

Unmasking rare *Ignatzschineria* bacteremia: Clinical history informs modern diagnostics

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OBJECTIVE: Demonstrate how clinical history and up-to-date microbiology knowledge led to the earlier and successful identification of bacteremia with a rare maggot-associated pathogen.

CASE SUMMARY: A 55-year-old female with uncontrolled diabetes and prior below-knee amputation presented with a diabetic foot infection complicated by maggot infestation. Blood cultures demonstrated polymicrobial bacteremia, including a Gram-negative bacillus resembling *Pasteurella*. Routine tests failed to identify this, automated GNI provided no identification, and VitekMS MALDI-TOF provided discrepant results. The isolate was referred for 16S sequencing. While awaiting 16S's result, the reference lab Bruker MALDI produced a high-scoring but unusual identification: "*Ignatzschineria* larvae." Microbiology trainees at the bench instantly recognized this organism's association with maggots. Because the ordering physician had specifically flagged the presence of maggot infestation, the microbiology team was able to establish a perfect correlation between an unusual organism and its characteristic clinical association. A detailed review of the newly added *Ignatzschineria* section of the Manual of Clinical Microbiology corroborated this identification. Based on compatible Gram stain, colony morphology, biochemicals, and clinical context, the laboratory promptly communicated this preliminary identification in the context of its relevance for this patient and its typical antimicrobial susceptibility to assist with clinical management while awaiting 16S. Two days later, 16S sequencing confirmed *Ignatzschineria*.

The patient received appropriate antimicrobials, followed by definitive source control with below-knee amputation and successful resolution of infection.

DISCUSSION: What would you do if you saw *Ignatzschineria* in a blood culture? Integration of patient history with advanced diagnostic methods is essential for accurate identification of rare pathogens in medical microbiology. *Ignatzschineria* causes human infections but is rarely seen, is challenging to identify, and has no antimicrobial breakpoints. This case demonstrates that the laboratory's awareness of clinical context can guide testing to suitable identification methods and keep clinical teams informed along the way.

CRP028

Paraburkholderia fungorum: A *Burkholderia mallei* imposter and unexpected blood culture contaminant in Canada and the US

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OBJECTIVES: (1) Alert labs and physicians to this slow-growing contaminant reported in Canada and several US states. (2) Request information from other Canadian labs that may see *Paraburkholderia* spp.

CASE SUMMARY: Between August and December 2024, blood cultures from three patients with unrelated medical concerns grew an unusual organism that was not identified with routine diagnostic methods. The organism grew after >50 hours incubation from aerobic vials only. Microscopy demonstrated small (not tiny), faint/bipolar staining Gram-negative bacilli. Unremarkable grey, non-hemolytic colonies grew slowly on blood agar (48–72 hr) with no growth on MacConkey agar (48 hr). Isolates tested weak/positive for catalase and negative for oxidase/indole/urease, which is compatible with *Burkholderia mallei*. Isolates were sent to the public health laboratory, and Risk Group 3 (RG3) pathogens were ruled out. 16S rDNA sequencing identified all three isolates as *Paraburkholderia fungorum*, consistent with their macroscopic, microscopic, and biochemical profiles (though usually oxidase positive). This environmental organism has been implicated in rare human infections; however, for these three patients, *P. fungorum* was determined to be a blood culture contaminant. These findings echoed a 2024 alert: the Minnesota Department of Health described a sharp increase in *P. fungorum* from blood cultures, where true bacteremia was thought unlikely after chart reviews by an Infectious Disease physician. This organism seems to be a recurring blood culture contaminant and has now been reported from multiple US states. Whole-genome sequencing will be used to assess the relatedness of these Canadian isolates with those from the United States.

DISCUSSION: *Paraburkholderia fungorum* is an environmental organism that mimics *B. mallei* phenotypes and is the subject of an ongoing investigation of possible blood culture vial contamination. To our knowledge, this is the first report outside the United States. Contact us if you see any *Paraburkholderia* species in your lab to help with this investigation.

CRP029

Candida blankii: A new emerging fungal threat?

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OBJECTIVE: *Candida blankii* is an emerging fungal pathogen that has been implicated in recent case reports of candidemia, osteoarticular infections, otomycosis, and respiratory colonization (in cystic fibrosis patients). Similarly to *Candida auris, C. blankii* has also been associated with outbreaks in the health care setting (eg, in neonates) and has demonstrated reduced susceptibility to azoles and echinocandins. Despite this, little is known about the pathogenicity and epidemiology of *C. blankii*, including its ability to colonize human skin or mucosa, because reliable identification of this organism remains a challenge in the lab. Furthermore, not all yeast, including *Candida* spp., may be identified to species level in the laboratory depending on the specimen type (eg, skin, respiratory). We describe the first case of *C. blankii* identified serendipitously at our institution.

CASE SUMMARY: A skin scraping from the leg of an adult inpatient was submitted to the microbiology laboratory. No fungal elements were seen on direct examination with calcofluor white. On day 12 of incubation, growth of yeast-like colonies was observed, and identification was attempted with MALDI-TOF MS. Use of the Bruker MALDI Biotyper® (MBT) BDAL V12.0 library yielded no positive identification for this isolate. The isolate was eventually identified as *C. blankii* using the mass spectrometry identification (MSI)-2 database (score of 51.22A) with confirmation by in-house ITS sequencing. The minimum inhibitory concentrations (MICs) after 48-hour incubation were fluconazole (64), voriconazole (4), micafungin (0.25), and amphotericin B (1).

DISCUSSION: *C. blankii* was identified as a likely skin colonizer at our institution and exhibited reduced susceptibility to azoles. This case highlights the importance of laboratories to consider species level identification of all yeasts, especially *Candida* spp., from most specimen types, as well as the ongoing need for improved fungal identification protocols to better understand the epidemiology and pathogenicity of new emerging multidrug resistant yeasts, such as *C. blankii*.

CRP030

Chagas meningoencephalitis and myocarditis from reactivation of occult chronic *Trypanosoma cruzi* infection after cardiac transplantation

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OBJECTIVES: Recognize manifestations of Chagas disease in the solid organ transplant (SOT) population. Explore diagnostics for Chagas central nervous system (CNS) infection. Demonstrate the role of high-dose benznidazole for treatment of Chagas meningoencephalitis.

CASE SUMMARY: A 51-year-old female from El Salvador underwent heart transplantation for presumed peripartum cardiomyopathy. She received anti-thymocyte globulin induction followed by tacrolimus, mycophenolate mofetil, and prednisone maintenance. Two months later, she presented with a 1-week history of confusion and progressive weakness, speech disturbance, right-sided facial droop, and hemiplegia, along with upgoing Babinski sign. Neuroimaging revealed subacute infarction with surrounding edema of the left basal ganglia, internal capsule, and thalamus suggesting early cerebritis/encephalitis. This was accompanied with new ventricular bigeminy with mild troponin elevation but normal cardiac function by echocardiography. Extensive review of referred-out testing revealed a prior positive IgG-ELISA serology for *Trypanosoma cruzi*. Chagas reactivation with CNS and cardiac involvement was suspected, prompting high-dose benznidazole. Blood and CSF smears were negative for trypomastigotes. Repeat *T. cruzi* serologies submitted to two reference laboratories were highly positive by IgG-ELISA and immunoblot with all six antigen targets detected. Allograft biopsy was negative for both *T.* cruzi PCR and cellular rejection. *T. cruzi* blood and CSF PCR were both positive. Explanted heart histopathology showed features of lymphocytic myocarditis without presence of amastigotes, but *T.* cruzi PCR was positive. Altogether, this substantiated the diagnosis of Chagas meningoencephalitis and graft myocarditis. With treatment, ventricular arrhythmia resolved and troponins normalized. Neurological deficits persisted but did not progress further.

DISCUSSION: The optimal management of Chagas disease in SOT remains unclear. While current practices include post-transplant serologic or PCR monitoring paired with pre-emptive therapy, prophylaxis may be considered in high-risk SOT recipients. In cases of suspected Chagas meningoencephalitis, molecular testing may be considered in blood and CSF. High-dose benznidazole may benefit those with refractory disease or CNS involvement.

CRP031

Paracoccus yeei: An emerging cause of peritoneal dialysis-associated peritonitis

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OBJECTIVE: Peritoneal dialysis–associated peritonitis is the most common infectious complication in patients receiving peritoneal dialysis (PD) and may result in hospitalization, PD catheter removal with transfer to hemodialysis, or death. We present a case of PD peritonitis caused by *Paracoccus yeei* in a patient with circulatory shock. This represents the first Canadian report of human infection caused by this organism.

CASE SUMMARY: A 74-year-old man on home PD for end-stage kidney disease presented to hospital with generalized weakness, mild abdominal pain, and hypotension requiring vasopressor support. He rapidly improved with empiric ceftriaxone and vancomycin, coming off pressors within 24 hours. PD fluid sampling revealed a cell count of 2,048 $\times$ 10^6/L (87% neutrophils), and Gram stain of PD fluid samples after 4 days of incubation in blood culture bottles revealed the presence of Gram-negative coccobacilli, after which his antimicrobial regimen was changed to intraperitoneal cefazolin and ceftazidime for PD peritonitis. Growth was observed on blood and chocolate agars, characterized by small, oxidase-positive and catalase-positive mucoid colonies. The organism was subsequently identified as *Paracoccus yeei* by MALDI-TOF. One week after hospital discharge, he returned to the emergency department with mixed septic/cardiogenic shock picture and was ultimately transitioned to comfort care.

DISCUSSION: *P. yeei* is one of over 80 species of the *Paracoccus* genus whose natural habitats are soil and marine environments. It is the first member of this genus to be associated with clinical disease in humans and has been reported to cause infection of the peritoneum, skin, biliary tract, central nervous system, cornea, myocardium, and bloodstream. Previous reports of *Paracoccus yeei* PD peritonitis have typically presented as abdominal pain with turbid peritoneal fluid, and most patients have responded to antimicrobial therapy without the need for PD catheter removal. However, there are no approved antimicrobial susceptibility testing methods or interpretation criteria for this organism.

CRP032

Staphylococcus aureus bacteremia with sternal osteomyelitis and superior vena cava mass: A rare paediatric case of complex infection

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OBJECTIVE: To highlight the challenges of diagnosing and treating musculoskeletal and endovascular infections in paediatric patients as a rare cause of a common respiratory presentation.

CASE SUMMARY: A previously healthy 16-year-old male presented to the emergency department with a 1-week history of upper respiratory symptoms, chest, and back pain, accompanied by fever. Despite normal chest X-ray and ECG findings, he was diagnosed with presumed musculoskeletal chest pain and discharged. Three days later, he re-presented with worsening pain and chest wall swelling and a high CRP, leading to a diagnosis of possible cellulitis or myositis. Chest CT revealed bilateral lung consolidations, anterior chest wall inflammatory changes, and a small left subpectoral fluid collection. Blood cultures grew *Staphylococcus aureus* (MSSA). The patient was admitted and treated empirically with antibiotics. MRI confirmed sternal osteomyelitis with bilateral chest wall abscesses and retrosternal extension. On day 3, he underwent debridement, but blood cultures remained positive for MSSA. A transthoracic echocardiogram (TTE) revealed a 10 × 7.5-mm mobile mass in the superior vena cava (SVC). After 5 days of IV antibiotics, blood cultures cleared, and the patient was discharged with outpatient parenteral antibiotics for 6 weeks. Over the course of treatment, the SVC mass shrank, resolving by week 4.

DISCUSSION: Our patient had sternal osteomyelitis with MSSA bacteremia and a superior vena cava pedunculated mass. Therefore, he was treated as a case of osteomyelitis and endovascular infection with a total of 6 weeks of IV cefazolin. Primary sternal osteomyelitis (PSOM) is typically acquired via hematogenous spread without trauma and is more common in males with predisposing conditions like sickle cell disease or diabetes. In addition, our patient also had superior vena cava (SVC) pedunculated mass and possibly linked to an embryonic remnant with endocarditis, which is rare in both paediatric and adult populations, especially without central lines.

POSTERS

P001

Evaluating Ambulatory Parenteral Therapy Program (APTP) for paediatric infectious conditions: Insights from Alberta Children's Hospital

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OBJECTIVES: (1) Describe the characteristics of patients referred to the APTP clinic, including type of infections and antibiotics used. (2) Determine the encountered complications including hospitalization and failure of APTP therapy.

METHOD: We have conducted a retrospective descriptive study examining paediatric patients under 18 years of age treated with intravenous antimicrobials as outpatients within the APTP program. Data were collected from electronic hospital records using patient identification numbers from May 1, 2023 to May 31, 2024. All data entries were recorded in RED-Cap as our data platform.

RESULTS: The study included 902 paediatric participants, with a balanced sex distribution of 455 males (50.4%) and 447 females (49.6%). The majority were aged 1–5 years (32.9%), followed by 6–10 years (26.9%). The most common diagnoses were cellulitis (15.7%), genitourinary (GU) infections (15.5%), dental infections (9.8%), and pneumonia (8.2%). Collectively, ear, nose, and throat (ENT) infections

were prevalent, representing 28% of cases. Ceftriaxone was the primary antibiotic for GU infections, while cefazolin was commonly used for cellulitis and dental infections. Of the total participants, 73 (8%) required hospitalization due to worsening infection or to increase the frequency of monitoring and IV antibiotics. Additionally, a statistically significant higher rate of admission was noted in males ($p = .03$). Most patients (97%) received peripheral IV access, with 96.3% reporting no issues. Only seven patients were lost to follow-up, and no mortalities were recorded. There were no significant associations between sex or age and hospital admissions.

CONCLUSION: This study underscores the importance of APTP in administering IV antibiotics safely in an outpatient setting. Supported by a multidisciplinary team, the program effectively treated common infectious conditions. Most patients maintained peripheral IV access without significant complications. While hospitalization rates were low, notable differences between male and female patients warrant further investigation into contributing factors to these disparities.

P002

A wastewater-based surveillance pilot program to detect, quantify, and correlate antibiotic usage in hospitals

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OBJECTIVE: Wastewater-based surveillance (WBS) is an emerging technology that can agnostically capture multiple parameters of relevance to population health. We leveraged an existing WBS network to develop a pilot program that can identify and quantify antibiotics in hospital effluent. We attempted to correlate the results with antibiotic utilization records from the same facilities to validate chemical targets found in wastewater as a representative measure of hospital antimicrobial usage.

METHOD: Wastewater was collected biweekly from February through October 2024 from one paediatric and two adult tertiary care hospitals. Ten antibiotics (five β-lactams, two fluoroquinolones, a sulfonamide, a nitroimidazole, and a tetracycline) were measured by filtering raw wastewater and injecting it directly into a liquid chromatography triple quadrupole mass spectrometer. Antimicrobial usage data from the same period measured as daily defined doses/1,000 patient days were collected from health databases for each facility and correlated with wastewater results using a Spearman's correlation test. Wastewater results were log-transformed and outliers removed using the ROUT method.

RESULTS: Moderate correlation (spearman R = 0.3–0.6) existed among most antibiotics measured in wastewater and those dispensed to hospitalized individuals between February and April (tetracycline, fluoroquinolone, nitroimidazole, β-lactam, and sulfa antibiotics). For some β-lactams this correlation decreased in the warmer months (May–August). We observed wastewater samples received at >20°C had significant degradation of certain targets (cefazolin, ceftriaxone, tazobactam; *t*-test $p = .003$, $p = .002$, and $p = .02$, respectively). The same temperature-dependent degradation was not present in distilled water samples used as a control when tested, suggesting biological factors contributed.

CONCLUSION: Hospitals are an ideal place to develop and model environmental antibiotic utilization through WBS. Our findings suggest that care must be taken when monitoring chemicals, particularly β-lactams, as they may be modified by β-lactamase–producing organisms, which are abundant in hospitals. Further validation and a deeper understanding of these challenges will strengthen WBS of antimicrobials across the One Health continuum.

P003

Examination of echinocandin appropriateness in hospitalized adult patients at a Canadian tertiary care centre

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OBJECTIVE: Antifungals are established antimicrobial stewardship (AMS) targets owing to toxicity, cost, and risk of inducing the development of antifungal resistance. At our

centre, echinocandin utilization has increased over time, but the degree of appropriateness is unknown. We piloted the addition of echinocandins to our prospective audit and feedback (PAF) program with a primary objective to evaluate appropriateness.

METHOD: This was a single-centre PAF study assessing echinocandins on formulary (micafungin and caspofungin). Incident echinocandin prescriptions for adult (age ≥18) inpatients at a Canadian tertiary care centre between June 1 and 30, 2024, were included. Contemporaneous verbal and written feedback to optimize the prescription was provided to the attending physician. The primary outcome was the percentage of appropriateness assessed against institutional prescribing guidelines and expert ASP opinion. Secondary outcomes were the volume of incident prescriptions, spectrum of indications, and appropriateness associated with infectious diseases (ID) specialist involvement.

RESULTS: There were 22 micafungin and 0 caspofungin prescriptions eligible for inclusion. The average patient age was 52 years (range 18–72), and 18/22 were male. The most frequent prescribing service was Critical Care (14/22). Of the 22 prescriptions, 17 (77%) were assessed appropriate or reasonable for patient-specific reasons. The most common indication was prophylaxis against invasive fungal infection in immunocompromised patients (8/22), particularly post-operative lung transplant recipients (5/22). Only four prescriptions were for fungemia. Overall, all initial echinocandin prescriptions were empiric in nature. Appropriateness was higher when ID specialists were involved (11/13, 85% versus 4/9, 44%; $p = .07$). Recommendations were provided in six prescriptions: two antifungal discontinuations, one rationalization to a narrower antifungal, one dose adjustment, and two ID consultations. The acceptance rate was 83.3% (5/6).

CONCLUSION: There may be an opportunity for AMS optimization of echinocandin prescriptions at our centre, but a larger study is needed to better understand baseline prescribing practices.

P004

The need for targeted antimicrobial treatment in paediatric head and neck infections: A review of anaerobic coverage

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OBJECTIVE: This narrative review aims to evaluate the role of anaerobic coverage in paediatric head and neck infections, focusing on the oral flora, susceptibility profiles of these organisms, and the role of extended anaerobic antimicrobial coverage (beta-lactam/beta-lactamase inhibitors or metronidazole) in treatment.

METHOD: A comprehensive literature review was conducted using PubMed and Google Scholar, examining review articles and primary studies (CC1) on antimicrobial susceptibility patterns of oral anaerobic flora in paediatric head and neck infections. The search strategy included terms such as "oral microbiome," "microbiome and caries," "microbiome periodontal disease," "pediatric oral microbiome," and "susceptibility of oral anaerobes." The review also explored the use of beta-lactams and the risks associated with extended anaerobic antimicrobial coverage, including treatment failure and antimicrobial resistance in both paediatrics and adult data.

RESULTS: A review of 10 studies on the oral microbiome and antimicrobial susceptibility patterns in paediatric head and neck infections indicated that the oral microbiome is significantly altered in disease states. In acute, non-invasive paediatric infections, Gram-positive anaerobes such as *Streptococcus* and *Peptostreptococcus* species predominated and were generally susceptible to penicillin-based therapies. Periodontal disease and dental caries contribute to an increased presence of Gram-negative anaerobes. In contrast, chronic and invasive infections were associated with more resistant Gram-negative anaerobes, including *Prevotella* and *Porphyromonas* species, which showed varying resistance to beta-lactams.

CONCLUSION: Paediatric acute head and neck infections are predominantly caused by pathogens susceptible to penicillin-based therapies, with amoxicillin suggested as the narrow-spectrum antibiotic of choice. However, in cases involving significant periodontal disease or chronic infections, resistant gram-negative anaerobes may be present. In such scenarios, beta-lactam/beta-lactamase inhibitor combinations or metronidazole should be considered to ensure optimal treatment

P005

Formulary restriction policy adherence assessment and characterization of current practice for selected antimicrobials

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OBJECTIVE: This study aims to evaluate adherence to formulary restrictions for three restricted antimicrobials, meropenem, daptomycin, and micafungin, at three hospitals in British Columbia (BC). It also examines the current practices of pharmacists in reviewing these medications.

METHOD: A retrospective chart review was conducted on adult patients (≥18 years old) receiving meropenem, daptomycin, or micafungin at three BC hospitals between April 2023 and March 2024. From 200 meropenem charts, 50 were randomly selected; all available daptomycin (22) and micafungin (19) charts were reviewed.

RESULTS: Adherence to formulary restrictions at prescribing was 70% for meropenem, 77% for daptomycin, and 79% for micafungin. After clinical pharmacist and antimicrobial stewardship (AMS) team interventions, adherence increased to 80% for meropenem and 88% for micafungin. Dispensary pharmacists did not initiate any interventions to improve adherence rates. Non-adherence was primarily due to unclarified penicillin allergies (meropenem), logistical challenges with the Community IV Program (daptomycin), and empiric fungal coverage for tertiary peritonitis (micafungin). Pharmacist documentation of restriction criteria reviews was infrequent.

CONCLUSION: Despite infrequent pharmacist documentation and intervention, adherence to formulary restrictions reached 77%–88%. Improving meropenem adherence requires maintaining up-to-date allergy records along with providing education on penicillin allergy assessments for the pharmacy team. For micafungin, involving infectious disease specialists in complex cases is recommended to ensure its appropriate use. Enhancing the EMR system with additional prescribing guidance could potentially improve prescriber awareness and the efficiency of pharmacy reviews.

P006

Using a planetary health lens to quantify our intravenous use of bioequivalent antimicrobials when oral administration is feasible

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OBJECTIVE: To quantify the proportion of patients receiving highly bioavailable antimicrobials intravenously when they could have been administered orally, and the related greenhouse gas emissions and antimicrobial cost.

METHOD: This was a retrospective chart review of inpatients who received IV azithromycin, ciprofloxacin, clindamycin, co-trimoxazole, fluconazole, levofloxacin, linezolid, metronidazole, moxifloxacin, and voriconazole at Vancouver General Hospital on five dates between August 2023 and April 2024.

RESULTS: A total of 128 patients were identified. Seventy-nine (62%) were eligible to receive at least one dose orally. The antimicrobials with the highest eligibility for IV-to-PO switch were azithromycin (73%) and metronidazole (71%). The most common infection types included intra-abdominal (33%) and respiratory (16%). The top medical services identified were General Surgery (38%) followed by Internal Medicine (19%) and Critical Care (14%). Over the five dates, the potential greenhouse gas savings were ∼82,000 g CO_2-eq. This is the equivalent of driving ∼400 km in a gasoline-powered car. The total potential cost savings over the study period was ∼$835.

CONCLUSION: Of the patients receiving highly bioavailable antimicrobials intravenously, 62% were eligible to receive at least one dose orally. There is a significant amount of greenhouse gas and antimicrobial cost savings in the IV-to-PO switch while maintaining excellent clinical outcomes. Education and antimicrobial stewardship opportunities exist to promote the IV-to-PO switch of highly bioavailable antimicrobials in eligible patients.

P007 – WITHDRAWN

P008

Antimicrobial use among adult inpatients in a network of Canadian acute care hospitals, 2009–2023

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OBJECTIVE: Inappropriate antimicrobial use contributes to antimicrobial resistance, an increasing threat to patient safety. This descriptive epidemiological study provides benchmark antimicrobial use (AMU) rates for adult inpatients in a sample of Canadian acute care hospitals over 15 years.

METHOD: Hospitals in the Canadian Nosocomial Infection Surveillance Program (CNISP), a network of 106 acute care hospitals across 10 provinces and 1 territory, submitted annual hospital-level AMU and patient-day data on select systemic antimicrobials from the 2009–2023 period. Data were analyzed using defined daily doses per 1,000 patient days (DDD/1,000PD) with trends assessed using the Mann-Kendall test (R 4.2.2).

RESULTS: Between 2009 and 2023, 20–36 hospitals (median: 21) submitted data each year. Hospitals were distributed across central (17%–65%), eastern (5%–29%), western (24%–64%), and northern (0%–4%) Canada. Most hospitals had between 200 and 500 beds (36%–67%). Overall, AMU rates (total DDDs per total patient days across all participating sites) significantly decreased ($p <$ .001), dropping from 654 to 446 DDD/1,000PD (–32%). AMU rates in non-ICU units significantly decreased (677 to 413 DDD/1,000PD, –39%, $p <$ .001) while remaining similar in ICUs (992 to 1,136 DDD/1,000PD, +15%, $p =$ .28). The three most commonly used antimicrobials were cefazolin, ciprofloxacin, and piperacillin/tazobactam from 2011 to 2015 and cefazolin, ceftriaxone, and piperacillin/tazobactam from 2016 to 2023. From 2009 to 2023, third-generation cephalosporin use significantly increased (37 to 78 DDD/1,000PD, +111%, $p <$ .001) while the use of broad-spectrum penicillins (105 to 65 DDD/1,000PD, –38%, $p =$ .02), quinolones (126 to 26 DDD/1,000PD, –79%, $p <$ .001), and carbapenems (26 to 22 DDD/1000PD, –15%, $p =$ .046) significantly decreased.

CONCLUSION: The 15-year AMU trends among adult inpatients in a subset of Canadian acute care hospitals revealed significant overall decreases, particularly in broad-spectrum penicillins, quinolones, and carbapenems. Limitations include the generalizability to all Canadian acute care hospitals and uncertainty due to fluctuations in annual hospital participation rates. As trends and hospital participation change over time, continued national surveillance remains essential for antimicrobial stewardship.

P009

Antibiotic prescribing for aspiration pneumonia in the ICU background: Aspiration pneumonia is a potential antibiotic stewardship target given that antibiotics appear to be often prescribed without robust diagnostic justification, particularly in critical care units

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OBJECTIVE: The primary objective of this study was to determine the proportion of critically ill patients who met published criteria for suspected or confirmed aspiration pneumonia after being treated for this indication. Secondary objectives include identifying risk factors associated with treatment for aspiration pneumonia but not meeting criteria, as well as identifying specific antibiotic regimens used and determining outcomes of aspiration pneumonia.

METHOD: We retrospectively reviewed antibiotic-treated patients in critical care units, focusing on those treated specifically for aspiration pneumonia. Patients were assessed based in defined clinical and radiographic criteria and either witnessed aspiration (confirmed) or risk factors for aspiration (suspected). Multivariable logistic regression was used to identify independent risk factors for outcomes of interest

RESULTS: Among 116 patients evaluated for aspiration pneumonia, 67 (57.76%) met the criteria for confirmed or suspected aspiration pneumonia. Of the total cohort, 35 patients (30.17%) had confirmed aspiration pneumonia while 63 patients (54.31%) were classified as having suspected aspiration pneumonia. Confirmed aspiration pneumonia cases were associated with intubation (OR: 2.44, 95% CI 1.02–6.35, $p =$ .05). Suspected cases were more likely admitted from non-ICU hospital units (OR: 2.92, 95% CI 1.33–6.68, $p =$ .01). Antibiotic prescriptions initiated on weekends were not significantly associated with increased odds for suspected or combined aspiration pneumonia compared to weekdays prescription (OR: 0.97, 95% CI 0.43–2.14, $p =$ .93).

CONCLUSION: About 40% of antibiotic courses for aspiration pneumonia do not meet the criteria for confirmed or suspected aspiration pneumonia, suggesting an important opportunity to improve antibiotic use. Antibiotic use not meeting the criteria was not significantly associated with prescriber role, time of prescription, or intubation status. Analysis on prescriptions and outcomes are ongoing.

P010 – WITHDRAWN

P011

Promoting the use of ceftriaxone for urinary tract infections caused by low-risk ampC-producing organisms: A quasi-experimental study

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OBJECTIVE: The Infectious Diseases Society of America recommended that for *Morganella morganii, Providencia* spp., and *Serratia marcescens*, organisms with low risk for inducing *ampC* production, treatment using third-generation cephalosporins can be based on susceptibility results. Our institution started releasing ceftriaxone susceptibilities for these organisms if grown from urine cultures. We evaluated if there were changes in antibiotic prescribing and clinical outcomes with the change in reporting.

METHODS: The microbiology laboratory modified reporting to release ceftriaxone susceptibility from urine cultures with a comment about the potential to develop resistance with prolonged therapy. To evaluate the impact of the new reporting protocol, a retrospective cohort of patients with a urine culture positive for *Serratia*, *Providencia,* or *Morganella* spp. was evaluated. We compared patients pre-intervention (September 2021 to December 2022) with those treated post-intervention (December 2022 to March 2024). The primary outcome was use of ceftriaxone compared to other antibiotics.

RESULTS: Fifty patients were included from the pre-intervention phase and 61 patients from the post-intervention phase. Median age was 78 years old (IQR 73–86), and 61 patients (55%) were male. Ceftriaxone use increased from 0% to 23% ($p < .001$), with a numerical reduction in ertapenem use (10% to 5%, $p = .46$). There was a significant reduction in oral ciprofloxacin use (60% to 38%, $p = .02$). Definitive oral antibiotic use decreased from 88% to 70% ($p = .04$). Treatment success (90% to 95%, $p = .46$) and readmissions (8% to 13%, $p = .54$) were similar for patients in both groups. One case of *C. difficile* infection occurred in the post-intervention group. None of the 14 patients who received ceftriaxone therapy developed resistance.

CONCLUSION: By reporting ceftriaxone susceptibilities for these organisms, we observed an increase in ceftriaxone utilization, with similar clinical outcomes. A significant decrease in definitive oral antibiotic and a numerical reduction of ertapenem use was also observed.

P012

Adult antimicrobial usage (AMU) surveillance in Newfoundland and Labrador (NL) hospitals

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OBJECTIVE: To report AMU surveillance conducted in acute care NL hospitals and compare to benchmark rates from Canadian Nosocomial Infection Surveillance Program (CNISP).

METHOD: AMU data collected from PYXIS/Carefusion™ and MedSelect/Centrack™ dispensing systems and hospital census data were reported as defined daily doses (DDD) and DDD/1,000 pt days for 2019–2023. Indication was not available. Ethics permission was not required, as identifiable data were not used.

RESULTS: Seven (2 urban, 5 rural) out of 12 large acute care hospitals in NL (58%) participated. Combined total AMU rate was 395 DDD/1,000 pt days, significantly less than CNISP mean AMU rate (468 DDD/1,000 pt days, $p = .013$). Combined AMU trended upward in four of five rural facilities but decreased in both urban facilities. Facility AMU rates ranged from 159 to 562 DDD/1,000 pt days ($p < .001$ for difference). Combined AMU rates for urban facilities were higher than rural facilities (506 versus 351, $p < .001$). Three facilities (two urban, one rural) had AMU exceeding the CNISP mean AMU rate. Among rural facilities, four out of five (80%) demonstrated increasing AMU rates, driven by increasing broad spectrum penicillin use. Fluoroquinolone AMU decreased, but rates up to 60% above CNISP mean rate were observed. Third-generation cephalosporin AMU increased, with highest rates in rural facilities. Carbapenem

AMU was stable and below CNISP mean AMU rate, except for one urban facility.

CONCLUSION: Inpatient AMU was lower than national rates and varied significantly between NL hospitals. Some rural sites used more antimicrobials than urban facilities during periods, highlighting the need for more stewardship intervention and standardization of usage. Not all hospitals were represented.

P013

Return on investment of an antibiotic audit and feedback program among family physicians in Ontario

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OBJECTIVE: To determine the return on investment (ROI) of an antibiotic audit and feedback (A&F) program from a Canadian public payer perspective.

METHOD: A pragmatic trial randomized 5,097 physicians in Ontario 4:1 to receive either an antibiotic A&F mailed letter or no letter in January 2022. A model was developed to calculate the monetary costs and savings associated with the program, integrating expenses from antibiotic prescriptions, adverse events, and severe bacterial infections. ROI was estimated by dividing the incremental savings of the program by the costs. An ROI $>$ 1 indicates monetary savings of the program exceed costs, whereas an ROI $<$ 1 indicates monetary costs exceed savings. We performed a probabilistic analysis with 5,000 simulations to estimate mean outcomes.

RESULTS: Trial results previously published demonstrated a significant 5% (95% CI 4%–6%) relative reduction in antibiotic prescribing at 6 months. Mean antibiotic cost savings per physician was –$53.36 (95% CI –$81.64 to –$25.08, $p < .001$) after 6 months. The three antibiotics responsible for the largest savings were azithromycin, amoxicillin/clavulanic acid, and nitrofurantoin. No significant differences were observed in costs from adverse events (mean difference = –$932.44, 95% CI –$3,089.94 to $1,225.09, $p = .397$) or severe bacterial infections (mean difference = –$391.89, 95% CI –$10,170.90 to $9,387.10, $p = .937$) between intervention and control groups. Costs from health care visits for diarrhea were significantly reduced in the intervention group. Total program costs and savings per physician were $5.34 (95% CI $5.32–$5.36) and $20.47 (95% CI $16.69–$24.26), respectively. The antibiotic A&F program resulted in an ROI of 3.92 (95% CI 3.91–4.64), meaning that for every dollar spent on the antibiotic A&F program there was a $3.92 return. Sensitivity analyses showed model results were robust to most parameters but sensitive to costs from severe bacterial infections.

CONCLUSION: The antibiotic A&F program was cost-saving to address overprescribing of unnecessary antibiotics by family physicians.

P014

Urinalysis: A simple but powerful tool for diagnostic and antimicrobial stewardship

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OBJECTIVE: Paediatric guidelines suggest not sending a urine culture if the urinalysis is normal in children over the age of 8 days, though it remains common practice in paediatric hospitals. Urine cultures that are reported with some growth of bacteria often prompt inappropriate treatment in this context. The aim of this study is to determine what proportion of urine cultures with bacteriuria also had an abnormal urinalysis.

METHOD: All urine cultures from children between 0 to 24 months of age at a large paediatric tertiary hospital were reviewed. Laboratory data and patient characteristics were collected. An abnormal urinalysis was defined as either a trace or greater leukocyte esterase or nitrite or a

microscopic exam of >5 WBCs per high-power field on urine microscopy.

RESULTS: A total of 896 urine cultures from 761 patients were included. Cultures were obtained from patients presenting to the ED in 62.6% while 22.2% were obtained from inpatients. The mean age was 6.1 months, and males accounted for 36.3%. In-and-out catheters ($N = 712$; 79.5%) and midstream urine ($N = 76$; 8.5%) were the most common specimens. A urinalysis was performed in 95.5% of cultures; 47.9% ($N = 410$) had a normal urinalysis. A normal urinalysis result was more often seen in no growth (63.2%) or no significant growth (62.0%) cultures. Abnormal urinalysis results were more likely if uropathogens were present in $>50 \times 106$ CFU/L. A uropathogen was reported in 314 cultures (35.0%), and pure growth was often observed ($N = 273$; 76.0%). No growth ($N = 410$; 45.8%) and no significant growth ($N = 142$; 15.9%) cultures were frequently observed.

CONCLUSION: Almost half of all urine specimens submitted for culture had a normal urinalysis, suggesting that the cultures were sent without interpretation of results. Using a urinalysis as a screening tool would be useful to prevent ordering of urine cultures. Exploring the clinical impact of urine culture results in these patients will be important.

P015

Tailoring antibiograms: Comparing resistance trends in hematological malignancy and solid organ transplant wards

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OBJECTIVE: Antimicrobial resistance varies across health care settings, and yet antibiograms are frequently presented as whole hospital antibiograms. Hospital A, a cancer-focused facility with dedicated hematological malignancy wards, and Hospital B, a larger general hospital with solid organ transplant wards, are affiliated with the same university and served by common medical staff. Despite their proximity, their distinct patient demographics may lead to different antimicrobial susceptibility patterns. This study compared resistance trends between the two hospitals and their highly specialized units.

METHOD: Antibiotic susceptibility of bacterial isolates from 2019–2023 at Hospital A and its hematological malignancy wards (Hospital A High-Risk [HA-HR]) and Hospital B and its solid organ transplant wards (Hospital B High-Risk [HB-HR]) were obtained and analyzed following CLSI M39. Species with less than 30 isolates or less were excluded from analyses. Data analyses were performed on Excel, and R statistical software was used for graph generation.

RESULTS: Antimicrobial susceptibility from Hospitals A and B were analyzed comparing their high-risk ward antibiograms to hospital-wide antibiograms. Antibiograms from both HA-HR and HB-HK showed lowered weighted percent susceptibility (62% and 61%, respectively) when compared to their respective hospital-wide antibiograms, HA and HB (79% and 75%, respectively). Upon comparing the two high-risk units, notable organism-drug discrepancies involved reduced *E. coli*–ciprofloxacin susceptibility at 12% for HA-HR compared with HB-HR while increased susceptibility was seen in HA-HR for *E. coli*–cefazolin (20%), *E. coli*–trimethoprim-sulfamethoxazole (18%), and *E. cloacae*–trimethoprim-sulfamethoxazole (19%). Increased methicillin-resistant coagulase-negative staphylococci (8%) was also noted in HA-HR. HA-HR showed a 9% and 8% reduction in weighted percent susceptibility compared to HA and HB, respectively, with the largest discrepancies seen in *E. coli* and CNST susceptibility.

CONCLUSION: These findings underscore the importance of using specialized antibiograms for high-risk units, as significant differences in resistance patterns between hospitals and wards highlight the need for more tailored antimicrobial stewardship.

P016 – WITHDRAWN

P017

Tracking Gram-negative organisms resistance: A decade of antibiotic trends in a tertiary care academic hospital

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OBJECTIVE: Annual antibiograms provide a snapshot of antimicrobial susceptibility but are limited by only presenting susceptibility reflecting one moment in time, making

the detection of emerging resistance challenging. This study aimed to assess susceptibility trends in a tertiary care hospital over the last 10 years.

METHOD: Antibiotic susceptibility data from blood and urine cultures (2013–2023) were obtained from annual antibiograms generated per the Clinical and Laboratory Standards Institute (CLSI) M39 guidelines. Updated CLSI M100 breakpoints were applied throughout the study period. Trends were analyzed using Excel.

RESULTS: *Escherichia coli, Klebsiella pneumoniae,* and *Pseudomonas aeruginosa* were the most prevalent Gram-negative organisms (GNO). Susceptibility for *E. coli* and *P. aeruginosa* blood isolates remained stable over the 10-year period, whereas gradual decreases in susceptibility to ceftriaxone, ciprofloxacin, and trimethoprim-sulfamethoxazole were noted in *K. pneumoniae*. Urinary *E. coli* demonstrated a steady decline in ciprofloxacin susceptibility over the 10-year period and a dramatic drop in tobramycin susceptibility noted in 2019 that has remained low since. A similar decline in tobramycin susceptibility was observed for urinary *K. pneumoniae,* along with gradual decreases in ceftriaxone, ciprofloxacin, ertapenem, and amikacin. Urinary *P. aeruginosa* maintained high susceptibility throughout the study period.

CONCLUSION: Tracking antimicrobial susceptibility trends over time and by different specimen types, rather than relying on static compiled annual data, is crucial for detecting emerging resistance. The trend in decreasing susceptibility in *K. pneumoniae* is concerning along with the dramatic drop in tobramycin susceptibility in urinary *E. coli* and *K. pneumoniae* and should be investigated further.

P018

Investigating the antibacterial activity of medicinal plant infusions against pathogenic bacteria

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OBJECTIVE: This study aimed to determine the antibacterial activity of the plant infusions, their combination therapy with antibiotics, and biochemical modes of action against bacterial pathogens.

METHOD: The infusions' antibacterial activity (minimum inhibitory concentrations [MICs] and minimum bactericidal concentrations [MBCs]) was evaluated using broth microdilution, the combination therapy was determined using the checkerboard assay, and biochemical modes of action was investigated using dye assays.

RESULTS: The MICs of the plant infusions ranged from 0.078 to 10 mg/mL, while the MBC ranged between 2.5 to 10 mg/mL, with 42% of the infusions showing good and moderate activity. In combination, using the checkerboard assay, the infusions with good MIC reduced antibiotics' MIC 128- to 500-fold while their MIC increased up to 4-fold. The antibiofilm activity of plant infusions on the prevention or destruction of preformed biofilm was investigated. The infusions prevented the formation of biofilm biomass at the initial time (T0h), with percentage inhibition values between 58% and 81%. Still, they had poor antibiofilm activity, with percentage inhibition values between 25% and 46% on pre-formed biofilms (T24h). Good inhibitory activity (>50% inhibition) at T0h indicates that prevention of biofilm attachment and growth proved to be easier to achieve than destruction of preformed biofilms (T24h). This research also investigated the cell membrane permeability potential and the impact of the infusions on cytoplasmic pH using Disc3 (5) and CFDA-SE assays, respectively. The infusions investigated caused cellular membranes' hyperpolarization, indicating membrane damage and changes in cytoplasmic pHint, resulting in antibacterial activity.

CONCLUSION: This study has shown that these infusions exhibit antibacterial potential and can be used as natural alternative antimicrobial agents to control pathogenic bacteria and reduce pressure on antibiotic

P019

Novel antibiotics: The promise of small-molecule iron inhibitors against multidrug-resistant Gram-negative superbugs

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OBJECTIVE: The menace of antimicrobial resistance is a global health problem and has been tipped as a silent pandemic after the abuse of various antibiotics use in health care settings during the COVID-19 pandemic. Currently, pathogenic bacteria such as *Acinetobacter baumannii* have developed resistance to all know antibiotics. Hence, there is a global need for the development of new and novel antibiotics. Iron is essential nutrient for bacterial growth. To be available to cells for growth, it is required to be released from iron-storage protein, BfrB, and its release blocked when in

excess. This cystolic iron level regulation is made possible by the interaction of BfrB and a cognate protein, Bfd. It is therefore proposed that the presence of small molecules that disrupt BfrB–Bfd interaction leads to cell death.

METHOD: Structure-based design of small molecules that disrupt the BfrB–Bfd interaction was used and *in vitro* compound susceptibility and time-kill assays against multidrug resistant *A. baumannii were assessed.*

RESULTS: The synthesized compounds demonstrated the potential to inhibit the growth of multidrug-resistant Gram-negative bacteria (*Acinetobacter baumannii*) in concentration-dependent manner similar to conventional antibiotics. There is the possibility to improve the bactericidal properties of the compound through the adjustments of the derivative substituents. The compounds demonstrated a clear bactericidal effect on *A. baumannii* 5075, a multidrug-resistant strain, with $>3\text{-Log}_{10}$ reduction at 5 hours, with no recovery at 3 hours and little recovery at 24 hours. Not only can the compound kill multidrug-resistant *A. baumannii*; it can also potentiate the activity of carbapenems (imipenem) against a carbapenem-resistant *Acinetobacter baumannii* as demonstrated by a more than eightfold decrease of imipenem MIC (1 μg/mL) with 7 μg/mL of KM-5-35.

CONCLUSION: The disruption of Bfr–Bfd interaction in bacterial cells not only causes cell death but could also potentiate the activities of other antimicrobial agents with different mechanisms of action against multidrug-resistant bacteria.

P020

Determination of antimicrobial, antibiofilm, and hemolytic activity of aurein-1.2 derivatives

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OBJECTIVE: Aurein-1.2 is a 13-amino-acid antimicrobial peptide secreted by the Green and Golden Bell frog, *Litoria aurea*, and the Southern Bell frog, *Litoria raniformis*. It exhibits powerful antimicrobial activity but unfortunately is dangerously hemolytic. This project aimed to design four derivatives to increase the antimicrobial and antibiofilm properties while minimizing erythrocyte cytotoxicity.

METHOD: Four derivatives of Aurein-1.2 (T1, T2, T3, and T4) were synthesized by substituting aspartate and glutamate with arginine residues and two isoleucine residues with tryptophan at varying positions. To analyze the antimicrobial activity of the derivatives, a minimum inhibitory concentration (MIC) assay was performed using the peptides at varying concentrations against *Escherichia coli* and multidrug-resistant *Escherichia coli*, *Salmonella typhimurium*, *Candida albicans*, *Staphylococcus aureus*, and methicillin-resistant *Staphylococcus aureus* (MRSA). Minimum biofilm eradication concentration (MBEC) assays were also performed to determine antibiofilm activity. Hemolytic activity against mammalian erythrocytes was analyzed using hemolytic assays with whole horse blood.

RESULTS: MIC results showed that T1 and T2 exhibited >90% cell death at 50 μg/mL, while T3 displayed similar activity at the same concentrations against all bacteria except for *Escherichia coli*, which required 100 μg/mL. T4 required 100 μg/mL for all tested organisms. T3 and T4 were active against *Escherichia coli* and *Staphylococcus aureus* biofilms with an MBEC of 31.25 μg/mL and 125 μg/ml, respectively. T1 and T3 showed no hemolytic activity at ≤10 μg/mL. T2 and T4 were hemolytic in all tested concentrations (10–500 μg/mL).

CONCLUSION: All peptide derivatives significantly increased the antimicrobial activity against Gram-negative bacteria while only T2 increased activity against Gram-positive bacteria. Derivatives T3 and T4 show high therapeutic potential against infectious biofilms, but further investigation is required to identify mechanisms of action. T1 and T3 were not hemolytic at low concentrations (≤10 μg/mL). T2 and T4 retained hemolytic activity like Aurein-1.2.

P021

Molecular characterization of drug resistance in uropathogenic *Escherichia coli*

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OBJECTIVE: The current study was intended to characterize the molecular mechanisms of resistance against ciprofloxacin (CIP) and cefotaxime (CTX) and the genetic relationship among uropathogenic *Escherichia coli* (UPEC).

METHOD: A total of 50 UPEC isolates resistant to CIP and CTX from a previous study were selected and

analyzed for plasmid-mediated quinolone resistance (PMQR) genes, extended-spectrum β-lactamase (ESBL) variants and mutations in target site in DNA *gyrA* and *parC* by sequencing. Molecular typing was also performed for clonal relationships among UPEC by ERIC PCR.

RESULTS: A total of 50 drug-resistant UPEC were selected that showed higher resistance against CIP (MIC > 500 μg/mL) and CTX (MIC > 128 μg/mL). PMQR genes were identified in 66% of isolates; 28% carried *qnrB* in combination with *qnrS*. The mutational profile of *gyrA* and *parC* genes revealed D87N and S80I as common substitutions respectively. Prevalence of *bla* CTX-M remained at 86% while *bla* TEM was 62% and *bla* SHV 6% among tested isolates. Genotypic analysis of CTX-M revealed that 80% belonged to CTX-M group 1 while 6% to CTX-M group 9. Sequence analysis of *bla* TEM, CTX-M group 1, and CTX-M group 9 showed *bla* TEM-1, CTX-M-15, and CTX-M 27 lineages respectively.

CONCLUSION: The current study indicated multiple carriages of ESBL genes with predominant CTX-M variants. Though *qnrS* was mainly found in ciprofloxacin-resistant isolates, mutations in the target site greatly elicit high quinolone resistance in UPEC strains. Considerable genetic diversity among drug-resistant UPEC isolates suggests the dissemination of drug resistance genes via horizontal transfer.

P022

In vitro activity of ceftriaxone versus members of the *Proteus vulgaris* group: A comparison of testing methods and evaluation for the paradoxical effect

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OBJECTIVE: Ceftriaxone has been observed to demonstrate paradoxical antibacterial activity versus *P. vulgaris*, with isolates inhibited *in vitro* at relatively low antibacterial concentrations but not high concentrations. The purpose of this study was to evaluate the *in vitro* activity of ceftriaxone versus a contemporary collection of *P. vulgaris* group clinical isolates and assess for the presence of paradoxical activity.

METHOD: Forty-eight *P. vulgaris* group clinical isolates were obtained from the CANWARD Study (2009–2022). Ceftriaxone susceptibility was determined by broth microdilution, broth macrodilution, and disk diffusion (DD) as described by CLSI, and by VITEK2®. DD was also performed using a higher inoculum (equivalent to a 1.0 McFarland Standard) and prolonged (48 hours) incubation. Current CLSI breakpoints were applied for all methods.

RESULTS: Variability in ceftriaxone susceptibility was observed depending on the test method. The percentage of isolates testing ceftriaxone resistant by DD (standard conditions), VITEK2®, broth macrodilution, and broth microdilution was 0%, 29.2%, 83.3%, and 87.5%, respectively. Essential agreement and categorical agreement between broth macrodilution and broth microdilution was 81.3% and 85.4%, while essential agreement and categorical agreement between broth macrodilution and VITEK2® was 18.8% and 39.6%. When DD was performed with a higher inoculum and prolonged incubation, 15 isolates demonstrated a clear inner zone of growth or colonies growing around the disk (ie, paradoxical activity). All 15 isolates had a ceftriaxone MIC of ≥64 μg/mL by broth macrodilution and broth microdilution, while 5 isolates had a VITEK2® MIC of ≤0.25 μg/mL.

CONCLUSION: In this study, ceftriaxone susceptibility of *P. vulgaris* group isolates was highly dependent on the test method. Further clinical data are required to determine whether ceftriaxone is in fact appropriate for the treatment of serious infectious due to members of the *P. vulgaris* group, and if so, what susceptibility testing method correlates best with clinical outcome.

P023

Evaluation of aztreonam/avibactam gradient test strip and aztreonam-ceftazidime/avibactam broth disk elution (BDE) method for susceptibility testing of metallo-β-lactamase positive carbapenemase-producing bacteria

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OBJECTIVE: This study compared the performance of an aztreonam/avibactam (ATM-AVI) gradient strip to the CLSI aztreonam plus ceftazidime-avibactam (ATM-CZA)

broth disk elution (BDE) method for antimicrobial susceptibility testing (AST) of carbapenemase-producing Enterobacterales (CPE) and *Stenotrophomonas maltophilia* isolates.

METHOD: A total of 36 CPE (18 clinical, 18 screening) and 9 *S. maltophilia* clinical isolates were tested using BDE and gradient strip methods. For gradient strip testing, MTS™ ATM-AVI gradient strips (Liofilchem) were utilized, following manufacturer recommendations with MIC interpretation according to EUCAST guidelines. For BDE, CLSI procedures were followed, using cation-adjusted Mueller-Hinton broth with ATM, CZA, or ATM-CZA disks. Results were compared for categorical agreement. For isolates demonstrating resistance, whole-genome sequencing was performed to identify the genetic mechanism of resistance. Quality control testing followed CLSI and manufacturer recommendations.

RESULTS: There were 30 NDM-, 4 NDM/OXA-48-, 1 KPC/NDM-, and 1 IMP-positive CPE isolates included in the study. Categorical agreement was 97.2% ($n = 36$) for CPE isolates. One *E. coli* (NDM) isolate initially showed discordance (gradient strip susceptible, BDE non-susceptible), but was later confirmed as susceptible after repeat BDE testing and whole-genome sequencing, which only detected a *PBP3* mutation (YRIK). Another *E. coli* (NDM/OXA-48) isolate was resistant by both BDE and gradient strip testing. Whole-genome sequencing revealed both a *PBP3* mutation (YRIK) and *CMY-42* (AMPC) gene, which confer high MICs to ATM-AVI when found in combination. For *S. maltophilia*, 88.9% ($n = 9$) of isolates were concordant. One discordant isolate (gradient strip susceptible, BDE non-susceptible) was later confirmed as susceptible after repeat BDE and gradient strip testing.

CONCLUSION: For CPE and *S. maltophilia*, both AST methods showed acceptable accuracy and reproducibility; however, the BDE method showed inconsistent results for clinical isolates with elevated but susceptible MICs. Discrepancy analysis, supported by genomic results, favoured the gradient strip method for accurate susceptibility interpretation.

P024

Whole-genome sequencing to assess genetic properties and antimicrobial resistance patterns of the eight novel v116 pneumococcal vaccine serotypes 15A, 15C, 16F, 23A, 23B, 24F, 31, 35B in Canada: CANWARD 2011–2020

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OBJECTIVE: To assess relationships among whole-genome sequence (WGS) characteristics, demographics, and antimicrobial resistance phenotypes for the eight unique pneumococcal serotypes (15A, 15C, 16F, 23A, 23B, 24F, 31, and 35B) covered by V116, a novel 21-valent pneumococcal conjugate vaccine developed specifically for use in adults.

METHOD: Pneumococcal isolates were collected by the CANWARD study from 2011 to 2020, inclusive, in collaboration with the Public Health Agency of Canada's National Microbiology Laboratory (NML). Serotypes were determined by Quellung reaction, and antimicrobial susceptibility testing was performed using the CLSI broth microdilution method. WGS was conducted by NML's DNA Core and analyzed using WADE (https://github.com/phac-nml/wade).

RESULTS: A total of 1,338 isolates were collected from respiratory samples (64.1%) and blood (35.3%); from males (59.4%) and females (40.6%); from those aged 0 to 17 (14.1%), 18 to 64 (51.6%) and ≥65 years (34.3%); and from Western Canada (37.0%), Ontario (22.7%), and Quebec/Maritimes (40.3%). Of isolates from those aged ≥65 years, 78.4% had a serotype covered by V116. The eight V116-unique serotypes covered 31.8% of isolates in those ≥65 years. V116 covered 93.0% of isolates with any resistance phenotype, and 92.1% and 94.5% of MDR and XDR isolates, respectively. Of the eight unique V116 serotypes, 15A and 23A demonstrated the highest antimicrobial resistance rates at 17.0% and 10.2% MDR, respectively; 6.7% of 15A isolates were XDR, and 50% (29/58) belonged to GPSC6. For 23A isolates, 34.4% (22/64) were GPSC5 and 37.5% (24/64) were GPSC7. A higher proportion of isolates from V116-unique serotypes (157/327; 48.1%) had one or more WGS resistance determinants, compared to all V116 serotypes (207/543; 38.1%).

CONCLUSION: The eight unique serotypes in V116 (15A, 15C, 16F, 23A, 23B, 24F, 31, and 35B) represented 31.8% of all isolates in persons ≥65 years. Unique serotypes 15A and 23A demonstrated the highest antimicrobial resistance, MDR, and XDR rates.

P025

When and how is IV dalbavancin used 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.

METHOD: 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™ (Research Electronic Data Capture), that allows clinicians across Canada to share their experiences treating patients with dalbavancin using an online survey: https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=TPMWJX98HL.

RESULTS: The results for 64 patients (as of December 19, 2024) are presented. The most common infections treated were acute bacterial skin/skin structure infection (53.1% of patients), bone/joint infection (20.3%), bloodstream/vascular infection (10.9%), and endocarditis (7.8%). Dalbavancin was used both as directed (78.1%) and empiric therapy (21.9%). Methicillin-resistant *Staphylococcus aureus* (MRSA) was the most common identified pathogen (64.1%), followed by *Streptococcus* spp. (9.4%), *Staphylococcus* spp. (9.4%), and unknown (9.4%). Dalbavancin was initiated in an inpatient treatment setting (eg, hospital ward, 45.3%), an outpatient treatment setting (eg, emergency department, 40.6%), an OPAT clinic (12.5%), or an infectious diseases clinic (1.6%). Dalbavancin was primarily used due to the convenience of a single-dose treatment (81.3%) or to facilitate early hospital discharge (10.9%). Dalbavancin was primarily used alone (81.3%) and most commonly using a single 1,500-mg dose (65.6%). Microbiological success (pathogen eradicated or presumed eradicated) occurred in 91.8% of known cases, while clinical success (cure and/or improvement) occurred in 90.0% 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 due to 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.

P026

Usage of IV amoxicillin/clavulanate in Canada: Results from the CLEAR registry

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

METHOD: 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™, allowing clinicians to share their experiences treating patients with IV amoxicillin/clavulanate using an online survey: https://rcsurvey.radyfhs.umanitoba.ca/surveys/?s=HH3RKLXJNCFDEHA9.

RESULTS: The results for 385 patients are presented. Treated infections included intra-abdominal (22.6%), acute

bacterial skin/skin structure (18.7%), community-acquired pneumonia (15.6%), cystitis/pyelonephritis (11.4%), and bone/joint (9.1%). IV amoxicillin/clavulanate was used both as directed (53.1%) and empiric therapy (46.9%). Causative pathogens were most commonly unknown (46.9%) or mixed infection (29.6%) followed by *Escherichia coli* (5.5%), *Streptococcus* spp. (5.5%), *Staphylococcus* spp. (4.4%), and *Enterococcus* spp. (4.2%). IV amoxicillin/clavulanate was primarily used instead of piperacillin/tazobactam (37.2%), when oral amoxicillin/clavulanate was needed but not feasible (25.5%), instead of ceftriaxone (14.3%), and as empiric treatment (9.1%). The most commonly administered dosage of IV amoxicillin/clavulanate was 1,000 mg/200 mg Q8H (70.4%). IV amoxicillin/clavulanate was primarily used alone (82.6%) but at times combined with other antimicrobials including vancomycin, a fluoroquinolone, or azithromycin. Microbiological success (pathogen eradicated or presumed eradicated) occurred in 83.5% of known cases, while clinical success (cure and/or improvement) occurred in 84.8% of known cases. Two of 385 (0.5%) patients reported an adverse effect (rash and transient leukopenia); neither resulted in drug discontinuation.

CONCLUSION: In Canada, IV amoxicillin/clavulanate is used as both directed and empiric therapy to treat on-label and off-label infections. It is primarily used instead of piperacillin/tazobactam or when oral amoxicillin/clavulanate is needed but not feasible. IV amoxicillin/clavulanate use is associated with high microbiological and clinical cure rates along with an excellent safety profile.

P027

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

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OBJECTIVE: We report the final data regarding IV fosfomycin usage in Canadian patients using data captured by the CLEAR registry.

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

RESULTS: Data were available for 116 patients (as of December 19, 2024). Infections treated included complicated urinary tract infection (cUTI, 29.3% of patients), bacteremia/sepsis ± a documented site of infection (21.6%), hospital-acquired bacterial pneumonia (12.1%), ventilator-associated bacterial pneumonia (10.3%), complicated intra-abdominal infection (6.9%), community-acquired bacterial pneumonia (4.3%), and endocarditis (3.4%). IV fosfomycin was used to treat Gram-negative (79.2%), Gram-positive (6.8%), or mixed (3.4%) infections. The most common pathogens treated were carbapenem-resistant *Enterobacterales* (CRE) (35.3%), MDR *Pseudomonas aeruginosa* (14.7%), extended-spectrum β-lactamase (ESBL)-producing *Enterobacterales* (15.5%), vancomycin-resistant *Enterococcus faecium* (VRE) (2.6%), and MRSA (1.7%). IV fosfomycin was used primarily as directed therapy (75.0%) and typically prescribed as part of combination therapy (73.3%) except when used to treat cUTI. Fosfomycin was prescribed due to resistance to other antimicrobial agents (69.0%), clinical failure of previous therapy (17.2%), or adverse effects associated with use of previous agents (12.9%). Microbiological success (pathogen eradicated/presumed eradicated) occurred in 85.3% and clinical success (clinical cure/improvement) in 69.5% of patients; 10.3% of patients died due to their infection. Adverse effects were not documented in 68.9% of patients, with two patients discontinuing therapy due to adverse effects (gastrointestinal and hypokalemia).

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 (eg, CRE) and as part of combination therapy. Its use is associated with relatively high microbiological and clinical cure rates and a very good safety profile.

P028

Molecular assessment of clarithromycin resistance in *Helicobacter pylori* in British Columbia

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OBJECTIVE: To determine the prevalence of clarithromycin-resistant *Helicobacter pylori* strains in British Columbia by employing both melting curve analysis and Sanger sequencing to identify resistance-associated genetic mutations. Additionally, the study aims to compare these molecular methods to demonstrate their equivalence in detecting resistance, thereby generating data to support antibiotic stewardship programs, optimize clarithromycin usage, and reduce the emergence of resistant *H. pylori* strains.

METHOD: From 2017 to 2022, biopsies and *Helicobacter pylori* isolates ($n = 63$) were collected from local hospitals in British Columbia. Genomic DNA was extracted using QIAGEN kits. Clarithromycin resistance mutations in the 23S rRNA gene were detected via real-time PCR and melting curve analysis on a Roche LightCycler 2.0. Additionally, samples underwent Sanger sequencing using an ABI 3130x Genetic Analyzer with BigDye™ reagents. Sequence data were analyzed with Geneious software to verify resistance-associated mutations.

RESULTS: Two major melting curve groups were identified: Group I (52°C–54°C) indicated clarithromycin-resistant *H. pylori* strains, while Group II (60°C–62°C) indicated clarithromycin-sensitive strains. The clarithromycin resistance rate was 84% (54/63). Sanger sequencing identified the resistance-associated single nucleotide polymorphism (SNP) A2142G or A2143G, whereas clarithromycin-sensitive strains showed no mutation in those two positions. The correlation between real-time PCR melting curve analysis and SNP profiles is 100%.

CONCLUSION: Both molecular assays effectively detect *H. pylori* and provide genotypic information on clarithromycin resistance. These methods are more sensitive and faster than traditional culture and E-test screening for identifying clarithromycin resistant strains. Although this study utilized passive surveillance rather than a controlled design, it revealed a high prevalence of clarithromycin-resistant *H. pylori* in British Columbia. These findings offer valuable insights to inform and optimize antibiotic usage in treatment protocols, supporting better clinical outcomes and antibiotic stewardship efforts.

P029

Recovering *Cutibacterium acnes* from bone and joint specimens: Experiences with prolonged incubation at two centres

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OBJECTIVE: *Cutibacterium acnes* is a fastidious, anaerobic, slow-growing bacterium implicated in bone and joint infections, particularly involving prosthetic material. Prolonged incubation is often recommended for prosthetic joint specimens despite no consensus on duration or methodology. We examined bone and joint cultures at two clinical microbiology laboratories to evaluate the impact of prolonged incubation on *C. acnes* recovery.

METHOD: We retrospectively studied positive *C. acnes* bone and joint cultures. At Centre 1 (January 2021–April 2024), all periprosthetic fluid and tissue specimens were incubated for 14 days both on Brucella vitamin K agar and in fastidious anaerobic broth. At Centre 2 (November 2022–December 2024), solely shoulder specimens including invasively obtained swabs, fluid, and tissues were incubated for 4 days on CDC anaerobic blood agar and 14 days in thioglycolate broth.

RESULTS: At Centre 1, 108 periprosthetic specimens grew *C. acnes*, including 60 (55.6%) shoulder, 31 (28.7%) hip, and 6 (5.6%) knee samples. Fifty-three (49.1%) and 92 (85.2%) samples grew *C. acnes* by day 4 and 7, respectively. The remaining 16 (14.8%) samples grew at or around day 14 at the time of the next scheduled read, and were more likely to be pure (100% versus 88.0%), isolated as a single colony or in broth only (43.8% versus 9.8%), and cultured from a hip

or knee sample (50.0% versus 31.5%). Of 50 *C. acnes* shoulder specimens at Centre 2, 38 (76.0%) and 46 (92.0%) of these samples grew *C. acnes* by day 4 and 7, respectively. All samples grew *C. acnes* by day 10.

CONCLUSION: Most *C. acnes* isolates were recovered in the first 7 days, with all samples at Centre 2 identified by day 10 of incubation. Prolonged incubation may favour *C. acnes* recovery in hip and knee specimens. Additional studies involving clinical outcomes can further inform specific guidance for culture duration and methodology.

P030

Hypervirulent *Klebsiella pneumoniae* infections in an urban, tertiary care hospital

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OBJECTIVE: Hypervirulent *Klebsiella pneumoniae* (hvKp) is associated with pyogenic liver abscess and metastatic disease to the eyes, lung, and central nervous system. We reviewed the clinical presentation and microbiology of hvKp cases identified at our tertiary care hospital.

METHOD: Patients with excessively mucoid isolates of *K. pneumoniae* were assessed using a string test. Serotyping and molecular testing were performed at the National Microbiology Laboratory. Isolates with serotyping and/or genes associated with hvKp (*rmpA, iroB, iucA, ybtA, clbA*, and *peg344*) identified between October 2022 and October 2024 were included. We performed a retrospective chart review of patient characteristics including sex, age, country of origin, travel history, diabetes history, and course in hospital.

RESULTS: Seven patients with hvKp-positive isolates (blood [6/7], liver aspirate [1/7]) were identified. Four isolates were string test positive. Two isolates did not serotype, but the remainder were K1 (3/5), K2 (1/5), and K5 (1/5). Identified genes were *rmpA* (7/7), *iroB* (7/7), *iucA* (5/7), *ybtA* (6/7), *clbA* (4/7), and *peg344* (7/7). The majority of patients were male (6/7) with an average age of 66, from Southeast Asia (6/7), with diabetes (4/7), and recent travel to Asia (4/7). All patients required hospital admission, with three requiring ICU admission. Average length of stay was 31.7 days. Sites of dissemination included liver (5/7), prostate (1/7), eyes (1/7), and biliary tree (1/7). Three isolates were pan-susceptible, and four isolates had intermediate susceptibility to one antimicrobial (cefazolin [3/7] and piperacillin-tazobactam [1/7]). Definitive treatment (average duration, 35.5 days) included ceftriaxone ($n = 4$), ceftriaxone/metronidazole ($n = 1$), amoxicillin-clavulanate ($n = 1$), and ciprofloxacin ($n = 1$). Thirty-day attributable mortality was 28.6%.

CONCLUSION: Male patients from Asia with diabetes appeared to be disproportionately affected by hvKp. No single serotype was responsible for all cases. Early identification of hvKp is important, especially with the risk for disseminated disease.

P031

Ungrouping the *Bacteroides fragilis* group: Species-level observations at a regional clinical microbiology laboratory

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OBJECTIVE: The *Bacteroides fragilis* group (BFG) is a collection of frequently isolated anaerobic bacteria associated with abdominal infections and sepsis. However, recent taxonomic changes and advances in bacterial identification challenge the continued use of this broad grouping. This study aimed to characterize the distribution of *Bacteroides*, *Parabacteroides*, and *Phocaeicola* species isolated at a regional reference clinical microbiology laboratory.

METHOD: We conducted a retrospective survey of all reported *Bacteroides*, *Parabacteroides*, and *Phocaeicola* species isolated from clinical specimens at our laboratory between November 2022 to December 2024. To remove duplicate samples, we counted one isolate per species per sample type (blood, swab, fluid, or tissue) for each patient. Statistical analysis was performed in R with Pearson's Chi-squared test.

RESULTS: A total of 804 *Bacteroides*, *Parabacteroides*, and *Phocaeicola* isolates were identified across 648 samples, including 431 (54.0%) abdominal/pelvic specimens, 165 (20.5%) blood cultures, and 187 (23.4%) arm/back/leg specimens. Only 138 (17.2%) isolates were identified as a

pure culture, including 116 blood cultures. Nearly all isolates ($N = 800$, 99.5%) were identified using MALDI-ToF mass spectrometry, of which *B. fragilis* ($N = 317$, 39.4%), *B. thetaiotaomicron* ($N = 125$, 15.5%), *B. ovatus* ($N = 92$, 11,4%), *Phocaeicola vulgatus* ($N = 59$, 7.3%), and *B. uniformis* ($N = 43$, 5.3%) were most frequently isolated. Species identification correlated with specimen source ($p = .013$) and sample type ($p = .022$) but not with pure culture ($p = .47$). *B. fragilis*, *B. uniformis*, and *P. vulgatus* were more associated with bacteremia while *B. thetaiotaomicron* and *B. ovatus* were more associated with abdominal/pelvic infections.

CONCLUSION: Clinical laboratories can routinely perform species-level identification of former and current BFG species. Species-level associations of *Bacteroides*, *Parabacteroides*, and *Phocaeicola* species support the discontinuation of this historic taxonomic designation.

P032

Lipidomics insights into antimicrobial resistance in *E. coli*

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OBJECTIVE: *Escherichia coli* is a major public health concern, causing over 2 million deaths annually worldwide. These infections are typically managed using antibiotics, but the alarming rise in antimicrobial resistance (AMR) is escalating toward a global health crisis (Leekitcharoenphon et al. Scientific Reports 2021). With antibiotic development pipelines nearly exhausted, novel therapeutic targets are urgently needed. While many AMR mechanisms are well characterized, the role of lipids remains underexplored. This project investigates the role of lipids in AMR through lipidomic profiling of *E. coli* strains.

METHOD: Six *E. coli* strains were grown in Mueller Hinton II broth at 37°C with shaking to an OD600 of 0.8–1.2. For the AMR tests, ampicillin was added at the strain's minimal inhibitory concentration (MIC), followed by incubation for 2, 4, 6, and 24 hours. Aliquots corresponding to 6×10^9 cells were pelleted, washed with cold PBS, and quenched with cold methanol. Lipids were extracted using methanol, dichloromethane, and 0.2M KCl with deuterated internal standards. Lipidomic analysis was performed using reversed-phase LC-MS/MS.

RESULTS: The lipidomic profiles of three ampicillin-resistant (AR_0084, AR_0019, AR_0020) and three susceptible strains (CDC 25922, AR_0077, CP9) revealed significant differences in lipid compositions, with complete separation by principal component analysis (PCA). Cardiolipins, phosphatidic acids, and phosphatidylethanolamines displayed substantial variations, with resistant strains showing higher odd-chain fatty acids. Exposure of the CDC control strain to ampicillin induced a significant increase of phosphatidylglycerol species over time (FDR-adjusted $p < .01$ and fold-change >1.5), whereas FA 18:1 and cardiolipins were reduced (FC < 0.67). These findings suggest early lipidomic shifts consistent with stress adaptation.

CONCLUSION: The observed lipid remodelling under antibiotic stress highlights the critical role of membrane and lipid dynamics in resistance mechanisms. We are now working to induce resistance in a susceptible strain to evaluate lipidomic changes associated with acquired resistance.

P033

Wastewater-based surveillance (WBS) of Shiga toxin–producing *Escherichia coli* (STEC) during a city-wide daycare outbreak

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OBJECTIVE: A daycare Shiga toxin–producing *Escherichia coli* (STEC) outbreak in August and September 2023 was one of the largest of its kind in Canada. The outbreak

involved 448 confirmed and suspected cases (38 children and 1 adult hospitalized) linked to sites with a shared central kitchen. We leveraged an existing municipal wastewater-based surveillance (WBS) network to explore whether this outbreak could be tracked over time.

METHOD: Composite 24-hour wastewater was collected weekly between June and November 2023 from municipal wastewater treatment plants (WWTPs), six neighbourhoods, and the regional paediatric hospital (RPH-1). Additional monthly samples were collected between March 2023 and March 2024 for WWTPs and RPH-1. Wastewater DNA extracts were assessed for STEC genomic targets, Shiga toxin-1 and -2 (*stx*$_1$, *stx*$_2$), intimin (*eae*), and LPS-O antigen specific for O157 (*rfbE*$_{O157}$), by multiplex qPCR. Targets were normalized by total 16S rRNA-for bacterial burden. Data were analyzed in Prism and compared using Spearman's rank correlation coefficient.

RESULTS: Strong correlation was observed for STEC targets across sites, ie. *stx*$_1$ versus *stx*$_2$, r = 0.7192, $p < .0001$; *stx*$_2$ versus *rfbE*$_{O157}$, r = 0.659, $p < .0001$; *eae* versus *rfbE*$_{O157}$, r = 0.6354, $p < .0001$. Large spikes in STEC gene targets were observed for RPH-1 increasing by a median 126-fold (*rfbE*$_{O157}$) and 2,509-fold (*stx*$_2$) in September 2023 compared to before/after the outbreak. Modest increases in STEC genomic targets were seen in most monitored neighbourhoods for *rfbE*$_{O157}$ and *stx*$_2$ relative to baseline values. Mean *rfbE*$_{O157}$ and *stx*$_2$ doubled across the city's WWTPs in August 2023. Smaller sewershed catchments exhibited much a larger variance in STEC genomic targets than did municipal WWTPs.

CONCLUSION: During a community-wide daycare STEC outbreak linked to shared support facilities, increases in STEC gene targets were detected across a range of scales and correlated well with each other. In the future, real-time WBS could be a useful tool to understand and track outbreaks of enteric pathogens such as STEC.

P034
Assessment of WASPLab® performance and optimal incubation time for urine cultures

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OBJECTIVE: To determine the clinical agreement of urine culture interpretation using 16h versus 18h digital images on WASPLab® in comparison with current manual interpretation of culture plates.

METHOD: A total of 299 urine samples were processed and incubated by the WASPLab® and by the current standalone WASP followed by manual incubation. WASPLab® incubation was set to 35°C in O_2 for COLOREX and in CO_2 for CNA and BAP. Images were taken in WASPLab® at 16 and 18 hours. Manual incubation for 18 hours was set to 35°C in O_2 for COLOREX, can, and BAP. The results obtained by digital image interpretation were compared with manual culture plate interpretation for clinical agreement with respect to colony counts and interpretative category (no growth, no significant growth, mixed, positive with organism identified). The image time (16 hours versus 18 hours) for clearest interpretation was documented. Clinical agreement was defined as a match in interpretative category or having extra growth in WASPLab®.

RESULTS: Clinical agreement was 98.9% (296/299) at 18 hours. Three samples showed a discrepancy because the manual method had no significant growth whereas the WASPLab® had no growth. In 7.6% (23/299) of samples having clinical agreement, there was extra growth of new organisms in WASPLab® that was not present with manual incubation. In 24% (72/294) of cultures, digital image reading at 18 hours was preferred to reading at 16 hours. Time preference was not recorded for 5 samples.

CONCLUSION: WASPLab® demonstrated acceptable performance for non-invasive and invasive urines. The samples showing extra growth indicate a potential benefit for using WASPLab®. The data showed that culture imaging at 18 hours was preferred to the same at 16 hours because colony morphology was more developed at 18 hours, resulting in more accurate digital interpretation by technologists and the most efficient operations. Future studies will be performed to evaluate Phenomatrix Plus®.

P035
Hypervirulent *Klebsiella pneumoniae* harbouring carbapenem resistance genes in Alberta, Canada, 2016–2024

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OBJECTIVE: Hypervirulent *Klebsiella pneumoniae* (hvKp) can cause invasive community-acquired infections in healthy adults. HvKp is usually susceptible to most antibiotics; however, hvKp gaining multidrug resistance, including to carbapenems, is emerging. Recent reports of the hypervirulent carbapenemase-producing *K. pneumoniae* (CpKp) ST23 lineage has raised alarms globally, making reporting of these cases significant. We screened all CpKp in Alberta for the presence of hypervirulence genes associated with the hypervirulent phenotype.

METHOD: *K. pneumoniae* from Alberta are submitted to the National Microbiology Laboratory for carbapenemase gene detection (KPC, NDM, OXA-48-type, IMP, VIM, GES, and NMC/IMI) by conventional PCR. Hypermucoviscous string-test was done on all isolates. Carbapenemase-positive isolates were sequenced using the Illumina NextSeq platform. Virulence genes (*ybt*, *clb*, *iuc*, *iro*, *rmpA*/*A2*) and score were determined using Kleborate. Between 2016 and 2024, 16 CpKp had Kleborate virulence scores of ≥3. Long-read sequencing was performed on these isolates using Oxford Nanopore Technologies. Hybrid genomes were assembled using Hybracter or Unicycler. Isolates were analyzed using Abricate, StarAMR, and MOB-Suite.

RESULTS: Phenotypically, 13/16 isolates were string-test negative. Among all isolates, virulence scores of 5 ($n = 1$), 4 ($n = 14$), and 3 ($n = 1$) were observed. There were eight sequence types (ST) in total, including one ST23. Carbapenemase genes included NDM ($n = 1$), OXA-48-type ($n = 7$), or both ($n = 8$). The ST23 isolate harboured *ybt* and *clb* on the chromosome, *iro* and *iuc* on a 230 kb IncFIB,IncHI1B virulence plasmid, and OXA-48 on a 92 kb IncFIA,IncFII plasmid. Interestingly, several isolates ($n = 7$) co-harboured virulence genes and NDM on the same plasmid.

CONCLUSION: Acquisition of carbapenemase genes by hvKp is of concern due to the combination of invasiveness and antibiotic resistance. Here, we identified a ST23 hvKp isolate in Canada with OXA-48 and seven isolates harbouring NDM on a virulence plasmid. Conventional hypermucoviscous string-test would not have detected 81% of these hvKp.

P036

Fast and user-friendly discrimination of highly virulent *Streptococcus agalactiae* clonal complexes by MALDI-TOF MS

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OBJECTIVE: *Streptococcus agalactiae* (GBS) is a common causative agent of neonatal bacterial meningitidis, burdened by high morbidity and mortality. Most cases are associated with a highly virulent clone, defined as serotype III and clonal complex 17 (CC17); in the 1990s, another clone (CC1) emerged as a significant cause of infection in newborns and adult immunocompromised patients. MALDI-TOF MS was investigated in this study for its potential to discriminate between the highly virulent GBS CC17 and CC1 clones.

METHOD: One-hundred and forty-three previously characterized GBS strains were included in this study, belonging to 19 sequence types and 6 clonal complexes, namely CC17 ($n = 80$), CC23 ($n = 16$), CC12 ($n = 15$), CC19 ($n = 14$), CC1 ($n = 11$), and CC498 ($n = 4$), and one isolate each belonging to ST26, ST41, and ST529. MALDI-TOF MS spectra were acquired with the MALDI Biotyper® system, using the default setting and procedure for routine measurement.

RESULTS: For both CC17 and CC1, a specific marker was found in the MALDI spectra. Most of CC17 (69/80; 86.3%) isolates showed the presence of a specific peak at 7,617 m/z, which was present in none of the other isolates (0/63), which all showed a peak at 7,637 m/z, absent in CC17. These peaks were found to be corresponding to two protein variants, determined by an amino acid exchange (R25H) in the *S. agalactiae* 50S ribosomal protein L35. In all CC1 isolates (11/11), a specific peak at 6,251 m/z was observed, which was absent in all other strains. This peak was found to be related to a 6250-Da ST1 specific protein.

CONCLUSION: MALDI-TOF MS was shown to discriminate highly virulent clones of *S. agalactiae*. The implementation of this potential subtyping application could allow prompt and extremely routine-friendly detection and screening of GBS isolates, which could represent a relevant aid in the prevention of the transmission from colonized mothers to newborns.

P037

Development and validation of a high-resolution melt assay for rapid detection of vancomycin resistance genes in *Enterococcus* species

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OBJECTIVE: Vancomycin-resistant enterococci (VRE), primarily *Enterococcus faecium* (VREfm) and *Enterococcus faecalis* (VREfc), are important nosocomial pathogens. Rapid identification of resistance genes (*vanA* and *vanB*) and species is essential for infection control and effective antimicrobial treatment. This study introduces a laboratory-developed high-resolution melt (HRM-VRE) assay for rapid, cost-effective, and accurate identification of VRE.

METHOD: HRM-VRE detects *vanA* and *vanB* resistance genes while differentiating *E. faecium* and *E. faecalis* based on melting temperature profiles. Two separate reactions were designed: one for *vanA* and *vanB* detection and another for species differentiation. Reactions utilized Qiagen Type-It HRM PCR Kit Master Mix performed on Bio-Rad CFX96. Validation included clinical VRE and non-VRE isolates, with parallel testing using conventional phenotypic methods.

RESULTS: HRM-VRE demonstrated 100% sensitivity and specificity (Table P037-1). No cross-reactivity or false positives occurred with common strains isolated from VRE chromogenic agar or vancomycin-sensitive enterococci. Integration into routine workflows will reduce VRE confirmation turnaround time to within 24 hours of detectable culture growth compared with a minimum of 3 days using traditional methods. The reagent cost per test for the HRM-VRE is estimated to be under $3 compared with commercial assays that typically range from $15 to $25.

CONCLUSION: HRM-VRE assay is an accurate, reliable, and time-efficient method for detecting VREfm and VREfc. As a lab-developed assay, it is considered cost effective compared to commercially available assays. Its high sensitivity and specificity combined with simultaneous detection of resistance genes and species make it suitable for routine diagnostic use, particularly in resource-limited settings.

Table P037-1: Validation results

Sensitivity	*n*	TP	FN
***E. faecalis* vanA**	5	5	0
***E. faecalis* vanB**	4	4	0
***E. faecium* vanA**	108	108	0
***E. faecium* vanB**	136	136	0
Specificity	***n***	**TN**	**FP**
***E. faecalis* VSE**	52	52	0
***E. faecium* VSE**	15	15	0
Other *Enterococcus* species	6	6	0
Non-*Enterococcus* organisms	33	33	0

P038

Validation of the BD Kiestra MRSA Application for detection of MRSA from surveillance specimens on BD BBL CHROMagar MRSA II

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OBJECTIVE: The BD Kiestra™ MRSA Application (MRSAApp) uses high-resolution plate images captured by the BD Kiestra™ Total Laboratory Automation (TLA) system for automated digital segregation of cultures planted on BD BBL™ CHROMagar® MRSA II plates (CA). Results generated by the MRSAApp are either growth of mauve colonies suggestive of MRSA or MRSA negative indicating no growth or absence of mauve colonies. This study evaluates the MRSAApp's accuracy in its result classification.

METHOD: Anterior nares or rectal swabs collected with a single ESwab (Copan) and nares/rectal swabs collected with a dual ESwab submitted for MRSA surveillance were included. Swabs were processed by TLA to CA and incubated at 37°C. Plates were imaged and analyzed by both the MRSAApp and medical laboratory technologists (MLT). Mauve colonies suggestive of MRSA were processed for confirmation using standard procedures by an MLT. The MRSAApp's segregation was retrospectively compared with final culture results to assess accuracy.

RESULTS: Of 2,524 consecutive MRSA surveillance swabs, 46 were confirmed MRSA positive (1.8% positivity rate).

The MRSAApp correctly classified 45/46 (97.8%) MRSA-positive swabs as potential MRSA, with one false negative due to a single mauve colony. Additionally, 168 specimens were classified as potential MRSA but did not yield MRSA, with the plates demonstrating lighter mauve colonies and/or agar discoloration at the inoculation site. Overall, the positive predictive value (PPV) of the MRSAApp was 21.1%, and the negative predictive value (NPV) was 99.96%.

CONCLUSION: MRSAApp is an effective tool for automated screening of MRSA plates. Although PPV was low, the high NPV would lead to a significant reduction of manual workload. With approximately 75,000 MRSA processed annually, MRSAApp could automatically segregate 92% of specimens as negative, with only 8% requiring manual MLT review. Enabling autoverification of negative cultures can further streamline workflow and optimize MLT time to prioritize workup of mauve colonies suggestive of MRSA.

P039

Microbiome analysis of bronchoalveolar lavage (BAL) specimens from immunocompromised patients with lower respiratory tract infections (LRTI) compared with those from healthy volunteers

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OBJECTIVE: Microbiological testing of BAL is vital for managing immunocompromised patients (IP) with LRTI, but standard methods are often limited by early antibiotic use and inability to detect atypical pathogens. Sequencing may reveal potential pathogens, but their clinical importance is often unclear. This study compared the BAL microbiomes of IP with LRTI to healthy volunteers, aiming to develop a 16S/18S rRNA gene-based targeted metagenomic approach for detecting bacterial and fungal pathogens.

METHOD: BAL specimens from healthy volunteers ($n = 20$) were collected during the COVID-19 vaccine trial, and residual BAL from IP ($n = 25$) were obtained from clinical virology laboratory after standard culture and PCR. 16S-18S rDNA amplicon Nanopore sequencing was performed. Raw reads were classified with Minimap classifier in Epi2Me using wf-16s.

RESULTS: Mean bacterial reads in BAL from healthy and immunocompromised individuals were 16,437 $\pm$ 37,073 and 6,222 $\pm$ 13,125, respectively, while fungal reads were insignificant in both groups. Relative abundances of species were uneven, with dominance of a single species over others in both groups (Berger Parker index 0.67 $\pm$ 0.22 versus 0.69 $\pm$ 0.19, $p = .9$; Pielou's evenness 0.31 $\pm$ 0.17 versus 0.27 $\pm$ 0.12, $p = .2$, respectively). However, species richness was significantly higher in the healthy group compared to IP (species richness 84.5 $\pm$ 29.6 versus 40.4 $\pm$ 18.2, $p < .001$; Shanon diversity index 1.37 $\pm$ 0.78 versus 0.97 $\pm$ 0.48, $p < .05$, respectively). Healthy BAL showed predominance of mixed anaerobic bacteria, unlike those from immunocompromised. *Prevotella* sp. was the dominant taxon in 95% of healthy BAL compared to only 16% in BAL from immunocompromised ($p < .001$). Several atypical pathogens, missed by culture, were detected in BAL from IP (35%) but not from healthy volunteers, including *Nocardia* sp., *Metamycoplasma* sp., *Lacticaseibacillus* sp., and *Trophyrema* sp.

CONCLUSION: Our results demonstrate the potential diagnostic value of the 16S/18S metagenomic approach for detecting pathogens in BAL specimens from IP with LRTI, although knowledge of commensal flora and further standardization are needed.

P040

Central nervous system tuberculosis in Alberta: A 9-year population-based retrospective cohort study

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OBJECTIVE: To evaluate demographics, epidemiology, diagnostic delays, cerebrospinal fluid (CSF) parameters, brain imaging findings, and treatment outcomes in patients with central nervous system tuberculosis (CNS-TB).

METHOD: We conducted a retrospective cohort study of patients with CNS-TB identified through physician-reviewed ICD codes from 2013 to 2021. Chart reviews were completed using health information systems. Cases were classified as tuberculous meningitis or CNS-TB without meningitis (eg, tuberculoma or abscess). Data collected included demographics (age, sex, country of birth), clinical parameters (HIV status, end-stage renal disease, diabetes, immunosuppression, smear status), and treatment factors

(drug resistance, medication regimens, outcome). CSF and imaging data were reviewed. 95% confidence intervals were used.

RESULTS: Fifty-two patients with tuberculous meningitis and eight with tuberculoma were identified. Forty percent of patients with TB meningitis had positive mycobacterial cultures, with 60% diagnosed clinically. Suboptimal specimen volume was noted in 43% of initial CSF mycobacterial cultures. Repeat LPs were performed for diagnostic purposes in 67% of cases. In patients with TB meningitis, mean cell count was 206 ± 71 cells, and mean lymphocyte proportion was 72 ± 8%. Twenty-seven percent of all cases were started on a five-drug regimen, with fluoroquinolone use noted in 73% of initial regimens. Mean daily rifampin dose was 11.2 ± 0.9 mg/kg. The median delay from symptom onset to treatment initiation was 33 days. Initial brain imaging showed typical "basilar," "posterior fossa," or "basal cistern" enhancement in 48% of cases, while 29% had normal imaging.

CONCLUSION: This study highlights opportunities to improve CNS-TB care in Canada, showcasing the epidemiologic factors and CSF/imaging finding seen in typical and atypical cases in high-income settings. Earlier recognition of these findings could help reduce diagnostic delays. Enhancing protocols for CSF mycobacterial culture collection may reduce unnecessary LPs and expedite diagnosis. Optimizing treatment regimens with CNS penetration, including appropriate rifampin dosing and use of fluoroquinolones or linezolid, warrants further research to improve outcomes.

P041

The association of immunocompromising conditions with mortality from blastomycosis in Manitoba

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OBJECTIVE: To characterize the clinical presentation and outcomes of immunocompromised patients hospitalized for blastomycosis compared to those without immune compromise.

METHOD: We performed a retrospective descriptive cohort study identifying adult patients hospitalized with microbial growth of *Blastomyces* spp. in Manitoba using the Provincial Lab Information System (PLIS) between January 2008 and May 2024. Immunocompromised conditions were defined as human immunodeficiency virus (HIV) and CD4 < 200, connective tissue disorder, solid tumor uncured by surgical resection, leukemia, lymphoma, or hematopoietic stem cell transplant within the year preceding hospitalization. We conducted descriptive analyses and statistical tests of comparisons between groups.

RESULTS: Of 271 patients with blastomycosis, we identified 122 unique hospitalizations. An immunocompromising condition was present in 16 patients (13%). Immunocompromised patients had a higher proportion of in-hospital mortality (31.3%; $n = 5$) compared to those without immune compromise (23.6%; $n = 25$). Need for intensive care unit (ICU) admissions were comparable (43.8% versus 40.6%), with similar ICU length of stay (19 versus 18 days). Total length of hospitalization was longer for immunocompromised patients (34 versus 25 days).

CONCLUSION: Immunocompromised patients represent a small proportion of patients requiring hospitalization for blastomycosis. Hospital mortality, need for ICU admission, and ICU length of stay were similar, regardless of immunocompromised status. Future studies are needed to determine the association of immunocompromised status with mortality after controlling for covariates that influence the outcome.

P042

Silent polyclonal infections in bacteremia: Survey of 10 major bacterial pathogens in the Calgary region

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OBJECTIVE: Bloodstream infections (BSI) cause over half a million cases annually in North America, resulting in 90,000 deaths. The success of clinical management of BSIs is critically reliant on the accurate determination of pathogen's antimicrobial resistance profile. Currently, microbial species and antimicrobial susceptibility patterns are based on phenotypes observed from single colonies picked from flagged blood culture bottles. This practice tends to underrepresent the true diversity of microbes circulating in BSIs because (1) only single isolates are picked for downstream laboratory analyses and (2) low microbial density in bacteremia can result in stochastic non-uniform distribution of circulating pathogens between blood culture bottles. Consequently, current laboratory methods cannot reliably assess the frequency of polyclonal infections, which involve multiple strains of the same species. These "silent" polyclonal infections may attribute to heterogeneity in resistance phenotypes, a phenomenon that may lead to treatment failures from an overgrowth of resistant strains. Currently, the incidence rate of polyclonal BSIs and the degree to which they contribute to heterogeneity in resistance have not been rigorously investigated.

METHOD: To address this, we harness the Calgary BSI cohort (2006–2022), comprising 38,000 BSI pathogens with whole-genome sequencing, systematic phenotypic data, and extensive electronic medical records, to identify examples of multiple infection in a large clinical cohort. Pairwise genetic distances were calculated to establish genetic relatedness thresholds for detecting polyclonal infections across 10 major BSI bacterial pathogens.

RESULTS: Among 1,847 multiple infection periods, polyclonal incidence rates ranged from 7.53% to 27.27% with *Enterococcus faecium,* a common nosocomial pathogen, showing a 21.33% polyclonal rate. Furthermore, over 95% of follow-up cultures with discordance in resistance profiles in *Staphylococcus aureus* and *Escherichia coli* were found in polyclonal infections.

CONCLUSION: These findings demonstrate the clinical relevance of identifying polyclonal BSIs to improve diagnostic accuracy and guide effective antimicrobial treatment.

P043

Clinical characteristics of varicella zoster virus (VZV) infections in adult solid organ transplant recipients

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OBJECTIVE: Data on varicella zoster virus (VZV) infections in solid organ transplant (SOT) recipients are limited. In our study, we aimed to investigate the clinical characteristics, outcomes, and complications of VZV infection in a large cohort of SOT patients presenting with microbiologically confirmed disease.

METHOD: We retrospectively reviewed the electronic medical and clinical microbiology records of SOT recipients who tested positive for VZV polymerase chain reaction (PCR) of any sample type between February 2013 and December 2022. Data collected included transplant organ type, immunosuppression, dissemination and visceral involvement, and complications such as post-herpetic neuralgia (PHN). An analysis of risk factors associated with disseminated infection was performed.

RESULTS: A total of 146 adult SOT patients with confirmed VZV infections were included in the study. Transplant types included lung ($n = 48$), kidney ($n = 48$), liver ($n = 19$), heart ($n = 25$), and other ($n = 6$). Median time to infection presentation was 640 days (IQR 290–2,251 days). Disseminated VZV infection was diagnosed in 59 of 138 patients (42.8%). Visceral involvement included ocular complications in 10 cases (6.8%), pneumonitis in 5 (3.4%), encephalitis in 3 (2%), and hepatitis in 2 (1.4%). PHN occurred in 33 patients (22.6%). One hundred and one patients (71.6%) required hospitalization, and five patients (3.4%) died within 30 days. The 1-year mortality rate was highest in the lung transplant group (12/48; 25%). No clear association was found between factors such as type of transplant, age, sex, immunosuppression, and the risk of disseminated disease, with the exception of a slightly higher overall mycophenolate mofetil dose in the latter group ($p = .066$).

CONCLUSION: We describe the clinical characteristics of VZV infection in a large cohort of SOT patients. Overall, hospitalization and disseminated infection were frequent, as well as visceral organ involvement. No clear risk factors were identified as predictive of dissemination.

P044

Characterizing the pathogens and antibiotic therapy for ventilator-associated pneumonia in chronically ventilated patients admitted to Vancouver General Hospital

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OBJECTIVE: To investigate any differences in the management of ventilator-associated pneumonia (VAP) in chronically ventilated patients at home versus at institution with respect to empiric/targeted antimicrobial choice (dose, route, frequency) and duration, and microbiological data (pathogens and susceptibilities).

METHOD: Retrospective chart review of all adult patients age ≥18 years on chronic ventilation admitted to Vancouver General Hospital (VGH) from November 1, 2022 to February 29, 2024.

RESULTS: A total of 21 chronically ventilated patients were analyzed (14 from institutions and 7 from home). Pseudomonas aeruginosa was the most common pathogen identified for both home ($n = 3$; 59%) and institutional ($n = 7$; 63%) settings. While patients from institutions have higher rates of recurrence ($n = 7$; 78%) compared to home patients ($n = 2$; 22%) and a history of multidrug-resistant strains ($n = 5$; 56%), there was no difference in clinical outcomes such as length of admission (median [IQR] days: institution 12.0 [8.9–25.4] versus home 10.0 [8.7–20.9]) and duration of treatment (mean ± SD: institution [10.0 ± 6.2] versus home [12.1 ± 6.1]). Additionally, there was no difference in antimicrobial choice and regimen for both empiric and targeted therapy.

CONCLUSION: No major differences exist in the management of VAP in chronically ventilated patients at home or at an institution, with prior microbiology history being a major driver for antimicrobial choice. Despite limitations, this project provides insight into opportunities for education, antimicrobial stewardship, and guidelines to better manage VAP in these patients.

P045

Performance of a nasal multiplex rapid antigen detection test (RADT) as a complement to nucleic acid amplification test (NAAT) to detect respiratory viruses in a paediatric emergency department setting

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OBJECTIVE: Respiratory viral infections, mainly with influenza, SARS-CoV-2, and respiratory syncytial virus (RSV), are reasons for consultation in paediatrics. Currently, their diagnosis is based on PCR testing, which is expensive, often run in batches, and requires highly trained personnel. The use of a point-of-care, multiplex RADT, which is inexpensive and easy to use, may increase patient fluidity in the emergency department (ED). This project describes performance characteristics of a nasal quadplex RADT in comparison with multiplex validated PCR.

METHOD: The residual fluid that remained in the device after RADT testing from patients evaluated at the CHU Sainte-Justine ED between October 10, 2024 and January 8, 2025, for whom the physician decided to do a nasal quadplex (COVID-19, Influenza A/B, and RSV antigen nasal test kit, Assure Tech), was harvested to purify nucleic acids. Consecutive specimens between October 10 and December 13, 2024 and between December 27, 2024 and January 7, 2025 were tested by our validated multiplex viral PCR (15 virus, Roche, TIB Mol Biol). Given the overwhelming prevalence of RSV early on, we opted to halt parallel testing until influenza circulation was documented.

RESULTS: Overall, 580 samples from unique patients were tested in parallel by both techniques. A total of 372 specimens were positive by PCR for at least one virus (influenza A: 44; influenza B: 10; RSV: 171; SARS-CoV-2: 27; others: 120). Concordances between the two analyses were 88.9% (95% CI 70.8–97.7) for SARS-CoV-2, 91.8% (95% CI 86.7–95.5) for RSV, 93.2 (95% CI 81.3–98.6) for influenza A, and 90.9% (95% CI 58.7–99.8) for influenza B. Compared to

PCR, RADT specificity was 100%, except for influenza B (one false positive, negative by PCR).

CONCLUSION: Our results indicate that the nasal multiplex RADT has characteristics that we considered acceptable for an ambulatory-setting paediatric population. The impact on patients' management and ED fluidity remains to be assessed.

P046

Estimates of paediatric community-acquired pneumonia incidence in high-income countries since 2010: A systematic review

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OBJECTIVE: Paediatric community-acquired pneumonia (CAP) is a significant cause of morbidity and mortality worldwide, being responsible for the deaths of more than 800,000 children per year. The burden of pneumonia in high-income nations after the inclusion of 13-valent pneumococcal conjugate vaccines in universal immunization programs has not been systematically evaluated. It is important to gauge the potential impact of expanded-valency pneumococcal vaccines and predict antimicrobial usage patterns.

METHOD: We conducted a systematic review of randomized controlled trials and observational studies reporting outcomes from 2010 onward. We searched MEDLINE, EMBASE, CINAHL, Global Health, and CENTRAL. We considered studies conducted in countries defined as high-income by World Bank criteria, including children aged 3 months or older with a clinical diagnosis of CAP. Our primary outcomes were the incidence of CAP and incidence of severe CAP (CAP requiring hospitalization).

RESULTS: There were 22 studies reporting overall CAP incidence and 33 studies reporting incidence of CAP requiring hospitalization. Incidence data showed substantial variability, likely due to heterogeneity of studies conducted in different regions and time periods with varying age groups and methodologies. Overall yearly CAP incidence ranged from 2.4 cases per 1,000 children to 29.97 per 1,000 children. Yearly incidence of CAP requiring hospitalization ranged from 0.29 per 1,000 children to 38.47 per 1,000 children.

CONCLUSION: This systematic review highlights considerable variability in paediatric CAP incidence across high-income countries, time periods, and age groups. However, CAP still appears to represent a significant child health issue even in regions that have the lowest incidence of disease despite widespread implementation of PCV13 vaccines.

P047

A clinical overview of utilization of Tocilizumab for COVID-19 at a tertiary care teaching organization in 2023

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OBJECTIVES: Tocilizumab is recommended in the management of COVID-19 in patients receiving dexamethasone and having increasing respiratory needs. The appropriateness of Tocilizumab for COVID-19 in Canada is unclear, given criteria of use from both the National Institutes of Health (NIH) and Ontario Science Table (OST) guidelines. The purpose of this review is to determine the appropriate utilization of Tocilizumab

METHODS: Retrospective review of patients receiving Tocilizumab for COVID-19 was completed from October 2023 to October 2024 at Hamilton Health Sciences. Appropriate use was defined as congruence with either NIH or OST guideline.

RESULTS: A total of 55 patients were included in the study; no patients were excluded. Of the 55 patients, 32 (58%) received their doses of Tocilizumab in the ICU. The critical care service was responsible for ordering 34/55 doses of Tocilizumab, while infectious diseases ordered only 4/55 doses of Tocilizumab. Among the 55 patients, 53 (96%) received dose banded doses of Tocilizumab, with only 2 patients receiving two doses. Mean age of patients was 72.5 years (IQR 65–82). Of the 55 patients 11 (20%) were mechanically ventilated, and the remaining 44 (80%) were on high-flow nasal cannula, BIPAP, or non-invasive ventilation. Dexamethasone was given to 53/55 (96%) of patients, while 27/55 (49%) patients received antivirals. The mean number of days from symptom onset to receiving Tocilizumab was approximately 6 (SD 5.7 days).

CONCLUSIONS: Overall, 51/55 (93%) courses of Tocilizumab were deemed appropriate based on the OST/NIH guidelines, as it was overwhelmingly being utilized in patients with worsening respiratory status at the time of presentation or worsening while on dexamethasone.

P048

COVID-19 among patients receiving bispecific T-cell engager therapy and chimeric antigen T-cell therapy for lymphoma: A single-centre retrospective cohort study

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OBJECTIVE: Bispecific T-cell engagers (BiTE) and chimeric antigen receptor (CAR) T-cell therapy have changed the treatment landscape of lymphomas. The outcome characteristics of COVID-19 among patients receiving either therapy remains poorly understood.

METHOD: In this retrospective cohort, we included patients with lymphoma who received BiTE or CAR T-cell therapy during COVID-19 pandemic. The accrual period extends from January 1, 2020 to December 31, 2023. We determined baseline characteristics, comorbidities, clinical data, and COVID-19 outcomes (14-day hospitalization, 21-day ICU admission, death). Chi-squared test and Fisher's exact test were used for categorical variables; Student *t*-test and Mann-Whitney test were used for continuous variables.

RESULTS: Thirty-eight patients (median age [IQR]: 66.5 [55–70.2] years, 65.8% female) were included. Therapies received included BiTE (31/38; 81.6%), CAR T-cell therapies (12/38; 31.5%), or both (5/38; 13.1%). Overall, 19 (50%) developed COVID-19; no differences were observed between proportion of COVID-19 infection among patients receiving BiTE or CAR T-cell therapies ($p = .636$). All patients received at least one dose of COVID-19 vaccination prior to infection. Four patients developed mild COVID-19 within 180 days of vaccination, of which half received only one dose. Twelve patients (31.6%) received tixagevimab/cilgavimab, of which three developed mild COVID-19 within 180 days of receiving the pre-exposure prophylaxis. Severe COVID-19 occurred in 4/19 (21.1%) patients, of which 1 received CAR T-cell therapy (no BiTE) and 3 received BiTE. Of these, three required ICU admission and mechanical ventilation and two died within 3 weeks after COVID-19 diagnosis (10.5%). Of those with severe COVID-19, coinfections reported included *Mycobacterium avium* ($n = 1$), *Klebsiella aerogenes* ($n = 1$), and Rhino/enterovirus ($n = 1$). All individuals with severe COVID-19 were infected after 180 days from last dose of vaccination or tixagevimab/cilgavimab.

CONCLUSION: Our preliminary data support the use of booster vaccine against COVID-19 every 6 months in high-risk individuals including those receiving BiTE and CAR T-cell therapies for lymphoma. Final analyses are forthcoming.

P049

M. abscessus soft tissue infections associated with lipolytic agents subcutaneous injection: An outbreak report and molecular epidemiology study

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OBJECTIVE: This study reports a *Mycobacterium abscessus* skin and soft tissue infection outbreak linked to mesotherapy treatments and validates a novel whole-genome sequencing (WGS)-based bioinformatic pipeline to identify such outbreaks and support public health investigations.

METHOD: A public health investigation including questionnaires sent to patients' infectious diseases physicians was performed to trace the timeline of events and establish the putative outbreak source. The complete genomes of six isolates from four patients were sequenced using a combination of Nanopore and Illumina technologies. Genomic *de novo* assembly was performed, and single nucleotide polymorphisms (SNPs) were identified using an external *M. abscessus* reference strain and a within-outbreak strain. Distance matrices and phylogenetic trees were generated using between isolates SNP distances.

RESULTS: Public health investigation and physicians' questionnaires suggested that all patients had received injections from the same esthetician within a 1-month period. Bioinformatics analyses revealed that all isolates were genomically nearly identical, differing by only 0 to 2 SNPs. A generated phylogenetic tree showed that these cases were genetically distinct both from other *M. abscessus* genomes obtained in Montréal and from reference genomes of *M. abscessus* subspecies.

CONCLUSION: Our findings indicate that merging Nanopore and Illumina data for WGS analysis can help identify whether different *M. abscessus* isolates have enough genomic similarities to suggest the possibility of a single outbreak. Those technologies and this approach could be used to support public health investigations, such as where there is epidemiological uncertainty regarding the relatedness of different cases.

P050

Validation of expedited antimicrobial susceptibility testing using short-incubation blood culture subcultures

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OBJECTIVE: Increasing antibiotic resistance demands more rapid AST solutions, especially in patients with sepsis and positive blood cultures. This study validates expedited AST using short-incubation blood culture subcultures (SIBC-AST).

METHOD: Conventional-AST from 18h-agar-subcultures and simulated SIBC-AST from 4h- and 10h-agar-subcultures were performed on 127 archived blood culture isolates, including *Enterobacterales* ($n = 56$), *Pseudomonas aeruginosa* ($n = 10$), *Stenotrophomonas maltophilia* ($n = 10$), *Acinetobacter* spp. ($n = 5$), staphylococci ($n = 20$), enterococci ($n = 17$), and streptococci ($n = 16$). AST methods included Vitek2-GN391/GP580 cards (bioMérieux), Oxoid disc-diffusion(DD) (ThermoFisher), E-test (bioMérieux), oxacillin/vancomycin/high-level aminoglycoside screens (ThermoFisher), βCARBA/βLACTA (Bio-Rad), and Clearview™ PBP2a-SA-culture-colony-test (Abbott). Percent of 4h- and 10h-subcultures with sufficient growth for AST was documented. Accuracy was assessed using CLSI M-52 for essential-agreement (≥90%), categorical-agreement (≥90%), very-major-errors (VME) (≤3%), major-errors (ME) (≤3%), and minor-errors (minE) (≤10%). Reproducibility and turnaround time were documented.

RESULTS: All subcultures had sufficient 4h and 10h growth for AST, except group A/C/G streptococci and viridans group streptococci 4h subcultures. Reproducibility was 100%, and performance met CLSI VME/ME/minE thresholds with the exception of minE (15%, 4%–37%) for Vitek2-GN391 piperacillin-tazobactam/nitrofurantoin against SPICE organisms using 4h- and 10h subcultures and ceftazidime against *Pseudomonas aeruginosa* using 4h subcultures. On average, SIBC-AST allowed AST to be available 13.6 hours earlier than conventional-AST, with results available 4.1 hours after simulated blood culture positivity for PBP2a, 4.5 hours for β-LACTA/β-CARBA, 13.8 hours for Vitek2, 24.4 hours for DD, and 28.0 hours for oxacillin/vancomycin/high-level aminoglycoside screens and E-test.

CONCLUSION: SIBC-AST is accurate, reproducible, and significantly reduces turnaround time, enabling targeted therapy on average 13.6 hours earlier, with earliest results for some methods as soon as 4.1 hours after blood culture positivity. SIBC-AST using conventional methods

offers a practical alternative to novel rapid AST solutions and should serve as the reference standard for comparison.

P051

Rapid identification of filamentous fungi using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS)

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OBJECTIVE: Rapid and accurate identification of filamentous fungi remains challenging in a clinical microbiology laboratory. Our study evaluated the performance of MALDI-TOF MS for identification of filamentous fungi isolated from clinical specimens.

METHOD: We conducted a retrospective study that included 73 clinical isolates of filamentous fungi commonly encountered in clinical specimens. The isolate was cultured on IMA and SAB-CG plates in parallel. The growth on days 3 and 7 was subject to MALDI-TOF-MS analysis using the mycelium transfer (MyT) extraction technique. Briefly, the MyT technique involves picking up the growth from the colony's edge in the presence of formic acid with a sterile toothpick, followed by spotting with matrix on the target plate for MALDI analysis against Bruker's filamentous fungi library. We calculated the accuracy of MALDI identification by MyT technique to both species and genus levels compared with the reference ID from the Public Health Ontario Laboratory. We also analyzed the impact of different culture media and incubation periods on the accuracy of MALDI identification.

RESULTS: Overall, the accuracy is 94.5% to the genus level and 92% to the species level. Of 40 *Aspergillus* isolates from 11 species, accuracy is 100% to genus and species level. We observed similar accuracy among *Mucorales*. IMA media are superior to SAB-CG with accuracy to genus and species level at 90% and 87%, respectively, while it is 81% and 78% for SAB-CG. We observed superior performance with growth at 3 days of incubation with accuracy of 94.5% at genus level and 92% at species level in comparison with 27.5% and 24.5% at 7 days of incubation.

CONCLUSION: MALDI analysis with the MyT technique provides accurate identification of commonly encountered filamentous fungi in a clinical microbiology laboratory. It also exhibits the advantage of early identification of young culture while morphological features are still developing for conventional identification.

P052

Performance of the BioGX and a lab-developed polymerase chain reaction tests to detect the presence of Shiga toxin subtypes 1 and 2 on the BD MAX platform

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OBJECTIVE: Shiga toxin–producing *Escherichia coli* (STEC) is a common foodborne illness that can lead to hemolytic uremic syndrome. Strains producing Shiga toxin 2 (Stx_2) carry increased risk, and identifying Stx2 strains lends importance to triaging public health investigations and therapy. However, most Health Canada–approved nucleic acid tests do not differentiate between *stx* strains, and currently approved tests rely on follow-up culture and/or insensitive enzyme immunoassays. We evaluated two stx_1/stx_2-differentiating polymerase chain reactions (PCRs) on the BDMax: BioGX (designed for the BDMax) and a lab-developed PCR test (LDT).

METHOD: BDMax ExK DNA-2 kits were used for extraction and the BDMax open protocol for analysis. BioGx and LDT were compared using spiked samples with Stx1- and Stx2-producing ATCC 35150 in serial dilutions of 10^3–10^1 CFU/mL in Tris-buffer and 10^6–10^3 CFU/mL in STEC-negative human feces. In parallel, BDMax Enteric Bacterial Panel (EBP) was run on feces as well as the LDT using eMag extraction and ABI 7500 PCR. BioGX was then selected for retrospective evaluation.

RESULTS: BioGX and LDT successfully amplified stx_1 and stx_2 targets. The limit of detection (LOD) for BioGX was 10^2 CFU/mL and the LDT was 10^3 CFU/mL. In feces, the LOD increased by 2 Logs for both assays. The BioGX LOD in feces was equivalent to that of the EBP Panel at 10^4 CFU/mL and LDT using the eMag/ABI. The LDT did not amplify on the BDMax extract and required the addition of 5 uL of BDMax elution buffer as diluent.

CONCLUSION: The BioGX assay offers a feasible option to differentiate *stx* strains with existing equipment and similar LOD as the BDMax screening assay. Evaluation with more

clinical samples is required to assess the performance of the BioGx assay. Further studies on optimizing the LDT for the BDMax are required.

P053

Verification of ceftazidime-avibactam and aztreonam synergy testing by broth disk elution (BDE) using *E. coli* AR0137 as a QC replacement

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OBJECTIVE: Therapeutic challenges remain with metallo-β-lactamase (MBL)-producing organisms, especially in settings with increased NDM prevalence. Susceptibility testing of aztreonam and ceftazidime-avibactam (ATM-CZA) combination is valuable for management and surveillance of infections caused by such organisms. Until recently, testing methods lacked standardization. In 2024, CLSI M100 Ed-34 introduced a validated broth disk elution (BDE) method to assess ATM-CZA *in vitro* activity, enhancing testing capabilities for numerous microbiology laboratories. This study aimed to verify the accuracy of ATM-CZA broth disk elution (BDE) in context of limited validation panel supply.

METHOD: *Enterobacterales* isolates from frozen stock of CDC Antimicrobial Resistance Bank with known reference ATM-CZA MICs were tested. QC included three ATCC strains and *E. coli* AR0137 (ATM-avibactam MIC of 16 μg/mL), replacing *E. coli* AR438 because of its unavailability. Identification and carbapenemase genes were confirmed using MALDI-TOF MS and CARBA-5 lateral flow assay/in-house PCR, respectively. For the BDE method, 5-mL cation-adjusted Mueller-Hinton broth (CAMHB) tubes were impregnated either with 30-μg ATM (Oxoid), 30/20-μg CZA (BD BBL Sensi-Disc), both disks ("ATM-CZA"), or no disk (growth control). Incubation and reading of turbidity followed the CLSI M100 Ed34 method. Results from BDE were compared with reference broth microdilution (BMD) ATM-CZA MICs available via CDC/Harris et al., 2023 for categorical agreement (CA).

RESULTS: Thirty-five isolates were included, predominantly composed of *Klebsiella pneumoniae* (10/35; 28.6%) and *Escherichia coli* (8/35; 22.9%). Among them, 54.3% carried MBLs. All isolates were susceptible to ATM-CZA by BMD. All QC organisms yielded the expected growth pattern. CA with retrospective BMD MICs was 97.1% (35/36) with 2.8% (1/36) major-error rate. The only discordant isolate was NDM-1-producing *Providencia rettgeri*, growing across ATM, CZA, and ATM-CZA tubes.

CONCLUSION: This study demonstrates acceptable performance of ATM-CZA BDE method, with *E. coli* AR0137 serving as a QC replacement for *E. coli* AR0348; however, resistance should be confirmed by an alternate method.

P054

Hepatitis C RNA reflex testing to improve turnaround time to diagnosis

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OBJECTIVE: Hepatitis C virus (HCV) can lead to severe complications if untreated, making a laboratory-confirmed diagnosis essential. Traditional HCV testing requires a two-step process where positive serology is further investigated with a plasma sample for HCV RNA, often resulting in delays and lost follow-up. In February 2023, HCV RNA reflex testing was implemented at our laboratory, allowing both HCV serology and molecular testing to be performed from a single serum sample. This quality improvement (QI) initiative aimed to enhance testing efficiency and patient engagement.

METHOD: Laboratory technologists identified first-time anti-HCV positive patients at the time of serology reporting and forwarded these serum samples to a reference laboratory for HCV RNA testing. Data were reviewed for 12 months before and after implementation (February 2022–February 2024). Turnaround times (TAT) from anti-HCV to HCV RNA results were compared using an unpaired *t*-test, while Fisher's exact test assessed follow-up care rates.

RESULTS: In the pre-QI period, 7/7 first-time anti-HCV–positive patients had follow-up HCV RNA ordered, with a mean TAT of 43.4 days; 5 (71%) tested positive for HCV RNA, and 3 (60%) received additional follow-up care. In the post-QI period, 24 serum samples were first-time anti-HCV positive with a mean TAT to HCV RNA result of 3 days ($p = .09$); 4 (17%) serum samples were rejected for HCV RNA in error, 13 (54%) tested positive for HCV RNA, and 11 (85%) received follow-up care ($p = .53$) on average 26 days later. An additional 18 serum samples were reflexed in error (not first-time anti-HCV positive).

CONCLUSION: The QI initiative demonstrated reduced TAT and improved follow-up care, although these changes were not statistically significant. Challenges, such as sample rejection and errors in reflexing non-eligible samples, indicate the need for ongoing refinement and monitoring to enhance HCV testing efficiency and patient outcomes.

P055

Evaluating laboratory reporting in superficial wound swabs with multiple Gram-negative bacilli identified

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OBJECTIVE: Gram-negative bacilli (GNB) isolated from superficial wound swabs may represent potential pathogens or commensals. The microbiology laboratory reports multiple GNB (MGNB) if two GNB are identified in any quantity with less than moderate polymorphonuclear cells (PMNs) seen in Gram smear or if three or more GNB are identified in any quantity with any amount of PMNs. A comment is added to contact the microbiology laboratory if further identification is clinically indicated. Our objective was to evaluate the significance of MGNB in aerobic wound swabs and to determine how additional GNB identification impacted patient management.

METHOD: All swab cultures at a large regional microbiology laboratory between May 1, 2023 and April 30, 2024 were included. Laboratory data and patient characteristics were collected. All requests for MGNB identification from a single hospital site were evaluated.

RESULTS: A total of 16,150 swabs were included and 2,636 (16.5%) reported MGNB. A total of 1,099 (41.6%) swabs from a single hospital site were further evaluated. Complete GNB identification was requested from 68 (6.2%) specimens. Pathogens reported included *Pseudomonas aeruginosa* ($N = 47$; 58.7%), *Staphylococcus aureus* ($N = 26$; 32.5%), and *Streptococcus pyogenes* ($N = 7$; 8.8%). There were 73 (53.6%) lower limb specimens, and most patients were admitted under Medicine ($N = 14$; 20.5%), with a mean age of 62.9 years. Comorbidities included diabetes ($N = 26$; 38.2%), vascular insufficiency ($N = 19$; 27.9%), malignancies ($N = 10$;14.7%), and immunosuppression ($N = 5$; 7.3%). The most common GNB identified were *P. aeruginosa* ($N = 49$; 36.5%), *Klebsiella* spp. ($N = 49$; 36.5%), *Escherichia coli* ($N = 42$; 31.3%), *Proteus* spp. ($N = 39$; 29.1%), *Enterobacter* spp. ($N = 35$; 26.1%), *Morganella* spp. ($N = 22$; 16.4%) and *Citrobacter* spp. ($N = 16$; 11.9%). Antibiotics were changed in 52 (76.4%) patients following MGNB identification. A carbapenem was prescribed in 23 (44.2%) patients.

CONCLUSION: Identification and reporting of MGNB from low-quality samples often leads to additional antibiotic prescriptions and escalation to carbapenem use. This study has identified an opportunity to introduce stewardship initiatives with respect to reporting of GNB that can otherwise be reported as commensal microbiota.

P056

Evaluation of the MALDI Biotyper® MBT subtyping module for detection of *Klebsiella pneumoniae* carbapenemase (KPC) in *Enterobacterales* in a clinical microbiology laboratory

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OBJECTIVE: Early detection of KPC-positive *Enterobacterales* is desirable to expedite initiation of appropriate antimicrobials and infection prevention and control (IPAC) measures. The Bruker MALDI Biotyper® MBT subtyping module can detect a specific peak at ~11,109 m/z in a subset of organisms carrying KPC-2 or KPC-3 carbapenemases. This allows simultaneous organism identification and KPC detection using routine MALDI-TOF MS workflows. The objective of this study was to evaluate the utility of MBT KPC subtyping at our site.

METHOD: A panel of *Enterobacterales* isolates were chosen from frozen clinical and Antimicrobial Resistance Isolate Bank (AR bank) libraries. Frozen isolates were subbed twice on blood agar plates, spotted to MALDI-TOF MS target plates using routine procedures, and run on two separate laboratory MALDI-TOF MS instruments. MBT subtyping was carried out automatically by the Bruker instruments simultaneously with identification. Detection of KPC was compared between MBT KPC subtyping and an in-house real-time PCR for carbapenemase-producing organisms (CPO PCR).

RESULTS: Of 93 total isolates, 58 (62.4%) were positive for KPC by CPO PCR (43 clinical and 19 AR bank isolates) and 35 were negative. Nine isolates (seven clinical and two AR bank) tested positive by MBT KPC subtyping. All nine were also positive by CPO PCR. MBT subtyping results were fully concordant between the two MALDI-TOF MS instruments. The overall sensitivity was 15.5% and the specificity was 100%. KPC subtype data was only available for AR bank isolates. Of those, 2/5 (40%) of KPC-2 and 0/14 of KPC-3 were positive by MBT subtyping.

CONCLUSION: The excellent specificity of this test suggests that it can triage KPC-positive isolates without additional steps, as results are generated automatically during routine MALDI-TOF MS identification. Clinically, this may allow an earlier switch to more appropriate antimicrobials and implementation of IPAC precautions. However, negative results cannot rule out KPC.

P057

Invasive Group A Streptococcus (iGAS) in Newfoundland and Labrador (NL): Recent epidemiology and risk factors

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OBJECTIVE: A provincial epidemic of iGAS was suspected. Both bacterial and host factors are implicated in the severity of infection. This project aims to describe the local epidemiology of iGAS in Newfoundland and Labrador over the past 10 years and assess whether any microbe or host risk factors could account for this increase in cases.

METHOD: A retrospective chart review included every invasive isolate in NL between January 1, 2014 and December 31, 2024. Reference genotyping from the National Microbiology Laboratory and clinical risk factors were collected, with HREB permission. Multivariate logistic regression was performed.

RESULTS: Two-hundred and thirty-six isolates of iGAS affecting 208 patients were included. Thirteen isolates could not be traced to a particular patient and were excluded from the study. Overall yearly incidence was 3.94 cases/100,000/year. Mean age was 49.51 years, and 44.2% were females. There was a significant epidemic between December 2023 and May 2024, with an incidence rate of 12.10 cases/100,000/year. When comparing cases before ($n = 141$) and after December 2023 ($n = 66$), there was a higher proportion of critical care admissions ($n = 20$, 15.3% versus $n = 23$, 35.9%, $p = .001$) and higher proportional mortality ($n = 10$, 7.6% versus $n = 10$, 15.4%, $p = .088$). There were no demographic differences between the pre- and post-outbreak groups. During the epidemic, 54.6% ($n = 36$) cases were caused by *emm1,* compared with 26.8% ($n = 38$) cases during the non-epidemic period ($p < .0001$). Age (OR = 1.11, $p < .001$), cardiac conditions (OR = 15.96, $p < .001$), and immunocompromising conditions (OR = 3.96, $p = .014$) were significant predictors of mortality. The *emm1* type (OR = 2.81, $p = .004$) was a significant predictor of critical care admission.

CONCLUSION: An iGAS epidemic was defined, with a high proportion of *emm1* genotype accounting for this outbreak. More work remains to determine whether a particular demographic is at higher risk of contracting an *emm1* variant.

P058

Evaluation of the Xpert® Xpress Strep A for detection of *Streptococcus pyogenes* from paediatric pleural fluids

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OBJECTIVE: Invasive Group A streptococcal infection (iGAS; *Streptococcus pyogenes*) incidence has increased in multiple countries since 2022, following the COVID-19 pandemic. Severe iGAS, including GAS pneumonia, requires prompt treatment and chemoprophylaxis for close contacts. Sterile site culture (eg, pleural fluid) is the diagnostic gold standard but is insensitive and may be compromised by pre-collection antibiotics. Xpert® Xpress Strep A (Cepheid) is a real-time (RT)-PCR targeting *spe*B gene that rapidly detects *S. pyogenes* from throat swabs. We evaluated its performance for *S. pyogenes* detection from paediatric pleural fluids.

METHOD: A convenience sample of 30 specimens – 29 clinical pleural fluids ($n = 7$ prospective; $n = 22$ frozen, retrospective from January 2023 to March 2024), and 1 ATCC 19615™ *S. pyogenes* spiked in pleural fluid – were tested with Xpert® Xpress Strep A on GeneXpert® instrument. Results were compared to composite reference: culture plus externally validated laboratory-developed (LD) RT-PCR targeting *spy* gene, with discrepancies resolved by alternative LDRT-PCR targeting *spe*B. True condition was accepted as when at least two-thirds of comparators matched. Limit of detection (LOD) was determined by spiked dilution series and probit analysis. Analytical reactivity and specificity were evaluated with $n = 6$ known *emm* types and $n = 8$ potential cross-reacting organisms, respectively.

RESULTS: Fifteen of 30 samples (50%) were positive by Xpert® and composite reference, while 7 of these were also culture positive (7/30; 23%). Xpert® demonstrated 100% positive percent agreement, negative percent agreement, and overall categorical agreement ($\kappa = 1$) with composite reference and individual LDRT-PCRs. There was 73% categorical agreement between Xpert® and culture alone ($\kappa = 0.47$). Analytical reactivity and specificity were 100%. LOD 1.5×10^1 (95% CI -8.2×10^2 to 8.5×10^2).

CONCLUSION: Xpert® performed well on pleural fluid, with 100% categorical agreement with composite reference, and was more sensitive than culture. Rapid turnaround time supports diagnostic utility. Future work should evaluate clinical and public health management impact and utility for other sterile body fluids.

P059

Evaluation of Seegene Novaplex™ dermatophyte assay to routine culture methods for diagnosis of onychomycosis

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OBJECTIVE: Diagnosis of dermatophyte infection by culture is slow, and direct detection methods such as potassium hydroxide (KOH) smear lack sensitivity. Molecular testing could improve accuracy and turnaround time, facilitating faster diagnosis and treatment. This study aims to evaluate the performance of the Novalplex™ dermatophyte assay (Seegene) compared with culture for diagnosis of onychomycosis.

METHOD: Residual nail material from 112 specimens that underwent routine fungal culture and KOH smear were stored at –80°C. Culture yielded 22 *Trichophyton mentagrophytes* complex (TMC), 34 *Trichophyton rubrum* complex (TRC), 1 *Epidermophyton floccosum*, and *3 C. albicans* while the remainder were negative (14) or positive for off-panel fungi (38). After undergoing a pretreatment, specimens underwent extraction on the Seegene STARlet system, then were run on the CFX-96 RTPCR system (Bio Rad), with results analyzed using Seegene software. When PCR results were discrepant from culture, specimens were classified as true positive if they were culture positive or PCR positive with either positive KOH smear or history of previous isolation in the patient. Accuracy, positive percent agreement (PPA), and negative percent agreement (NPA) were calculated for PCR and culture compared to consensus results.

RESULTS: PCR accuracy was 80.36% compared with culture, before resolution of discrepancies. Discordant results included 8 culture-positive/PCR-negative samples, 12 culture-negative/PCR-positive samples, and 2 TMC culture-positive that were dual PCR-positive for TMC and TRC. After resolution of discrepancies, overall PPA, NPA, and accuracy for PCR were, respectively, 87.88%, 86.96%, and 87.50% and for culture were 88.24%, 100.00%, and 92.86%. For PCR targets, PPA, NPA, and accuracy for TRC were, respectively, 90.24%, 97.18%, and 96.64% and for TMC were 91.30%, 97.75%, and 96.43%.

CONCLUSION: Despite the use of archived specimens, molecular testing performed comparably with dermatophyte culture. Discrepancies may be attributed to heterogeneity of fungal elements within nails, with more visibly infected portions set up initially for culture.

P060

Evaluation of the QIAstat-Dx® Gastrointestinal Panel 2 for the detection of viral, parasitic, and bacterial pathogens in Fecalswab specimens

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OBJECTIVE: This study evaluates the performance of the QIAstat-Dx® Gastrointestinal Panel 2 (GIP2) (Qiagen) for the detection of gastrointestinal pathogens from Fecalswab® specimens (Copan).

METHOD: For most targets, specimens were tested initially on the Allplex™ GI assays (Seegene). For *P. shigelloides*, specimens were initially tested on BIOFIRE® GI Panel (BF-GIP) (Biomerieux). After initial testing, specimens were stored at –80°C. Two hundred specimens were tested on the GIP2. Discordants with Allplex™ were tested on BF-GIP or Xpert® Norovirus (Cepheid), while discordants for *P. shigelloides* were tested by culture. Consensus results were obtained based on agreement of at least two of three tests. Accuracy as well as percent positive and negative agreement (PPA, PNA) were calculated overall and on a per-target basis.

RESULTS: Compared to original testing results, the accuracy was 99.72% (95% CI 99.16%–99.61%), while PPA and PNA were 90.34% (95% CI 85.85%–93.77%) and 99.89% (95% CI 99.74%–99.96%), respectively. After resolution of discrepancies, the accuracy was 99.69% (95% CI 99.49%–99.82%), PPA was 93.99% (95% CI 90.12%–96.68%) and PNA was 99.98% (95% CI 99.88%–100.00%). For bacterial targets, PPA was 100.00% (95% CI 96.92%–100.00%) and PNA was 99.96% (95% CI 99.79%–100.00%). For parasitic targets, PPA was 97.30% (95% CI 85.84%–99.93%) and PNA was 100.00% (95% CI 99.52%–100.00%). However, viral targets had a PPA and PNA of 83.33% (95% CI 73.19%–90.82%) and 100.0% (99.67%–100.00%), respectively.

CONCLUSION: Overall, the QIAstat-Dx® GIP2 performed well in detection of bacterial and parasitic targets, but suboptimal performance for viral targets was observed from FecalSwab specimens.

P061

Association of sleep, exercise, and other lifestyle factors with respiratory infection in a prospective cohort study of university students

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OBJECTIVE: Lifestyle factors such as adequate sleep and exercise have been associated with protection from respiratory infections in various study populations. In a previous study, we found that sleep and exercise were associated with fewer rhinovirus infections in university students. The current study was designed to carefully measure various lifestyle factors (sleep, exercise, and stress) and to examine their association with symptoms of respiratory infection in a cohort study of university students.

METHOD: We invited full-time university students to fill out weekly online questionnaires and optionally to self-collect oral-nasal swabs for viral infection from September to December 2024. All participants provided informed consent. They were at least 17 years of age and self-identified as generally healthy with no known immunocompromised condition or treatment for chronic illnesses. Students reported respiratory symptoms, sleep, and other lifestyle factors (exercise, stress). Swabs were performed weekly with an additional swab completed 48–72 hours upon self-reported sickness.

RESULTS: A total of 150 subjects provided baseline and at least one follow-up questionnaire and completed over 1,200 questionnaires. In the optional testing arm, 114 subjects provided over 700 self-collected weekly oral-nasal swabs. Forty (26.7%) identified as men, 108 (72.0%) as women, and 2 (1.4%) as non-binary. Median age was 19 years (Q1, Q3: 18, 21). During follow-up, 102 (68.0%) of participants recorded respiratory illness, including 38 (37.3%), 25 (24.5%), and 39 (38.2%) with one, two, or more than two episodes, respectively. Mean (SD) sleep duration of 7.0 (0.9) hours, exercise intensity index of

10.6 (2.6), and total stress score of 8.3 (1.5) were found but not associated with illness overall. Respiratory infection lab data analysis is currently ongoing.

CONCLUSION: In contrast with our previous study, we found no overall association between lifestyle factors (sleep, exercise, and stress) and infection. A detailed temporal analysis with lab-confirmed infection will be conducted to provide more insight.

P062

Validation of *Plasmodium* detection assays with heat-inactivated clinical whole-blood specimens for hemorrhagic fever suspects from malaria-endemic areas

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OBJECTIVE: In cases of suspected viral hemorrhagic fever, malaria needs to be ruled out urgently, as it is a more common cause of fever in a returning traveller, and dual infections can occur. Typically this involves preparation of thin smears with methanol fixation and heat inactivation. Newer testing algorithms for malaria incorporate rapid antigen detection tests (RDTs) and loop-mediated isothermal amplification (LAMP). Ebola virus can be inactivated in whole blood using heat treatment. However, it is unknown how heat inactivation of whole blood prior to use with RDTs and LAMP impacts the sensitivity of these tests. We aimed to evaluate the use of heat inactivation on common malaria diagnostics to develop a protocol for safer handling of samples from patients with suspected viral hemorrhagic fever.

METHOD: Thirty EDTA whole-blood specimens stored at −80°C previously positive by LAMP and 24 samples previously positive by BinaxNOW RDT were included. Thin smears confirmed a mix of *P. falciparum* ($N = 19$ LAMP and BinaxNOW, parasitemia 0%–0.94%), *P. vivax* ($N = 2$ LAMP, $N = 1$ BinaxNOW), *P. ovale* ($N = 6$ LAMP, $N = 3$ BinaxNOW) and *P. malariae* ($N = 3$ LAMP, $N = 1$ BinaxNOW). One-milliliter aliquots were heated in a heating block set to 60°C for 60 minutes, centrifuged (10,000 rpm for 10 min), and then tested using BinaxNOW (Abbott) or LAMP (Alethia, Meridian Bioscience) following manufacturer protocols.

RESULTS: For LAMP the positive agreement between heat-inactivated and untreated specimens was 100% (95% CI 88–100). Only 63% (95% CI 41–81) of BinaxNOW samples remained positive for at least one antigen, and only 33% (95% CI 16–55) had all of the same antigens detected after heat inactivation. When the individual antigens are considered, HRP-2 had higher agreement (79% [95% CI 54–94]) compared to aldolase (7% [95% CI 0–34]).

CONCLUSION: If heat inactivation is used for suspected hemorrhagic fever, the accuracy of *Plasmodium*-LAMP remains unchanged while that of BinaxNOW decreases significantly.

P063

Comparative performance of Xpert® Xpress Strep A and ID NOW™ Strep A assays using ESwab™ media for Group A *Streptococcus* detection

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OBJECTIVE: Group A *Streptococcus* (GAS) is the leading bacterial cause of pharyngitis and can result in severe complications if untreated. Rapid and accurate diagnostics are crucial for distinguishing GAS infections from viral causes and guiding appropriate management. This study evaluated the diagnostic performance of two commercially available, Health Canada–approved molecular assays – Xpert® Xpress Strep A and ID NOW™ Strep A – using Copan Liquid Amies Elution Swab (ESwab™) media, a widely available transport media that can be used for either culture or molecular detection of bacterial pathogens.

METHOD: Throat swab samples from paediatric patients (≤19 years old) were submitted from the emergency department of a children's hospital as part of routine clinical care. Swabs were vortexed prior to pipetting 200 µl of ESwab™ media for testing on both molecular platforms. A composite reference standard was applied; a true-positive result

was defined as either culture positivity or detection by two independent molecular assays.

RESULTS: A total of 106 swabs collected between February 2 and 21, 2024 were included in the evaluation. Each swab was processed for bacterial culture and testing on both molecular assays. The Xpert® Xpress Strep A assay achieved a sensitivity of 100%, specificity of 98.7%, PPV of 97.4%, NPV of 100%, and diagnostic accuracy of 99.1%. The ID NOW™ Strep A assay demonstrated a sensitivity of 100%, specificity of 97.3%, PPV of 94.3%, NPV of 100%, and diagnostic accuracy of 98.1%. Both assays exhibited high concordance with throat culture, with invalid result rates being minimal (<1%) for both.

CONCLUSION: ESwab™ media demonstrated excellent performance in detecting GAS on both molecular platforms, even though it is not the manufacturer-recommended sample type for the ID NOW™ Strep A assay. Utilizing ESwab™ media enables reflex culture, susceptibility testing, and/or additional molecular analysis, thereby streamlining the diagnostic process and improving patient care.

P064 – WITHDRAWN

P065 Clinical assay validation and bioinformatic pipeline considerations of amplicon-based respiratory syncytial virus whole-genome sequencing

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OBJECTIVE: Respiratory syncytial virus (RSV) whole-genome sequencing (WGS) is a useful method for genomic surveillance and informing hospital infection control. Implementing RSV WGS for routine clinical diagnostics requires thorough laboratory and bioinformatic validation. We evaluated upstream WGS laboratory protocols and bioinformatic pipelines for implementing accurate RSV sequencing in clinical settings.

METHOD: A combination of 34 RSV-A and RSV-B samples were collected in universal transport media or a guanidine-based molecular media. RNA was extracted using the bioMerieux NucliSENS and Promega Viral High-Throughput kits. Amplicon-based WGS was performed with a modified Nanopore Midnight protocol. Samples were analyzed using three different reference-based pipelines: RSV-GenoScan, IRMA, and artic-rsv. Pipelines were selected based on Nanopore compatibility, open-source availability, and useability. Nextclade was used for RSV subtype and clade classification. Bioinformatic pipelines were compared following Clinical & Laboratory Standard Institute (CLSI) MM09 guidelines, which outline criteria for continuous documentation monitoring, ease of installation, integration with other programs, and access to a test set.

RESULTS: Cycle threshold (Ct) ranged from 19.89 to 31.51 across collection media types and RNA extraction methods. All pipelines yielded concordant RSV subtype and clade classification results with 100% agreement. Median sequencing depth ranged from 270 to 6,246, and genome coverage ranged from 90.96% to 100%. The pipelines met most CLSI MM09 guidelines for sequencing. However, there were limitations in ease of installation, regularly updated documentation, and software versioning.

CONCLUSION: RSV sequences were successfully generated using different extraction methods, a range of Cts, and various bioinformatic pipelines. Guidelines such as CLSI MM09 provide a useful resource when selecting analysis methods. Other factors such as useability, run time, and computational performance should also be considered. The clinical implementation of RSV WGS is a vital tool for effective RSV surveillance, particularly in the era of newly developed RSV vaccines.

P066 Prediction of antibiotics resistance of *Staphylococcus aureus* from genomic data through machine learning

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OBJECTIVE: *Staphylococcus aureus* is a leading bacterial pathogen, contributing to over 1 million deaths and 34 million years of life lost globally. Its ability to acquire resistance to multiple antimicrobials has resulted in the emergence of multidrug-resistant *S. aureus* (MDR-SA), a pathogen with diverse antimicrobial resistance (AMR) profiles. This diversity poses significant challenges for clinical management and public health. Understanding the relationship between *S. aureus* genomic profiles and their resistance phenotypes is crucial for antimicrobial stewardship and targeted interventions.

METHOD: To address this issue, we utilized the Calgary Bloodstream Infection (BSI) cohort, which spans from 2006 to 2022 and includes data on 38,614 BSI pathogens collected from the Calgary region (ResistanceDB.org). This cohort provides comprehensive data, including whole-genome sequencing, phenotypic resistance profiles, and extensive electronic medical records, enabling the study of multiple infections in a large clinical population. We applied machine learning (ML) and network visualization techniques to analyze the resistance profiles of 8,484 *S. aureus* isolates. Specifically, we used association mining to identify MDR patterns, defined as combinations of two or more antimicrobial resistance traits, and predicted the genomic associations between these traits.

RESULTS: Our ML-based genetic analysis accurately predicted methicillin resistance with 97% accuracy and achieved over 90% accuracy in classifying resistance phenotypes for other antibiotic classes. This approach validated established associations between genomic composition and phenotypic MDR traits in *S. aureus*. Excitingly, we identified potentially novel genes and genetic regions linked to AMR.

CONCLUSION: The application of ML enabled the efficient prediction of correlation between *S. aureus* resistance traits and genomic composition. The discovery of novel genes offers additional targets for antimicrobial drug development and broadens the spectrum of known resistance determinants. Lastly, the highly generalizable ML model serves as a robust tool for tracking and monitoring clinically relevant MDR markers across diverse bacterial populations.

P067

DISCO-LAMP: A novel multiplexed diagnostic platform for malaria

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OBJECTIVE: Malaria, caused by *Plasmodium* species, continues to be a significant global health issue, and infectious disease diagnostics are equally critical in Alberta and worldwide. Existing tools like microscopy and PCR have limitations, including high costs, labor intensity, and suboptimal sensitivity and specificity. DISCO (diverse infections screening via colors in one-pot)-LAMP addresses these gaps by integrating multiplex loop-mediated isothermal amplification (Mx-LAMP) with automated opto-electrical sensing and machine learning (ML) for rapid, accurate, and cost-effective pathogen detection.

METHOD: DISCO-LAMP targets *Plasmodium genus* (PAN), *P. falciparum (Pf)*, *P. vivax (Pv)*, and an internal actin control (IAC). The diagnostic platform amplifies target DNA within 30 minutes at 62°C using species-specific primers and probes in a one-tube reaction. A miniaturized device integrates optical fibers, LEDs, and unique dual-mode sensors consisting of a mini-spectrophotometer and a camera to detect fluorescent signals emitted by pathogen-specific probes. Regression and classification ML models enhance the analysis by quantifying DNA concentrations and enable real-time performance by supporting both qualitative and quantitative monitoring. Validation with 355 clinical samples involves benchmarking performance against a commercial Loopamp™ Malaria detection kit (Human Diagnostics).

RESULTS: Preliminary tests on 100 samples achieved 98.5% sensitivity and 100% specificity within 20 minutes of time-to-positivity, detecting DNA concentrations as low as 1–10 copies/µL for PAN, Pf, and Pv.

CONCLUSION: DISCO-LAMP bridges a critical gap in diagnostics by offering a portable, fully automated solution tailored for resource-limited settings and near-patient testing, which can also be extended to detect other diverse pathogens. The platform automation streamlines workflows, enabling rapid and consistent screening in diverse settings. Moreover, the device can be deployed in airports to screen travelers returning from regions with endemic diseases, supporting public health initiatives globally. It ensures timely detection and treatment for vulnerable groups, including pregnant women and children, promoting equitable access to health care.

P068

Loop-mediated isothermal amplification (LAMP) assay for the detection of antimicrobial resistance in *E. coli* bloodstream infections

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OBJECTIVE: *E. coli* bloodstream infection (BSI) mortality rates are exacerbated by the global rise in antimicrobial resistance (AMR). Conventional antimicrobial susceptibility testing requires days to determine bacterial antibiotic resistance profiles from the time of a positive blood culture. Inappropriate antibiotic treatment due to resistance to common first-line treatments results in increased patient mortality. This research aims to develop a rapid molecular test to detect key resistance genes against third-generation cephalosporins and carbapenems in *E. coli* BSIs using an affordable in-house diagnostic platform, the White Pearl.

METHOD: A loop-mediated isothermal amplification (LAMP) assay was designed to target the most prevalent extended-spectrum beta lactamases (ESBLs), AmpC, and carbapenemase genes in *E. coli* BSIs, including CTX-M-1-group, CTX-M-9-group, CMY-2 group, OXA-48-likes, KPCs, and NDMs. It also detects *E. coli* ST131, a highly virulent strain linked to increased mortality in BSIs from urinary sources, often co-occurring with fluoroquinolone resistance.

The assay was optimized using a statistical method known as a definitive screening design and validated on 35 clinical *E. coli* isolates, with at least 10 positives per target. Whole-genome sequencing (WGS) served as the gold standard for comparison.

Further testing on contrived samples is ongoing, utilizing blood culture bottles incubated for 8 hours and spiked with bacteria at $\sim 10^8$ CFU/mL. DNA extraction is performed through a 100-fold dilution followed by a 10-minute incubation at 95°C.

RESULTS: The *E. coli* panel demonstrated 100% sensitivity and 97.1% specificity on clinical isolates. Preliminary tests on contrived samples suggest similar performance. The LAMP assay takes 45 minutes from sample extraction to result.

CONCLUSION: The LAMP assay effectively detects major resistance genes in *E. coli* BSIs and correlates well with WGS data. Its low production cost and portability on the White Pearl platform make it suitable for rapid diagnostic use in resource-limited settings, supporting antimicrobial stewardship.

P069

Anaplasma phagocytophilum DNA detection in anonymized human samples previously tested for Lyme antibodies in a Canadian province

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OBJECTIVE: Anaplasmosis is caused by the bacteria *Anaplasma phagocytophilum*. It is a vector-borne disease transmitted by the tick *Ixodes scapularis*. Between 2012 and 2022, only two human cases of anaplasmosis were reported in our province, despite a growth of 7 to 57 annual cases of Lyme disease from 2012 to 2022 and a neighbouring Canadian jurisdiction reporting 199 cases between 2017 and 2022. Recent active tick surveillance provincially indicated an *Anaplasma phagocytophilum* prevalence of 4.1%, suggesting possible clinical underdiagnosis. Therefore, residual anonymized sera submitted for Lyme antibody screening from August 2022 to July 2023 were tested for *Anaplasma*.

METHOD: Frozen anonymized residual serum samples submitted for Lyme antibody screening collected between August 2022 and July 2023 were thawed and tested by real-time PCR for *Anaplasma phagocytophilum* DNA. Limited demographic information was recorded for each sample: age, forward sortation area, and health region. Results of

Lyme antibody testing were unavailable. Positivity rates both overall and by demographic indicator were calculated, where possible.

RESULTS: *Anaplasma* DNA was detected in 7 out of 1,444 samples tested (0.48%) during a 12-month period (0.8 cases/100,000 samples). Six out of seven positive samples (85.7%) originated from a southern health region known for higher Lyme detection rates. There were no positive samples in patients younger than 40 years of age.

CONCLUSION: *Anaplasma phagocytophylum* is present in human samples submitted for Lyme antibody testing in our population. It is possible that some of the patients tested for Lyme disease might have also been tested for *Anaplasma* NAAT and serology. Anaplasmosis is likely underdiagnosed, as the symptoms are non-specific and the disease is not widely recognized. Education on emerging and established tickborne illnesses is needed to enhance diagnostic suspicion and demand for testing.

P070

A review of the clinical utility of PJP PCR from nasopharyngeal swabs at a Canadian tertiary care centre

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OBJECTIVE: *Pneumocystis jirovecii* is an opportunistic pathogen with increasing disease incidence in non-HIV immunocompromised hosts. Microbiologic confirmation of *P. jirovecii* pneumonia (PJP) remains a challenge in patients in whom invasive testing (eg, bronchoscopy or sputum induction) may not be feasible due to safety concerns (eg, patient is too frail or hypoxic) or testing unavailability. In these situations, nasopharyngeal (NP) swabs represent an attractive alternative due to their minimally invasive nature, although the clinical performance of this specimen type remains unclear. We assessed the local utilization of this specimen type for PJP real-time PCR.

METHOD: Forty NP swabs tested using the RealStar® PJP PCR kit between December 2022 to November 2024 were retrospectively reviewed for clinical performance. Demographic characteristics, risk factors for PJP, clinical presentation, suitability for bronchoscopy, receipt of PJP prophylaxis, and initiation of empiric PJP treatment were included in the analysis.

RESULTS: There were 11 positive, 3 indeterminate (Ct value 34-40), and 26 negative PJP PCR results among our tested NP swabs. All patients with positive PJP PCR results had an EORTC/MSG described host risk factor for PJP, hypoxemia, bilateral ground-glass opacities on chest imaging, and had not been receiving PJP prophylaxis. The majority (8/11; 73%) had also been initiated empirically on PJP treatment at the time of test request. Overall, the positive percent agreement of PJP PCR with clinical diagnosis was 75% (9/12) and the negative percent agreement was 92% (23/25). Most patients (29/40; 73%) did not have additional specimens sent for PJP testing.

CONCLUSION: PJP PCR may be considered under specific circumstances for microbiologic confirmation from NP swabs in patients with compatible risk factors for PJP and in whom PJP is highly suspected but invasive testing cannot be performed. Prospective paired studies are required to further evaluate the performance of PJP PCR from NP swabs versus BAL specimens.

P071

A temperature–time anti-*Treponema pallidum* (syphilis) stability study using a spike and recovery method

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OBJECTIVE: Our laboratory identified a gap in test kit package insert shipping temperature/time instructions for EDTA specimens collected for syphilis testing. Testing for *Treponema pallidum* (syphilis) antibodies is performed using the Newmarket Biomedical PK7400 TP HA REAGENT on the PK7400 Automated Microplate System (Beckman Coulter Brea, CA).

The PK7400 TP HA REAGENT package insert states EDTA specimens can be stored at 2–8°C up to 7 days. EDTA specimens are stored at 18–24°C and transported at

2–25°C (ambient temperature) from CBS collection sites to the testing laboratories.

A sample stability study was conducted to determine whether syphilis antibodies in EDTA specimens would degrade and result in a false-negative result if specimens were exposed to 18–25°C storage/transport conditions until testing.

METHOD: A spike and recovery method was used to create 10 reactive syphilis specimens by spiking EDTA whole-blood specimens with confirmed syphilis-reactive serum. Clinical laboratory specimens provided clinically diagnosed, de-identified, non-donor serum samples with a rapid plasma regain (RPR) value of 1:32. Once spiked, each EDTA whole-blood specimen was split into two. One specimen was immediately tested (Time 0) and the second was stored at 18–25°C for a minimum of 72 hours prior to testing (Time 1).

RESULTS: All specimens tested at Time 0 were reactive for syphilis antibodies and remained reactive following testing (Time 1) after 72 hours 1 minute to 74 hours 43 minutes at ambient temperature storage.

CONCLUSION: In this spike-recovery model, our evidence supports that syphilis antibodies in EDTA specimens will continue to be detected by the PK7400 TP HA assay after storage/transport at ambient temperature ranges for 72–74 hours. It is unlikely that syphilis-reactive EDTA whole-blood specimens transported to our laboratories at ambient temperature for 72–74 hours would be false negative in the PK7400 TP HA assay.

P072

Comparative evaluation of chromogenic media for detection of uropathogens using the BD Kiestra total laboratory automation system

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OBJECTIVE: Microbiology laboratories receive high volumes of urine specimens for culture. Many cultures yield mixed growth, adding additional workload with limited clinical value. Laboratory workflows of urine culture processing can be improved with the adoption of chromogenic media and artificial intelligence analysis. The objective of this study is to evaluate the microbiological performance of various chromogenic media compared to current laboratory procedures.

METHOD: Urine samples received in the laboratory were inoculated to Blood and MacConkey agar using the BD Kiestra InoqulA (10 ul) or manually (1 ul). Cultures were incubated, imaged in BD ReadA compacts at 15 hours, and reported as per protocol. A selection of urine samples was inoculated in parallel to the following chromogenic media: BD BBL CHROMagar Orientation (BD), Micronostyx Colorex agar (MSX), Oxoid Brilliance UTI (OX). Inoculated plates were incubated and imaged at 18 hours. Chromogenic media cultures were compared to conventional testing results.

RESULTS: A total of 665 urine specimens were included. Midstream urine ($N = 473$; 71.1%), in-and-out catheters ($N = 73$; 11.0%), and indwelling catheters ($N = 72$; 10.8%) were the most common urine sources. Clinical samples were reported with a uropathogen ($N = 174$; 26.1%), as no significant growth ($N = 217$; 32.6%), no growth ($N = 187$; 28.1%), or mixed ($N = 87$; 13.1%). Overall, these results were similar among all three chromogenic media. Discordant results between those reported from clinical specimens and each chromogenic media (OX $N = 67$; MSX $N = 63$; BD $N = 60$) were identified. Major discordant results (ie, missing a uropathogen) were uncommon among all media (OX $N = 4$; MSX $N = 10$; BD $N = 6$). The most common minor errors include reporting no significant growth in previously reported no-growth cultures ($N = 51$), reporting no growth in previously reported no-significant-growth cultures ($N = 48$), and reporting a uropathogen in a previously reported mixed culture ($N = 40$). All chromogenic media performed similarly in identifying uropathogens.

CONCLUSION: All chromogenic media evaluated performed similarly and can be used to replace current urine culture testing.

P073

Evaluation of an automated nucleic acid extraction platform for quantitative polymerase chain reaction–based malaria parasite detection and species differentiation from whole blood

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OBJECTIVE: Nucleic acid extraction is a critical component of malaria molecular testing performance. Manual silica spin column-based workflows perform well and are widely adopted but are labour intensive and time consuming. Furthermore, whole blood is a complex sample type that requires extensive washing to remove PCR inhibitors (eg, heme). This study aimed to evaluate the performance of an automated magnetic nanoparticle-based extraction system, the EMAG (bioMérieux), against a manual workflow for detection and differentiation of *Plasmodium* species by laboratory-developed test (LDT) quantitative polymerase chain reaction (qPCR).

METHOD: *Plasmodium*-positive and -negative whole-blood samples spanning a range of parasite burdens and *P. falciparum* control material from the World Health Organization were included in the study. All samples were extracted with the QIAamp Blood Mini Kit (Qiagen; manual workflow) and bioMérieux EMAG NucliSENS platforms (EMAG; study workflow). Extraction performance was evaluated by comparing qualitative detection of *Plasmodium* spp. and LDT qPCR cycle threshold (Ct) and LoD values across both extraction methods. Hands-on technologist time was documented for each workflow.

RESULTS: A total of 58 samples were selected, including *P. falciparum* ($n = 24$), *P. malariae* ($n = 2$), *P. ovale* ($n = 4$), *P. vivax* ($n = 8$), and *P. falciparum/P. vivax* mixed infection ($n = 1$), with Ct values ranging from 19 to 33. All 39 positive samples, including the 1 mixed sample, were detected with the two workflows. The mean Ct difference between Qiagen and EMAG-extracted clinical samples was −0.14 (SD = 1.21). Both extraction methods demonstrated LoD ≤ 7 copies/reaction for *P. falciparum*. The average hands-on time per sample was 1 hour for Qiagen compared with 15 minutes for EMAG.

CONCLUSION: These findings support the performance of the EMAG automated extraction platform compared with a routine manual workflow in a public health reference laboratory setting. Implementation of an automated workflow presents the potential to reduce hands-on laboratory technologist time and increase capacity for malaria testing.

P074
Multi-site validation of the automated AIX1000 RPR platform for improved reproducibility and scalability

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OBJECTIVE: Syphilis rates are rising across Canada, with a particularly alarming increase in Saskatchewan's northern regions. Syphilis, caused by the spirochete *Treponema pallidum*, requires early detection and treatment to prevent progression to more severe stages of disease. To address the need for scalable and consistent syphilis testing, the AIX1000, an automated RPR (rapid plasma reagin) platform, was implemented and validated in Saskatoon and Regina. This platform can accommodate higher testing volumes with shorter turnaround times and mitigate the inherent subjectivity of manual RPR interpretation.

METHOD: A total of 177 samples were tested via manual RPR and the AIX1000 platform. Of these, 90 samples were tested at two separate sites for an in-depth comparison. Agreement between sites was assessed for both manual and automated platforms.

RESULTS: When comparing the performance of manual RPR to the AIX1000, all results agreed within two dilutions. Ninety-four percent agreed within one dilution, and 58% agreed exactly. For samples that were tested via manual RPR and AIX1000 at two sites, agreement within two dilutions via manual RPR was observed for all, 95% within one dilution, and 50% agreeing exactly. In contrast, the AIX1000 demonstrated higher reproducibility between the two sites, as agreement within one dilution was observed for all samples and exact agreement was observed for 77% of samples.

CONCLUSION: In addition to having a faster turnaround time and higher throughput capabilities, the AIX1000 platform exhibited superior reproducibility compared with traditional manual RPR testing, highlighting its potential as a more reliable and scalable solution for syphilis testing in high-burden regions.

P075 – WITHDRAWN

P076 Strategies for culture-independent sequencing of *Helicobacter pylori* and *in silico* prediction of antibiotic resistance

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OBJECTIVE: Colonization of the stomach by *Helicobacter pylori* (*Hp*) is a risk factor for peptic ulcers and gastric cancer. *Hp* treatment is complicated by the emergence of antibiotic-resistant strains. When empiric eradication therapy is unsuccessful, current recommendations include endoscopic biopsy and phenotypic antibiotic susceptibility testing of *Hp* cultures. Here we describe the development of culture-independent, stool-based sequencing methods for faster and less invasive prediction of antibiotic resistance in *Hp*.

METHOD: DNA extracts were prepared from clinical stool samples positive for the *Hp* fecal antigen test as well as contrived stool samples spiked with *Hp*. Four different sequencing methods were evaluated, including traditional "shotgun" metagenomic sequencing and three targeted methods: (1) tiled amplicon sequencing, (2) CRISPR/Cas9-directed sequencing, and (3) bait capture enrichment sequencing.

RESULTS: Analysis of shotgun sequencing data indicates that the abundance of *Hp* DNA in clinical stool samples is too low for reliable *in silico* prediction of antibiotic resistance using a traditional metagenomics approach. Targeted sequencing methods have the potential to detect mutations in genes associated with antibiotic resistance. The tiled primer scheme supports PCR amplification of eight gene targets associated with resistance to metronidazole, amoxicillin, levofloxacin, and rifabutin. We have also designed guide RNAs that efficiently direct Cas9 cleavage of sequences adjacent to genes linked to clarithromycin and tetracycline resistance. Pan-genome alignments from a globally representative set of *Hp* assemblies have been prepared and are being used to design hybridization probes (baits) for enriched sequencing of additional resistance gene targets.

CONCLUSION: Due to the low abundance of *Hp* DNA in stool, shotgun sequencing is not feasible for culture-independent detection of antibiotic resistance genes. In contrast, targeted sequencing methods are promising options to achieve improved sensitivity for identification of *Hp* antibiotic resistance determinants.

P077

Diagnostic performance of the Xpert® MTB/RIF Ultra assay for detecting *Mycobacterium tuberculosis* in Hamilton, Ontario

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OBJECTIVE: This study evaluated the diagnostic performance and clinical impact of the Xpert® MTB/RIF Ultra (Xpert Ultra) assay in identifying MTB in lower respiratory and cerebrospinal fluid samples at the Hamilton Regional Laboratory in Hamilton, ON.

METHOD: Xpert Ultra performance was verified using 29 clinical samples (20 sputum and 9 BAL) previously tested by smear and culture at Toronto Public Health Laboratory (TPHO), 14 control (MMQCI) and 3 CAP survey samples, and 11 simulated CSF specimens. Post-implementation, 44 respiratory specimens tested by Xpert Ultra assay were compared to standard TB smear and culture performed at the reference laboratory.

RESULTS: In the verification study, Xpert Ultra demonstrated 100% inter-assay reproducibility, and for detection of MTB and rifampin resistance (RIF), the assay demonstrated 100% concordance with expected results in the control samples. In the clinical samples, combining data from the verification and post-implementation study (n = 73), the assay demonstrated a sensitivity of 100% (95% CI 78.2%–100%) and a specificity of 94.8% (95% CI 85.6%–98.9%) for detection of MTB compared to culture results. Xpert Ultra identified MTB in four AFB-negative/MTB culture–positive specimens resulting in earlier initiation of treatment in three patients by 19–21 days. Three Xpert Ultra–positive specimens were AFB positive/MTB culture negative, the latter from patients with a history of TB. The TAT for the Xpert Ultra was 24 hours compared to 4.6 days and 17 days for the reference lab TB PCR (from smear) and positive culture, respectively.

CONCLUSION: The Xpert® MTB/RIF Ultra assay demonstrated excellent diagnostic accuracy for MTB detection and significantly reduced result turnaround time. Further studies to assess its impact on patient management and isolation protocols are ongoing.

P078

Low occupational risk of Mpox (clade 2b) transmission from routine handling of patient specimens in a provincial public health clinical microbiology laboratory

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OBJECTIVE: The Mpox virus is classified as a Risk Group 3 human pathogen. Following the May 2022 multi-country outbreak, many Canadian laboratories implemented enhanced safety measures for PCR testing of clinical specimens, including containment level (CL)-3 processing, enhanced CL-2 precautions, and viral inactivation prior to CL-2 testing. In March 2023, the Public Health Agency of Canada (PHAC) recommended specimen handling in CL-2 settings with routine universal precautions.

METHOD: After a local risk assessment (LRA), our provincial public health clinical microbiology laboratory adopted routine universal precautions (needleless) for handling query-Mpox specimens on July 27, 2022. A literature review, conducted for the LRA, revealed no reports of Mpox transmission to clinical microbiology laboratory staff. Review also demonstrated that asymptomatic Mpox infection is rare, occurring mainly in patients with high-risk behaviour. Locally, Mpox cases are routinely reported to Public Health, which conducts detailed contact tracing interviews.

RESULTS: Between July 27, 2022 and December 15, 2024, our laboratory processed 1,669 specimens for Mpox testing, with an 8.4% positivity rate (140 positive specimens from 43 patients). Positive specimens included blood, urine, nasopharyngeal/throat swabs, and lesion swabs from skin, genital, rectal, and lip/mouth areas. The median cycle threshold value was 22.6 cycles (range: 17.5–39.8). Based on Public Health contact tracing, no confirmed Mpox infections were attributed to occupational exposure during this period. All Mpox isolates tested were of clade 2b/IIb.

CONCLUSION: Specimen handling with routine universal precautions (that uses no sharps) over 17 months resulted in no recorded occupational Mpox transmission among laboratory staff. Despite limitations such as small sample size, lack of serology testing, absence of detailed staff interviews, and reporting bias from the original literature review, these findings support current recommendations and low occupational risk of Mpox (clade 2b) transmission in clinical diagnostic laboratories when using routine universal precautions in a CL-2 setting.

P079

MRSA Clonal dynamics before and during the COVID-19 pandemic: A genomic investigation

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OBJECTIVE: The COVID-19 pandemic created an unprecedented environment for infectious diseases, potentially reshaping the epidemiology of multidrug-resistant pathogens such as methicillin-resistant *Staphylococcus aureus* (MRSA). Public health measures altered antibiotic and disinfectant use, and disruptions to health care access may have driven shifts in MRSA transmission and clonal dynamics. Before the pandemic, Ontario saw a shift from predominantly hospital-associated (HA) MRSA clonal complex (CC)5 strains to community-associated (CA) CC8 strains, yet the province lacks comprehensive genomic surveillance to monitor such trends. Understanding

these shifts is crucial to addressing the evolving threat of MRSA, particularly during public health crises.

OBJECTIVE: To investigate the genomic epidemiology of MRSA before and during the pandemic, with a focus on potential changes in clonal dynamics and genetic features.

METHOD: Whole-genome sequencing was performed on 382 MRSA isolates collected from patients (predominantly outpatient and emergency room attendees) at Toronto's Mount Sinai Hospital between 2018 and 2022. Genomic data were integrated with clinical, epidemiological, and laboratory information for analysis.

RESULTS: CC8 (222/382; 58.1%) and CC5 (66/382; 17.3%) were the dominant clonal complexes, with the pre-pandemic rise in CC8 plateauing during the pandemic. Additionally, AMR genes differed compared to pre-pandemic. For example, *erm*-mediated erythromycin resistance decreased from 22.4% (pre-pandemic) to 7.3% (pandemic), despite a relatively stable 73% phenotypic erythromycin resistance. Furthermore, the prevalence of plasmid-associated *qac* genes doubled during the pandemic (4.7% to 9.5%, $p = .068$), reflecting a potential increase in biocide tolerance.

CONCLUSION: The pandemic may have impacted MRSA strain dynamics, with a notable plateau in CC8 dominance and shifts in genetic attributes, including resistance determinants. These findings highlight the complex interplay between public health measures and pathogen evolution. Expanding this preliminary study to a province-wide genomic surveillance effort will follow to unravel the long-term impacts of the pandemic and guide targeted interventions against MRSA.

P080

Community-associated Methicillin-resistant *Staphylococcus aureus* bloodstream infections among people who inject drugs admitted to hospitals in Canada (2010–2023): Data from the Canadian Nosocomial Infection Surveillance Program

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OBJECTIVE: People who inject drugs (PWID) are at risk of complications like methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infections (BSI). This study, using data from the Canadian Nosocomial Infection Surveillance Program (CNISP), compares characteristics of community-associated (CA) MRSA BSIs in PWID versus non-PWID.

METHOD: CA-MRSA BSIs (2010–2023) were identified in participating hospitals using standardized definitions. Those ≥12 years were included while those missing injection drug use and isolate typing/antimicrobial susceptibility data were excluded. Differences between groups were assessed using Wilcoxon rank sum test, χ^2, or Fisher's exact tests, with $\alpha \leq 0.05$.

RESULTS: All statistical comparisons were significant at $p < .001$ unless otherwise specified. Each year, between 18 and 44 hospitals reported CA-MRSA BSI cases ($n = 2{,}875$). The majority of cases were from the Western region (57%), with PWID accounting for 40% of cases overall ($n = 1{,}136$, range: 21%–49%) and varying by region: 42% Western, 34% Central, and 45% Eastern. Compared to non-PWID, PWID were younger (96% under 60 versus 48%) and more likely to be female (49% versus 32%). PWID had a higher proportion of endocarditis (26% versus 4.4%) but

better 30-day survival (90% versus 81%). However, cases among PWID with endocarditis and/or osteomyelitis were more likely to remain hospitalized at 30 days ($p < .05$). Vancomycin use was more frequent among PWID, pre (78% versus 58%) and post (87% versus 79%) positive blood culture. Overall, isolates had slightly higher resistance to select antimicrobials in non-PWID versus PWID. However, the most prevalent spa type, t008 (47% overall; 55% PWID versus 42% non-PWID), showed higher resistance in PWID versus non-PWID to clindamycin (25% versus 12%) and ciprofloxacin (93% versus 88%, $p < .05$).

CONCLUSION: CNISP data show a significant proportion of CA-MRSA BSI occur among PWID. This population is younger and experiences greater morbidity. Further research is needed to better understand risk factors and optimize management strategies for PWID.

P081

Evaluation of FT-IR for the differentiation of *Campylobacter jejuni* strains regarding their potential to induce Guillain-Barré syndrome

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OBJECTIVE: *Campylobacter jejuni*, the leading cause of bacterial gastroenteritis, can trigger post-infectious Guillain-Barré syndrome (GBS) due to molecular mimicry with gangliosides at the Ranvier nodes. The structurally analogous substance involved is a sialylated lipooligosaccharide (LOS) on the bacterial surface, for the synthesis of which the two alleles of the alpha-2,3 sialyltransferase (*cstII* or *cstIII*) serve as key enzymes. Strains that produce a sialylated LOS exhibit increased epithelial invasiveness and are more likely to be associated with bloody diarrhea. We evaluated the performance of FT-IRS spectroscopy for the discrimination of *C. jejuni* strains producing a sialylated LOS from those with a non-sialylated LOS.

METHOD: A total of 28 whole-genome–sequenced *Campylobacter jejuni* isolates were investigated, groups and carrying the cstII or cstIII genes, or lacking any alpha-2,3 sialyltransferase. Fourier-transform infrared (FT-IR) analysis was conducted using the IR Biotyper® system. Exploratory data analysis was performed using hierarchical cluster analysis (HCA), principal component analysis (PCA), and linear discriminant analysis (LDA).

RESULTS: Exploratory data analysis revealed that the *C. jejuni* isolates cluster significantly in relation to the presence or absence of one of the *cst* alleles (Figure P081-1). Furthermore, within the *cstIII*-positive cluster, a distinct subgrouping was observed that correlated entirely with the presence or absence of the two genes encoding a heterodimeric Tlp7, which functions as a formic acid chemotaxis receptor.

Figure P081-1: Dendrogram showing the IRBT clustering (on the left side) and its correlation with genomic data (on the right side, namely isolate name, group, *dtlp7*, *cst*, clonal complex, sequence type and source of isolation—from left to right).

CONCLUSION: FT-IR methodology has demonstrated the potential to distinguish between *C. jejuni* strains that produce a sialylated LOS, which can trigger GBS, and those with non-sialylated LOS. Consequently, this approach could serve as a rapid and user-friendly solution for routine workflows. Further studies involving a larger number of strains are essential to confirm and reinforce these promising preliminary findings.

P082

Implementation of multiplex bacterial pneumonia PCR in hospital and community settings: Saskatoon, Saskatchewan

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OBJECTIVE: Pneumonia is a pulmonary infection caused by a diverse array of bacterial, fungal, and viral pathogens. Identifying bacterial pathogens in suspected pneumonia cases traditionally relies on microbiological cultures, which yield results within 24–72 hours post-respiratory sampling. Saskatchewan has implemented a multiplexed PCR assay that concurrently detects and identifies seven pneumonia-associated respiratory bacteria. The SeeGene Allplex™ PneumoBacter Assay targets *Bordetella parapertussis* (BPP), *Bordetella pertussis* (BP), *Chlamydophila pneumoniae* (CP), *Haemophilus influenzae* (HI), *Legionella pneumophila* (LP), *Mycoplasma pneumoniae* (MP), and *Streptococcus pneumoniae* (SP). This submission aims to present the data collected from community and inpatient populations subjected to this diagnostic test.

METHOD: In March 2024, the Microbiology Laboratory at Royal University Hospital validated and implemented the SeeGene Allplex™ PneumoBacter Assay. This assay was authorized for use on all respiratory specimens, and the data presented were collected as part of routine prospective laboratory testing. The subsequent analysis was performed using R-Studio.

RESULTS: This abstract presents data from March to November 2024, during which 1,075 tests were ordered. Of the specimens collected, 544 (50.65%) were from female patients and 422 were from paediatric patients. Seventy-three percent of the specimens were from the upper respiratory tract. The assay demonstrated an average monthly positivity rate of 27.2%. A significant proportion (38.2%) of specimens tested positive for SP, HI, both SP and HI, or a co-infection with another target. Additionally, 4.6% of specimens were positive for BP, 0.2% for BPP, 0.4% for CP, 0.4% for LP, and 12.8% for MP.

CONCLUSION: The implementation of the PneumoBacter Assay significantly improved the turnaround time for diagnosing atypical pneumonia by eliminating the need for additional testing. However, it introduced complexity and utilization issues due to the detection of HI and SP. Based on these findings, RUH is modifying the testing and reporting algorithm to address these challenges.

P083

Validation of a real-time polymerase chain reaction (RT-PCR) assay for the detection of *Pneumocystis jirovecii* on the BD MAX Open System

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OBJECTIVE: *Pneumocystis jirovecii* pneumonia (PJP) is a serious opportunistic fungal disease that primarily affects immunocompromised patients, including those with HIV. Accurate diagnosis of PJP is challenging due to the low sensitivity of conventional staining methods and the non-cultivable nature of the organism. To address these diagnostic obstacles, we developed and validated an RT-PCR assay targeting the major surface glycoprotein (MSG) gene of *P. jirovecii* on the BD MAX Open System. We also conducted a prospective study to establish an appropriate cycle threshold (Ct) cutoff for bronchoalveolar lavage (BAL) specimens.

METHOD: The performance characteristics of the assay were investigated using contrived specimens prepared from negative patient BAL. DNA extraction and PCR were carried out on the BD MAX Open System, utilizing the BD Max ExK DNA-2 kit (Becton, Dickinson and Company) and an in-house PCR master mix. The master mix included Luna Universal Probe One-Step RT-qPCR Master Mix (New England Biolabs) with primers and probes detecting the MSG gene and RNase P as internal control. In the prospective study, PCR was performed for a period of 6 months (May to November 2024) on 190 patient BAL specimens that underwent Calcofluor white staining. Ct values

were correlated with clinical data to determine the cutoff threshold.

RESULTS: The analytical specificity of the assay was 97.5% with precision (CV) ranging from 1.4 to 2.6% over 4 days. The accuracy was 96.67% (95% CI 88.47%–99.59%) while the analytical sensitivity was 1,266 copies per mL. A Ct value greater than 40 indicated a negative result, while a Ct between 31 and 40 signified low-level and less than or equal to 30 demonstrated high-level detection of *P. jirovecii*.

CONCLUSION: This PCR assay shows acceptable performance characteristics for PJP screening from BAL specimens, with an average cost of CA$22.05 per sample, and offers an expedited diagnostic method for this potentially life-threatening infection.

P084

Whole-genome sequencing reveals the circulation of multiple human coronavirus OC43 genotypes in Ontario

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OBJECTIVE: To develop a whole-genome sequencing assay to investigate the genomic epidemiology of human coronavirus OC43 (HCoV-OC43) isolated in Ontario during the 2022/2023 and 2023/2024 respiratory disease seasons.

METHOD: PrimalScheme v1.4.1 designed multiplex primers to generate overlapping amplicons for sequencing of HCoV-OC43 genomes. 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, minimap2 to align reads, iVar to remove primer sequences, medaka consensus, medaka variants, and bcf-tools to construct a consensus genome.

RESULTS: Thirty 1100-bp amplicons were designed to amplify HCoV-OC43 genomes. Two-hundred and ninety-six unique HCoV-OC43-positive samples with Ct < 38 were attempted, and 248 (83.8%) samples met sequencing quality metrics. Sequence alignment against known HCoV-OC43 genotypes (A–K) revealed the presence of genotypes F, J, I/K, and other genomes that do not group with genotypes A–K. Samples from a long-term care outbreak of HCoV-OC43 grouped within a cluster.

CONCLUSION: We have designed a two-pool multiplex PCR to amplify HCoV-OC43 genomes for WGS on the ONT platform. HCoV-OC43 isolates collected from the 2022/2023 and 2023/2024 respiratory seasons revealed multiple HCoV-OC43 genotypes currently circulating in Ontario.

P085

Development of a dual diagnostic and prognostic electrochemical biosensor for predicting infection burden in malaria in pregnancy (MIP)

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OBJECTIVE: MiP often presents with a prognosis of increased risk of maternal death, miscarriage, stillbirth, and neonatal death. Current approved malaria diagnostics suffer from poor sensitivities, and RDTs can present with false positives attributed to the deletion of the RDT target HRP-2 protein by *Plasmodium* strains. Additionally, an increasing number of publications are highlighting the association of key metabolite biomarkers with severity of infection. Therefore, this work investigates a point-of-care electrochemical platform screening for both diagnostic and prognostic markers with high sensitivity and specificity.

METHOD: The bioelectric interface is capable of label-free detection of DNA hybridization events between probes and sequences specific to *P.falciparum, P.vivax,* and conserved sequences across the *Plasmodium* genus (PAN). Additionally, DNA aptamers in the prognostic component with high specificity assess upregulation of markers associated with severe disease. Discrete electrochemical data and patient data serve as inputs to a random forest model for the prediction of patient outcomes. Patient samples and data from a cohort of pregnant women in Ethiopia are employed to interrogate this novel electrochemical platform and accompanying machine learning prediction tool.

RESULTS: Preliminary experimentation highlights the ability of this aptameric biosensing approach to discriminate the presence of a key metabolite with a clinically

relevant sub-μM limit of detection and a linear working range of 1 to 10 μM in contrived samples, and metabolite identification observed in spiked whole-blood samples. Additional data will be provided for the detection of a series of additional metabolites within our custom electrochemical platform. Performance metrics of the machine learning model in patient risk stratification will also be reported.

CONCLUSION: By integrating biosensing and machine learning, this approach offers a novel point-of-care tool to address a pressing gap in MiP diagnostics and provide a robust, accessible platform to inform clinical decisions and improve maternal and neonatal outcomes.

P086
Wastewater-based surveillance of respiratory viruses and correlation with clinical data

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OBJECTIVE: The pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has highlighted the public health and epidemiological utility of monitoring pathogenic viruses in wastewater. Our goal was to develop and validate an efficient approach for the surveillance of multiple respiratory viruses in wastewater that are of concern to public health, addressing the unmet need for unbiased surveillance of respiratory viruses as a supplement to clinical testing data.

METHOD: Three times weekly, 24-hour composite samples of wastewater raw influent were collected from a large local wastewater treatment plant. Using a vacuum membrane–based method, the samples were extracted within 7 days of collection. A sensitive multiplex quantitative polymerase chain reaction (qPCR) assay was developed, optimized, and validated for targets of interest: SARS-CoV-2, influenza A, influenza B, and respiratory syncytial virus (RSV). Quantitative data was normalized using pepper mild mottle virus (PMMoV). Results were tracked and compared to weekly reports from the regional clinical laboratory that serves all four city hospitals.

RESULTS: SARS-CoV-2 was detected every week throughout the test period and correlated well with clinical results. Influenza A and RSV began in the non-detectable range, increasing during their corresponding seasonal increase. Influenza A and RSV quantitation in wastewater correlated well with local clinical testing.

CONCLUSION: We successfully developed and validated a sensitive and specific qPCR assay for the routine wastewater-based surveillance of the respiratory viruses SARS-CoV-2, influenza A, influenza B, and RSV. We obtained quantitative data that were compared with clinical results from the same regional population, showing a strong correlation, including the seasonal increase in respiratory viral infections. This method can be utilized to further expand the repertoire of viral targets of interest, especially those with a direct impact on public health.

P087 – WITHDRAWN

P088 – WITHDRAWN

P089
Comparative diagnostic evaluation of three polymerase chain reaction assays for the detection and differentiation of *Plasmodium* species: A retrospective study in two Canadian reference laboratories

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OBJECTIVE: Accurate and timely diagnosis of malaria is critical for favourable clinical outcomes. Multiplex quantitative polymerase chain reaction (qPCR) provides a robust diagnostic option, but data on assay comparability are limited. This study aimed to evaluate the test performance of two commercial qPCR assays against a composite reference in two Canadian reference laboratories (Laboratory A and B).

METHOD: A convenience set of clinical whole-blood samples positive for *Plasmodium* species was selected. Each sample was initially characterized by a composite reference of microscopy, malaria rapid diagnostic test, and laboratory-developed test (LDT) qPCR. Additional testing with two qPCR assays, the Novaplex Malaria Assay (SeeGene) and RealStar Malaria PCR Kit (Altona), was

performed at each laboratory. The evaluation included qualitative detection of *Plasmodium* spp., species differentiation, and semi-quantitative detection using cycle threshold (Ct) for parasitic burden.

RESULTS: Thirty-nine positive samples were selected, including 19 *Plasmodium falciparum* (Lab A|B; 9|10), 4 *P. malariae* (2|2), 8 *P. ovale* (4|4), and 8 *P. vivax* (4|4). Compared with LDT, the SeeGene assay showed an overall percent agreement (OPA) of 95.1% (95% confidence interval [CI] 83.5–99.4), and the Altona assay showed an OPA of 97.5% (95% Cl 86.8–99.9). There were two false-positive *P. knowlesi* co-detections by SeeGene in a *P. malariae* case, with Pk Ct 31.6 and 29.1. Conversely, Altona had one false-positive *P. vivax* co-detection in a *P. malariae* case, with Pv Ct 41.3. Overall, the mean Ct difference between the SeeGene and Altona assays was –2.2 (95% CI, –7.85 to 3.44), and the greatest difference was observed for *P. falciparum* with up to 7.5 Ct difference.

CONCLUSION: These findings support reasonable diagnostic performance of two commercial qPCR assays for malaria. However, false-positive co-detections and systemic Ct shift patterns require further investigation to better understand the potential impact prior to clinical implementation.

P090

Comparison of bioinformatic assemblers for phylogenetic analysis of viral metagenomic sequencing from nosocomial respiratory outbreaks

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OBJECTIVE: Metagenomic sequencing (mGS) is a useful tool for identifying pathogens in patient specimens. In the case of nosocomial outbreaks of respiratory viruses, there is the potential to identify the strain as well as determine relatedness to other outbreak samples. Here we compare the analytical performance of multiple bioinformatic assemblers using metagenomic sequencing (mGS) data from multiple nosocomial outbreaks of RNA respiratory viruses.

METHOD: Samples from five nosocomial respiratory virus outbreaks from multiple institutions collected between 2022 and 2023 were sequenced (Table P090-1). Residual extracted RNA was combined with random hexamers and used for cDNA synthesis. cDNA was sequenced on the Illumina Miniseq platform. Reads corresponding to human reference genome hg38 were mapped using Bowtie2, and the filtered alignments were subtracted using samtools view and converted to fastq using samtools fastx. Data from each sample were analyzed using four assemblers (MEGAHIT, rnaSPAdes, metaviralSPAdes, and coronaSPAdes), and the results compared outbreak samples.

RESULTS: mGS confirmed the same viral identification as by RT-PCR and were able to provide typing for coronavirus and parainfluenza virus. Differences were observed between assemblers in the size of the largest contig generated and the mean genome percentage when compared to a reference genome. Notably, coronaSPAdes only produced data on samples from two outbreaks of seasonal coronavirus (CoVs) and yielded higher genome fractions than the other

Table P090-1: Respiratory outbreaks

Outbreak	Virus identified by RT-PCR	Sequenced samples (n)	Virus identified by sequencing	Reference genome
A	Human metapneumovirus (HMPV)	3	HMPV	NC_039199.1 Human metapneumovirus isolate 00-1
B	Human coronavirus	3	Human coronavirus HKU1	NC_006577.2 Human coronavirus HKU1
C	Human coronavirus	3	Human coronavirus OC43	NC_006213.1 Human coronavirus OC43 strain ATCC VR-759
D	Human Rhino/enterovirus	4	Rhinovirus	OQ791521.1 Rhinovirus A31 isolate RV-A31/USA/4T3/2009
E	Human parainfluenza virus	7	Human parainfluenza virus 3	NC_001796.2 Human parainfluenza virus 3

pipelines, indicating it was better for analysis of CoVs. Additionally, only two of the assemblers generated useable data for the rhino/enterovirus outbreak and were able to identify the virus as rhinovirus type A31.

CONCLUSION: Assemblers showed differences including in the average genome fraction, which may affect characterization of the viral sequences for outbreak analysis. Viral metagenomic sequencing may be most effectively applied as a rule-out test for determining whether two patients are infected by different strains of a particular virus.

P091

Malaria Magnetic Bind & Boil (MMBB): A rapid and affordable near-patient nucleic acid extraction approach for the detection of malaria species using loop-mediated isothermal amplification

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OBJECTIVE: Malaria elimination efforts require diagnostic tools capable of detecting submicroscopic parasitemia at the point of care (POC). While rapid diagnostic tests (RDTs) are practical and affordable, their high limit of detection (LoD) and poor performance with non-*falciparum* species reduce their utility. Sensitive assays, such as a loop-mediated isothermal amplification (LAMP), show promise but are limited by current extraction methods, which are equipment intensive, costly, and time consuming. This study introduces an innovative extraction approach combining a novel in-house buffer with magnetic beads.

METHOD: Cultured *Plasmodium falciparum* samples were processed with Buffer EN and Beads A (Xpedite Diagnostics), followed by 3 minutes at room temperature. After

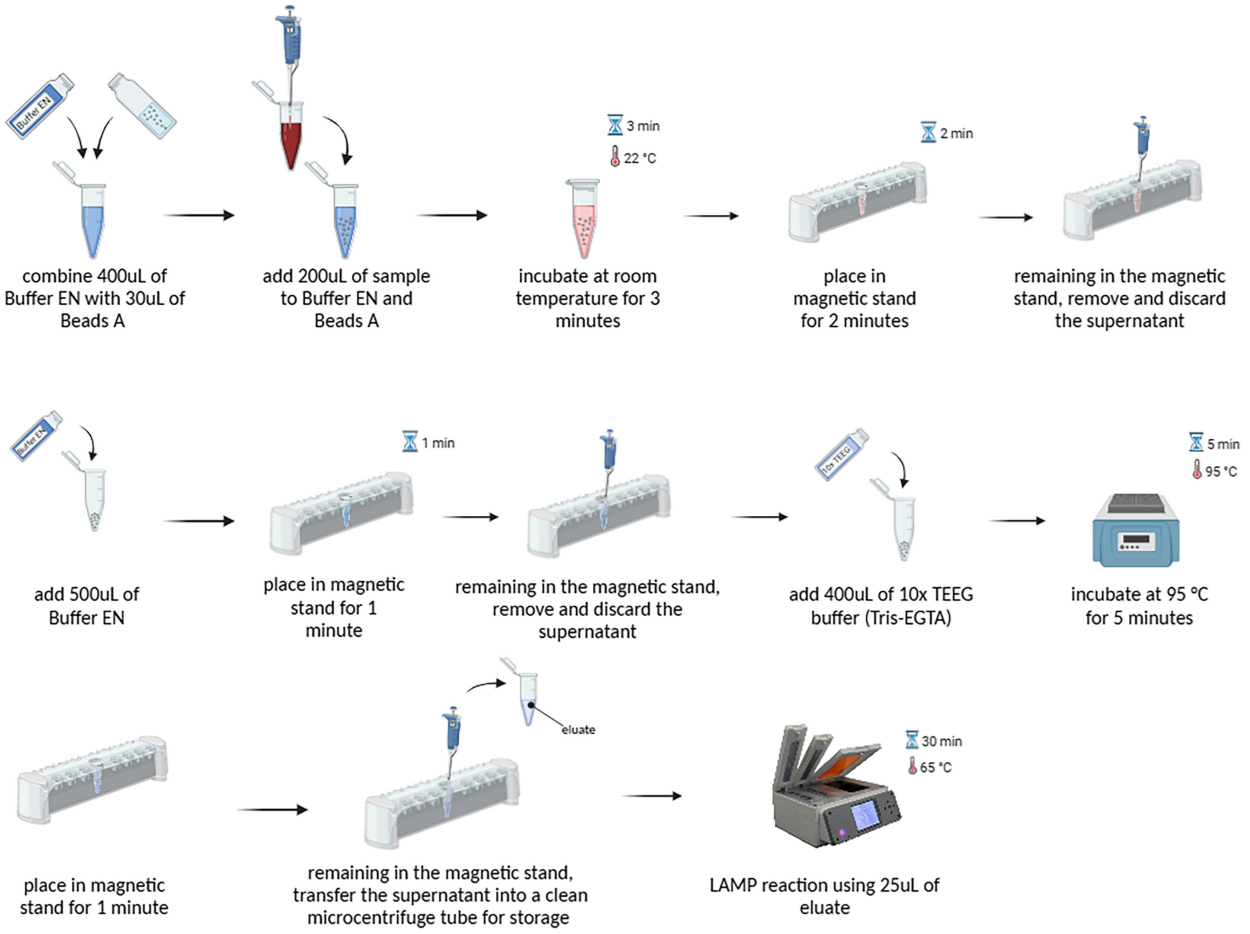

Figure P091-1: Malaria Magnetic Bind & Boil (MMBB) method.

placing samples on a magnetic rack for 2 minutes, the supernatant was removed. Another volume of Buffer EN was added and removed, then samples were placed on the magnetic stand for 1 minute to remove any remaining supernatant. Nucleic acids were extracted with 10× TEEG buffer (Tris-EGTA) at 95 °C for 5 minutes. Eluates were used directly in a 25-µL LAMP reaction to detect *Plasmodium* spp., *P. falciparum*, *P. vivax*, and human actin. Sample boiling and LAMP amplification occurred on an-inhouse device, called the White Pearl. Performance was compared to the Loopamp PURE DNA extraction kit (Human Diagnostics). Clinical validation results with patient isolates is presented at the conference (Figure P091-1).

RESULTS: The mean time to positivity for a 0.01% parasitemia sample was 13.9 (±1.9) minutes for the *P.f* assay with an LoD of 50 to 500 parasite/uL attained at a 40-minute cutoff. Ongoing optimization aims to improve LoD, sensitivity, and specificity. An in-depth study will be presented at the conference.

CONCLUSION: The MMBB method extracts nucleic acids from blood and proves compatible with LAMP in under 10 minutes at low cost ($1.00 CAD/extraction). Requiring minimal laboratory equipment, MMBB is well suited for near-patient diagnostics in resource-limited settings.

P092

Addressing stool complexity in automated DNA extraction: Retrospective evaluation of two commercial automated DNA Extraction platforms for gastrointestinal protozoa

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OBJECTIVE: High-quality nucleic acid extraction is critical to ensure the accuracy of molecular detection of gastrointestinal (GI) protozoa of medical importance. While commercial automated DNA extraction platforms have been widely adopted in clinical laboratories, the complex composition and inhibitory nature of stool and GI protozoa cysts' resilience present notable challenges for efficient automated nucleic acid extraction. This study aimed to compare the test performance of two automated DNA extraction platforms for molecular detection of gastrointestinal protozoa in human stool.

METHOD: A convenient set of unpreserved stool samples and stool preserved in COPAN FecalSwab containers was collected from hospital laboratories. Unpreserved stool samples were prepared into COPAN FecalSwab following a defined concentration. All samples were pre-treated with a 1-minute bead-beating step before extraction in parallel with the bioMérieux EMAG NucliSENS platforms (EMAG) and Promega Maxwell RSC (Promega). Extraction performance was evaluated by comparing the qPCR cycle threshold (Ct) values of the same sample from each platform, using a commercial qPCR, the RIDA®GENE Parasitic Stool Panel I, and a laboratory-developed test (LDT) qPCR for *Cyclospora* spp. only.

RESULTS: A total of 19 clinical COPAN FecalSwab stool samples and 2 unpreserved stool samples were included in the study (FecalSwab: *Entamoeba histolytica* [$n = 7$]; *Giardia lamblia* [$n = 6$]; *Cryptosporidium* spp. [$n = 6$]; unpreserved stool: *Cyclospora* spp. [$n = 2$]). The average Ct difference between EMAG and Promega-extracted samples tested by RidaGene was 0.9 (95% confidence interval [CI] −1.5 to 3.3). The Ct differences between EMAG and Promega-extracted samples tested by LDT qPCR for the two *Cyclospora* spp. samples were 2.5 and 2.2, respectively.

CONCLUSION: These findings demonstrate the similar performance of two commercial automated DNA extraction systems for detecting stool protozoa when combined with an upstream bead-beating step. These results support the potential use of these systems to enhance routine clinical laboratory workflows compared to manual DNA extraction workflows.

P093

Evaluation of bead-beating pre-treatment and two commercial quantitative polymerase chain reaction assays for detection of gastrointestinal protozoa

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OBJECTIVE: Gastrointestinal (GI) protozoa are among the leading causes of diarrhea worldwide. Quantitative polymerase chain reaction (qPCR) is a promising diagnostic tool for stool testing, but the rarity of infections in non-endemic settings has limited validation efforts. This study aimed to compare the utility of a bead-beating pre-treatment as well as the diagnostic performance of two commercial multiplex qPCR assays for the detection of *Giardia lamblia*, *Cryptosporidium* spp., and *Entamoeba histolytica*.

METHOD: A convenience set of fecal swab specimens was selected. Testing was performed by either FilmArray GI Panel (BioFire) or Allplex GI-Parasite Assay (SeeGene). Samples also underwent DNA extraction via the EMAG NucliSENS platform (bioMérieux), with and without bead-beating pre-treatment, to assess the effect of mechanical disruption. The extracted DNA was tested using the Allplex GI-Parasite Assay (SeeGene) and the Parasitic Stool Panel (RidaGene). Performance was evaluated by calculating the percent agreement between the SeeGene and RidaGene results and by comparing cycle threshold (Ct) values.

RESULTS: A total of 55 samples were included in the study (*Cryptosporidium* spp. [$n = 15$], *G. lamblia* [$n = 37$], *E. histolytica* [$n = 1$], mixed [$n = 2$]). For *Cryptosporidium* spp., the PPA between SeeGene and RidaGene was 100% (95% CI [confidence interval] 73.5%–100%), and the NPA was 97.7% (95% CI, 87.7%–99.9%). For *Giardia lamblia*, the PPA was 94.7% (95% CI 82.3%–99.4%), and the NPA was 100% (95% CI 80.5%–100%). Overall, bead-beating was associated with lower or similar Ct for most samples, except five samples (*Cryptosporidium* spp. [$n = 1$], *G. lamblia* [$n = 4$]), where a higher Ct (Ct difference >2) was observed.

CONCLUSION: The results from this study demonstrated the variable performance of two commonly used commercial qPCR assays for GI protozoa and underscored the need for target-specific data in multiplexed molecular evaluations. Bead-beating largely improved the detection of *Giardia lamblia* and *Cryptosporidium* spp. Confirmatory testing by conventional modalities or an additional qPCR may be required.

P094

Validation of the Copan Liquid Amies Elution (ESwab®) for collection, transport, and testing of vaginal specimens for *Trichomonas vaginalis* on the OSOM Trichomonas Rapid Test

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OBJECTIVE: To validate the ESwab as the medium for the collection, transport, and testing on the OSOM Trichomonas Rapid Test.

METHOD: We evaluated 115 specimens from female patients with per vaginal discharge that submitted both an e-swab and a dry swab for bacterial vaginosis/yeast and trichomonas evaluations, respectively. We compared dry swab against the ESwab. We tested the ESwab immediately upon arrival and weeks later.

RESULTS: We found a 99.2% concordance between the ESwab and dry swab methods. In addition, the ESwab maintained trichomonas antigen stability for several months when maintained at refrigeration temperature.

CONCLUSION: The ESwab is appropriate for the collection, transport, and testing of per vaginal discharge specimens requesting evaluation of *T. vaginalis*.

P095

Comparative performance of VITEK 2 Advanced Expert System (AES) versus BD Phoenixä CPO Detect Test for detection of carbapanemase-producing organisms (CPOs)

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OBJECTIVE: Recent iterations of commercial antimicrobial susceptibility testing (cAST) systems incorporate advanced technologies for screening resistant phenotypes, including carbapenemase-producing organisms (CPOs). VITEK 2 uses an Advanced Expert System (AES) to validate AST results, cross-reference them with a database of susceptibility patterns, and infer resistance mechanisms. BD Phoenix employs a detection well with meropenem, doripenem, and cloxacillin. This study aimed to evaluate the performance of VITEK 2 AES during its implementation against BD Phoenix CPO Detect Test (CPO-DT) as a potential replacement for CPO screening workflow.

METHOD: Seventy-two frozen *Enterobacterales* isolates from CDC Antimicrobial Resistance (AR) Bank with known carbapenemase genes and clinical/surveillance samples (from 2022–2023) were included. Carbapenemase genes were confirmed by CARBA5 lateral flow assay/in-house PCR. Isolates were subsequently tested according to CLSI M100-Ed34 breakpoints on VITEK 2 AES (v.9.02) using GN391 card, and BD Phoenix M50 using the NMIC-450/NMIC-451 panels. CPO detection results from both cAST systems were compared with molecular results.

RESULTS: Of the 72 isolates, 58 (80.6%) harboured confirmed carbapenemases: 32.8% KPC, 24.1% NDM, 29.3% OXA-48; 6.9% other; and 6.9% combined. Using molecular testing as reference standard, VITEK 2 AES had lower sensitivity than BD Phoenix CPO-DT (79.3%, 95% CI 66.2–89.2] versus 86.2% [95% CI 74.6–93.2]). More CPOs were undetected by VITEK 2 (16.7% [12/72]) than BD Phoenix (11.1% [8/72]). Among the undetected VITEK 2 CPOs (5 KPC, 7 OXA-48), 75% (9/12) had Meropenem MIC $\leq$ 0.25 µg/mL. Adding a VITEK 2 bioART rule to flag ertapenem MIC $\geq$ 0.25 mg/mL or meropenem 0.5 mg/mL increase VITEK 2 sensitivity to 91% (53/58). Lastly, specificity was >90% for both cAST.

CONCLUSION: Compared to BD Phoenix, VITEK 2 AES has acceptable specificity but may potentially miss detection of CPO with low-level resistance to ertapenem or meropenem. Adding a VITEK 2 bioART rule to flag potential CPO isolates improves detection by AES.

P096

A changing HIV demographic: A retrospective cohort study describing negative outcomes in a growing HIV population

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OBJECTIVE:

1. Understand the changing HIV demographic in Canada, especially in the prairie provinces.

2. Understand the negative health outcomes faced by this population.

3. Appreciate the syndemic nature of injection drug use, HIV, houselessness, and the effect this interaction has on negative health outcomes.

METHOD: This was a retrospective cohort study of all people 18 years and older newly diagnosed with HIV in Manitoba, Canada, between January 1, 2018 and December 31, 2023. Negative outcomes were defined as not connected to care, unsuppressed viral load, not on antiretrovirals, hospitalization after HIV diagnosis, development of AIDS, and death. Population variables were determined using frequencies for categorical variables and medians for continuous variables with interquartile range. A multivariate analysis using Poisson log regression was conducted to compare variables to negative outcomes. A community-based research approach was applied.

RESULTS: This population was composed of 44.8% females, 60.9% identified as heterosexual, with 56.2% reporting injection drug use, 35.1% reporting houselessness, and 40.3% reporting a mental health condition. Amongst females, 81.8% reported at least one of either houselessness, mental health condition, or injection drug use. Preliminary data suggest a significant association between houselessness, methamphetamine use, and female sex with lack of connection to care and unsuppressed viral load. The mortality rate is approaching 10% in a population with a median age of 35. Further data analysis continues.

CONCLUSION: Manitoba's HIV population is unique, made up of nearly 50% females, high levels of injection drug use, and houselessness. Preliminary data suggest the HIV services in place are not meeting the needs of this unique population, which has low engagement care and a high mortality rate. Further data analysis continues.

P097

Lung inflammation and fibrosis for targeted intervention to modulate early lung dysfunction in HIV-infected: LIFETIME Study

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OBJECTIVE: To investigate the role of genetic polymorphisms, inflammation, tissue damage, and fibrosis in pulmonary functional deterioration in HIV+ patients with community-acquired pneumonia (CAP) and to test *in vitro* interventions targeting key pathways using advanced kinomics.

METHOD: This prospective observational study involved three cohorts: HIV+/CAP+, HIV+/CAP, and HIV-/CAP+ in Medellín, Colombia. Participants undergwent pulmonary function testing, blood sampling, and induced sputum collection at baseline and during a 2-year follow up. Biomarkers of inflammation and fibrosis were measured using multiplex assays. Genetic variants linked to lung dysfunction were identified via whole-exome sequencing, and kinome arrays test therapeutic compounds *in vitro* using epithelial cell models.

RESULTS: In a prior cohort (2016–2018), 64 participants were included: HIV and CAP ($n = 27$), CAP ($n = 7$), and HIV ($n = 30$). Alterations in lung microbiota composition were observed, with dominant phyla including *Firmicutes, Proteobacteria,* and *Fusobacteria* and genera such as *Streptococcus, Haemophilus,* and *Veillonella*. Co-infection with HIV and CAP was associated with reduced microbial diversity, elevated inflammatory mediators (eg, IL-6, IL-8, MCP-1), and significant pulmonary dysfunction (eg, reduced FEF25, FEF25-75, FEV1), particularly in those with CD4 < 200 cells/μL. Building on these findings, a new cohort has been established: HIV+/CAP− ($n = 33$), HIV−/CAP+ ($n = 2$), HIV+/CAP+ ($n = 1$), and controls ($n = 33$). A biobank of bronchoalveolar lavage fluid, induced sputum, plasma, and other samples complemented these analyses. Preliminary findings showed distinct inflammatory profiles, small airways involvement, and elevated fibrosis markers in HIV+ patients.

CONCLUSION: This study elucidated mechanisms of HIV-associated pulmonary dysfunction, linking inflammation, genetic polymorphisms, and fibrosis. Insights from kinomics testing and longitudinal data informed therapeutic strategies and laid the groundwork for clinical trials.

P098
Antimicrobial use and infection control among patients with influenza

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OBJECTIVE: Annual influenza infections lead to increased hospitalizations, health care costs, and productivity losses due to illness-related absenteeism. Canadian guidelines recommend starting antiviral treatment, including oseltamivir, as soon as possible for adults hospitalized with influenza regardless of illness duration prior to hospitalization. Also, delayed diagnosis and implementation of precautions can contribute to nosocomial transmission and outbreaks. In this study, we aimed to review the local practice of antiviral use and precautions among adult inpatients with influenza to guide future interventions.

METHOD: A retrospective review was conducted based on positive influenza test reports for hospitalized patients and patients who visited urban Nova Scotian emergency departments during the 2023–2024 influenza season. Using a randomized sample, we measured the number of patients who received antiviral medications appropriately and the appropriateness of Infection Prevention and Control (IPAC) precautions.

RESULTS: We reviewed 126 patients randomized from 567 total influenza cases. IPAC measures were implemented and clearly documented in only 27.8% of patients at the time the swab was done. Only 6 of the 126 patients received oseltamivir empirically before the positive influenza swab result. Overall, 50% of patients received oseltamivir, and 81% of those who needed oxygen were prescribed oseltamivir. The mean time to starting oseltamivir from the time of testing was 34 hours, and the time to start after the time of result return was 10.5 hours.

CONCLUSION: Our study demonstrated an insufficient documentation for the time of IPAC measure implementation. There was a suboptimal use of oseltamivir

during influenza season with substantial delays in initiating therapy.

P099

Integrating AI into infection control: Evaluating the accuracy and consistency of four leading platforms across three regions

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OBJECTIVE: The study aimed to assess the accuracy and consistency of AI responses on specific infection control measures, comparing them to CDC guidelines. It also assessed how AI platforms perform in dealing with complex infection control scenarios.

METHOD: A comparative analysis of four AI platforms (ChatGPT, Meta AI, OpenEvidence, Copilot) was conducted by presenting them with structured questions and clinical case scenarios on varicella and measles. AI responses were evaluated for accuracy based on alignment with CDC guidelines, while platform accessibility was tested from Canada, Malaysia, and the UK. Regional variations in AI responses were analyzed to assess the consistency of outputs across geographic locations.

RESULTS: All four AI platforms provided generally accurate information on infection control measures for varicella and measles, but discrepancies were noted. ChatGPT and Meta AI largely aligned with CDC recommendations while OpenEvidence and Copilot omitted key features like the epidemiological criteria for confirming varicella cases. Meta AI also lacked a complete explanation of the laboratory criterion for varicella. Regional differences emerged in post-exposure prophylaxis (PEP) and treatment recommendations for measles, with Copilot and OpenEvidence showing significant variations. Meta AI was unavailable in Malaysia. Additionally, response consistency varied, with ChatGPT showing inconsistencies in case definitions and treatment guidance and Copilot displaying regional variations in PEP recommendations.

CONCLUSION: AI platforms demonstrate potential in supporting infection control but exhibit regional variability in responses, highlighting the need for standardized, region-specific protocols. These findings emphasize the importance of ongoing development and refinement of AI tools to ensure their global applicability and accuracy in health care. Consultation with an Infection Prevention and Control physician remains essential when dealing with complex infection control issues.

P100

How effective are continuous masking policies in reducing transmission of respiratory viral infections in hospitals? A systematic review

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OBJECTIVE: There is a need for strategies to reduce respiratory viral infection (RVIs) transmission in hospitals. One proposal is the implementation of mandatory continuous masking policies. However, the effectiveness of such policies in mitigating the spread of RVIs is unclear. We conducted a systematic review of the literature to determine the effectiveness of continuous masking in reducing the incidence and transmission of RVIs amongst patients and health care workers (HCWs) in hospital settings.

METHOD: We systematically searched electronic databases for original articles. Two reviewers screened studies. One reviewer extracted the data from selected studies according to a predetermined data extraction form. Results

were summarized narratively. Joanna Briggs Institute tools will be used for quality assessment.

RESULTS: Of the 3,691 studies identified, 17 met eligibility criteria. Twelve studies were conducted in single-centre adult hospitals and four in paediatric hospitals, with two of those in neonatal centers. One study was conducted using a hospital system. Infections included influenza A and B, parainfluenza 1-3, adenovirus, respiratory syncytial virus (RSV), traditional human coronavirus strains, human metapneumovirus, SARS-CoV-2, and rhinovirus/enterovirus. Eight of the studies assessed the impact of a masking policy on infection rate in patients. All eight reported that masking policies reduce transmission of infection in patients. Of the nine studies that assessed the impact of a masking policy on infection rate in HCWs, seven were associated with reductions in infection transmission in HCWs, whereas two showed no statistically significant change.

CONCLUSION: Our findings suggest that masking policies may play a role in RVI prevention, but there are significant limitations with the use of observational design and the masking in conjunction with other prevention measures. However, assessment of the quality of the papers is pending. Future directions include assessing secondary outcomes such as masking adherence and patient morbidity and mortality as well as assessing adjusted analyses from confounding that are critically important.

P101

Management and paediatric considerations during a measles outbreak in a tertiary care paediatric hospital

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OBJECTIVE: A measles outbreak occurred at a tertiary care paediatric hospital between February 2 and April 20, 2024, affecting paediatric patients, health care workers (HCWs), and the broader community. Despite an effective vaccine, measles remains a public health challenge. We report the outbreak's epidemiology, exposure risks, health care provider protocols, and its financial impact.

METHOD: This observational study used data from clinical reports, exposure assessments, and public health surveillance. It focused on paediatric patients, HCWs, and secondary exposed individuals. Incidence rates, descriptive epidemiology, and comparative analyses were performed.

RESULTS: The outbreak included 19 confirmed cases of the B3 strain, with an epicentre in the emergency department, affecting 13 paediatric patients (68%) and 6 adults (31.5%), including 4 HCWs. Ages ranged from 2 months to 46 years, with a median age of 18 months. Seventy-two percent of cases were unvaccinated. There were five hospitalizations (26%) and no deaths. Key responses included the use of personal protective equipment and pre-triage isolation of suspected cases in negative pressure rooms. Over 1,800 HCWs had their immunity status verified. Post-exposure vaccines were administered to 200 children, while 399 HCWs received a dose. Post-exposure immunoglobulins (Ig) were administered to 131 infants intramuscular, and 5 immunocompromised children or pregnant women received intravenous doses. The financial impact amounted to $68,078 in salaries and $22,205 in Ig use.

CONCLUSION: This outbreak highlights the urgent need for improved built environment and infrastructure to decrease the risk of transmission and proactive preventive measures. Emergency departments and outpatient clinics should have sufficient negative pressure rooms. Proactive vaccination and staff immunity verification are essential for improving public health preparedness and responses to future outbreaks.

P102

Hepatitis B in Alberta, Saskatchewan, and Manitoba compared to Canada from 1980 to 2023

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OBJECTIVE: To describe hepatitis B virus (HBV) incidence in Alberta, Saskatchewan, and Manitoba compared to Canada from 1980 to 2023, analyze the influence of age and sex, and identify gaps and opportunities for public health and clinical practice.

METHOD: This is an ecological study. Data were drawn from publicly available HBV reports published by the governments of Alberta, Saskatchewan, Manitoba, and Canada. Variables included the number of HBV acute, chronic, and unspecified cases, rate/100,000 population; and proportion of diagnoses by sex (female/male), age, ethnicity, and associated risk factors. We reported the incidence of HBV by sex, age, and ethnicity annually when data were available.

RESULTS: Canada's HBV infection rates rose from 1980 (4.75/100,000) to 1989 (21.95/100,000). After vaccination programs were introduced in the 1990s (Alberta and Saskatchewan: 1995; Manitoba: 1998), acute HBV rates declined nationally from 10.80/100,000 (1990) to 0.30/100,000 (2021). Total Canadian HBV cases increased in 2004–2019 (927–4912) due to a rise in chronic HBV cases (64–3,790). Saskatchewan's acute HBV rates declined between 2010 and 2018 (0.95/100,000–0.09/100,000). Manitoba's chronic HBV rates increased between 2014 and 2019 (5.4/100,000–20.5/100,000), aligning with national trends. Alberta's acute HBV rates fluctuated, decreasing from 1984 to 2006 (8.9/100,000–0.8/100,000), spiking in 2007 (23.0/100,000) and 2010 (18.1/100,000), before declining from 2011 to 2023 (0.6/100,000–0.3/100,000). Alberta reached the highest cumulative HBV rates in 2008–2019 across all study regions. Males, particularly those aged 40–59 years, accounted for the highest percentage of total HBV cases nationally. In Manitoba, males represented ≈60% of cases. Province-specific data on sex and age of cases were usually underreported.

CONCLUSION: Despite declining acute HBV rates in Canada since the introduction of the vaccine, the rise in chronic HBV cases highlights a significant ongoing illness burden. This is particularly relevant given the significant morbidity and mortality associated with HBV among Canadians. Limited reporting of age, sex, and ethnicity, especially in the provinces, highlights the urgent need for improved surveillance to guide effective public health strategies.

P103

Recommendations for detection of *Legionella* species by culture for hospitalized at-risk populations: A structured narrative literature review

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OBJECTIVE: *Legionella* spp. is found in aqueous environments and have been implicated in multiple health care outbreaks. There are currently no national Canadian guidelines or expert consensus on acceptable limits of *Legionella* detection in drinking water within health care settings.

METHOD: We conducted a structured narrative review using discrete search terms applied to three databases, PubMed (1978–2024), OVID (1946–2024), and The Outbreak Database (1936–2023), for reports of nosocomial *Legionella* transmission in English using COVIDENCE, along with a grey literature search of guidelines published by Canadian and international bodies. Outbreaks were included if they contained quantification of *Legionella* spp. Quality was assessed using Joanna Briggs Institute (JBI) and/or modified JBI criteria. Two reviewers conducted title/abstract screening of a random subset of 5% of records, and a single reviewer conducted the remainder of screening, selection, and data extraction. Four reviewers screened guidelines, and they were included if a specific recommendation regarding *Legionella* detection limits was included.

RESULTS: Our database search produced 2,006 records. After duplicate removal and exclusion of inappropriate

references, 252 studies remained, and 33 studies underwent full review and data extraction. There was wide variation of quantifiable *Legionella* detected in the context of nosocomial transmission, but the vast majority (82%) of outbreaks were associated with a detection of ≥1 CFU/ml. Of 15 *Legionella* control guidelines identified, 12 (80%) recommend non-detectable levels for at-risk patient populations when specified, or otherwise <1 CFU/ml. Quality of included studies was high (52%), moderate (39%), and low (9%).

CONCLUSION: Our narrative review of outbreaks and guidelines are generally consistent in recommending either undetectable *Legionella* in the context of at-risk hospital patients and <1 CFU/mL in all other health care contexts. Our findings suggest a threshold of <1 CFU/mL should be adopted as the Canadian standard and will be valuable for hospitals across Canada considering their local practices.

P104
Clinical implications of microbial misclassification in bloodstream infections: Insights from whole-genome sequencing of the Calgary BSI cohort

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OBJECTIVE: Bloodstream infections (BSIs) pose a significant health risk to patients and major costs to the health care system. Microbial identification via MALDI-TOF mass spectrometry, while rapid and effective for many pathogens, lacks the resolution to distinguish closely related species. The clinical significance of this misclassification is poorly understood.

METHOD: Using whole-genome sequencing (WGS) data from the Calgary BSI cohort – a comprehensive collection of over 38,000 isolates collected in southern Alberta from 2006 to 2022 (ResistanceDB.org) – we systematically evaluated MALDI-TOF MS species identification that were discordant with genomic classifications. We found multiple examples of these among isolates putatively identified as *Klebsiella pneumoniae* (*K. variicola*, $n = 364$, 21.3%; *K. quasipneumoniae*, $n = 87$, 5.3%), *Klebsiella oxytoca* (*K. grimontii*, $n = 59$, 9.9%; *K. michiganensis*, $n = 202$, 38.2%), and *Enterococcus faecium* (*E. lactis*, $n = 39$, 5.9% misclassification). The clinical implications of clinical misidentification of bacteremia species were assessed using patient characteristics.

RESULTS: Our data revealed wide-ranging impacts of species misclassifications, with many having no effect. For instance, species misidentified as *K. pneumoniae* showed no significant differences in clinical outcomes. In contrast, species misidentified as *K. oxytoca* and *E. faecium* showed notable differences in outcomes and antibiotic resistance. One example is that *K. grimontii* BSIs were associated with significantly longer hospital stays and higher treatment costs compared *to K. oxytoca*. Similarly, *E. lactis* exhibited markedly lower mortality rates and reduced antibiotic resistance profiles compared to correctly identified *E. faecium*.

CONCLUSION: Our analyses showed that at least five organisms are subject to this problem and are linked to significant differences in clinical manifestations. These findings underscore the need for higher-resolution diagnostic tools to improve species-level identification and optimize clinical management of infections.

P105 – WITHDRAWN

P106 Implementation of in-house TB PCR testing to reduce test turnaround time and airborne isolation days

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OBJECTIVE: Early diagnosis of tuberculosis (TB) has traditionally relied on sputum microscopy (acid-fast bacilli/AFB smear) combined with PCR confirmation of positives. A positive smear is sufficient to diagnose TB, but three negative smears are required to rule out TB. Sputum microscopy is often performed at a reference laboratory, and the turnaround time (TAT) is several days. Final

confirmation requires culture, which takes up to 7 weeks. This can result in delays in treatment for positive cases and prolonged airborne isolation for negative cases. The PCR-based Xpert MTB/RIF Ultra (Ultra) assay is rapid and easy to use. We evaluated its performance characteristics and the impact on turnaround time (TAT), duration, and cost of isolation.

METHOD: Ultra testing was performed at Unity Health in Toronto, Canada, from April through December 2024. Unprocessed sputum (1 mL) from patients suspected of pulmonary TB without recent anti-TB therapy was used. Sequential sputa were collected at least 1 hour apart, either in parallel or in addition to sputa collected for routine testing. De-isolation decision-making by infection prevention and control was based on clinical assessment, microscopy, and culture results, not Ultra results.

RESULTS: Of 163 sputa tested (107 patients), 11% of tests and 13% of patients tested Ultra positive. Compared to first sputa, Ultra had 100% sensitivity for AFB-positive, culture-positive specimens, 63.6% sensitivity for AFB-negative, culture-positive specimens, and 98.6% specificity. Patients without TB spent a median of 8 days in isolation. The median reduction was 2.5 days TAT compared to AFB smear. Based on the cost of a private room, Ultra would save approximately $988 per patient.

CONCLUSION: The Ultra assay demonstrated excellent sensitivity and specificity for smear-positive cases and reduced TAT relative to conventional diagnostics. Implementation of Ultra PCR outside of reference laboratories would permit more timely diagnosis and will reduce costs and duration in isolation.

P107

Assessing the public health impact of the adjuvanted respiratory syncytial virus prefusion F protein (RSVPreF3) vaccine in 50–59-year-old Canadian adults at increased risk for RSV during three full RSV seasons

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OBJECTIVE: Adults with comorbidities are at an increased risk for more severe respiratory syncytial virus (RSV) disease, compared with other populations. We evaluated the public health impact of the adjuvanted RSV prefusion F protein (adjuvanted RSVPreF3) vaccine (approved in Canada for ≥60-year-olds and 50–59-year-olds at increased risk for RSV) in Canadian 50–59-year-olds with comorbidities.

METHOD: A static multi-cohort Markov model (deterministic run) was used to assess the impact of one-time vaccination with the adjuvanted RSVPreF3 vaccine over a 5-year horizon (1-month-long cycle) versus no vaccine. The base-case analyses individually modelled symptomatic RSV cases in 50–59-year-olds with selected comorbidities: chronic obstructive pulmonary disease (COPD), diabetes, asthma, coronary artery disease (CAD), congestive heart failure (CHF), and chronic kidney disease (CKD). Vaccination coverage of 35% was applied, based on existing adjuvanted vaccine coverage. Vaccine efficacy assumptions incorporated three RSV seasons. RSV health care resource utilization and epidemiology (including upper/lower respiratory tract disease [URTD/LRTD]) inputs were obtained from literature using available Canadian estimates, preceding COVID-19 public health measures. Vaccination was assumed to occur in October of Year 1.

RESULTS: In patients with COPD, the adjuvanted RSVPreF3 vaccine would prevent 15,255 RSV cases (URTD: 4,019; LRTD: 11,237), 809 hospitalizations, 430 emergency department visits, 85 deaths, 10,173 outpatient visits, and 6,427 antibiotic prescriptions, versus no vaccination. Additionally, the vaccine would prevent 23,827 RSV cases (patients with diabetes), 20,582 cases (patients with asthma), 5,164 cases (patients with CAD), 2,105 cases (patients with CHF), and 5,386 cases (patients with CKD). The number needed to vaccinate to avoid one RSV-related event among patients with COPD was 10 (infection), 184 (hospitalization), and 1,747 (death), and varied for other comorbidities.

CONCLUSION: The adjuvanted RSVPreF3 vaccine may substantially reduce the public health burden of RSV in the Canadian population of 50–59-year-olds at increased risk for severe RSV disease due to comorbidities.

P108

Health care–associated infections and antimicrobial use among Canadian paediatric inpatients: 2024 Point Prevalence Survey results from the Canadian Nosocomial Infection Surveillance Program (CNISP)

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OBJECTIVE: CNISP conducts periodic point prevalence surveys to assess health care–associated infections (HAIs) and antimicrobial use (AMU) in paediatric populations. This study provides an update with 2024 data from Canadian acute care hospitals.

METHOD: Hospitals surveyed patients over a 24-hour period from February to March 2024. Variables captured included HAIs, microorganisms and antimicrobial resistant organisms (AROs), the use of additional precautions and AMU. Descriptive statistics for the results are presented.

RESULTS: Among 62 participating hospitals, 33 reported data on paediatric inpatients (<18 years). There were 1,549 paediatric patients surveyed. One or more HAIs were identified in 6.5% (95% CI 5.4–7.9) of patients (n = 101). Infants (ages 1 month to 2 years) and children (ages 2 to 12 years) made up the highest proportion of patients with HAIs (48% and 29%, respectively). The most common HAIs were bloodstream (24%) and viral respiratory infections ([VRI] 20%), followed by ventilator-associated pneumonia (20%). Among patients with HAIs, eight (7.9%) were caused by AROs: five extended spectrum beta-lactamase–producing organisms and three methicillin-resistant *Staphylococcus aureus*. Device-associated infections accounted for 41% of all HAIs. Of the 718 patients admitted to the ICU, 48 had an HAI (6.7%), with pneumonia, representing over half of those reported (52%). Nearly one-third of patients (443/1,549; 29%, 95% CI 26–31) were on additional precautions; most were on droplet and contact precautions (292/443; 66%), while 29% were on contact only (127/443). VRIs (excluding COVID-19) were the most common reason for additional precautions (223/1,549; 14%). Systemic antimicrobial agents were administered to 34% of patients (524/1,549), with β-lactams/penicillins and third-generation cephalosporins used most frequently (25% and 16% of all antimicrobials, respectively).

CONCLUSION: These findings highlight the burden of HAIs, device-associated infections, and AMU among Canadian paediatric inpatients, emphasizing the need for continued surveillance.

P109

A dramatic rise in carbapenemase-producing *Enterobacterales* after a 3-year decline following the COVID-19 pandemic

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OBJECTIVE: Carbapenemase-producing *Enterobacterales* (CPE), linked to international travel from high-prevalence regions, pose a significant public health threat. During the COVID-19 pandemic, global travel restrictions and COVID-19 public health measures were associated with a marked decline in CPE cases in a tertiary care microbiology laboratory serving a metropolitan area. In 2024, the number of international flights returned to pre-pandemic levels and pandemic-related public health measures have eased. This study evaluated trends in CPE frequency pre-pandemic, during the pandemic, and in the post-pandemic period including 2024.

METHOD: The annual numbers of CPE and carbapenemases (excluding duplicates) from 2009 to 2024, adjusted per 1,000,000 bacteriology and CPE-screening cultures, were calculated and displayed graphically. Trends across two periods, 2009–2019 (pre–COVID-19) and 2019–2024 (post–COVID-19) were analyzed. Statistical analysis was performed using the Chi-squared test for trend with GraphPad Instat.

RESULTS: Between 2009 and 2019, the number of CPE per 1,000,000 cultures per year increased steadily from 5 to 161 (p < .0001). However, during the pandemic, CPE cases per 1,000,000 cultures decreased from 161 in 2019 to 74 in 2022 (p = .009). In 2023 and 2024, CPE cases per 1,000,000 cultures rose to 140 in 2023, then surged to 207

in 2024 ($p = .0009$), at a higher rate (67 cases per 1,000,000 cultures/year) than that seen in the pre-COVID period (19 cases per 1,000,000 cultures/year). This resurgence was particularly driven by a rise in New Delhi metallo-β-lactamase (NDM), although a rise in KPC, IMP, VIM, and OXA-48 carbapenemase-producing strains was also noted.

CONCLUSION: Following a significant decline during the COVID-19 pandemic, the number of CPE per 1,000,000 cultures has rebounded to levels surpassing the pre-pandemic rates. This resurgence is correlated with the resumption of global travel and the easing of COVID-19–related public health measures, likely facilitating the reintroduction of CPE in the community.

P110

Mind the gap: The evolution of provincial infection prevention and control practices against antimicrobial-resistant organisms

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OBJECTIVE: To address the rise of antimicrobial resistance (AMR) globally, the Pan-Canadian Action Plan on AMR prioritizes surveillance and infection prevention and control (IPAC). National IPAC guidelines recommend screening programs and Additional Precautions (AP) for antimicrobial-resistant organisms (AROs). However, data on the implementation of these programs and their evolution over time are lacking. To address this gap, this province-wide study described hospital IPAC trends over 8 years.

METHOD: Annual surveys of all hospital corporations provincially since 2016 have assessed the IPAC programs in place for methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), extended spectrum beta-lactamase-producing organisms (ESBL), and carbapenemase-producing organisms (CPO). Survey questions regarding emerging *Candida auris (C. auris)* were added in 2020 and 2023. Differences in proportions between 2016 and 2023 were analyzed using Chi-squared tests.

RESULTS: The number of hospital corporations changed annually, reflecting newly formed corporations. Response rates of hospital corporations from 2016 to 2023 increased from 52.6% to 82.9% (112/213 to 116/140; $p < .01$). The proportions of hospital corporations with IPAC screening programs from 2016 to 2023 have been stable for MRSA (100% to 100%; $p = 1.00$), decreasing for VRE (79.1% to 69.0%; $p = .10$), stable for ESBL (38.8% to 39.7%; $p = .95$), and increasing for CPO (56.3% to 70.7%; $p = .03$). The proportion with IPAC screening programs for *C. auris* from 2020 to 2023 has increased (9.5% to 19.8%; $p = .09$). The proportions of hospital corporations who applied AP from 2016 to 2023 have been stable for MRSA (100% to 100%; $p = 1.00$), decreasing for VRE (84.6% to 75.0%; $p = .09$), decreasing for ESBL (87.9% to 69.0%; $p < .01$), and stable for CPO (100% to 96.5%; $p = .17$). In 2023, 86.7% of hospital corporations applied AP for *C. auris*.

CONCLUSION: Provincial IPAC trends reveal evolving AMR priorities, variations in practices, and significant gaps. Strengthening screening programs for CPO and *C. auris* is critical.

P111

Genomic epidemiology of Vancomycin-resistant *E. faecium* from two academic hospitals, 2020–2024

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OBJECTIVE: Vancomycin-resistant *Enterococci* (VRE) remain a significant infection control challenge in hospitals. Whole-genome sequencing is a valuable tool for gaining insight into the population of organisms circulating in health care facilities, and we use this methodology to describe the local genomic epidemiology of Vancomycin-resistant *Enterococcus faecium* (VREfm).

METHOD: A total of 271 unique clinical VREfm isolates collected between 2020 and 2024 from multiple acute care

hospitals were subjected to WGS on the Illumina MiniSeq platform. We investigated population structure through *in silico* multi-locus sequence typing (MLST) and variable length *k*-mer (VLK) typing via popPUNK using a global database of *E. faecium* genome sequences. We determined the pangenome of these isolates and estimate a phylogenetic tree from the aligned core. Lastly, the distribution of Vancomycin resistance of these isolates using AMRfinderplus was determined.

RESULTS: Two-hundred and sixty-two (97%) of our isolates were classified as ST80 (65%), ST17 (24%), ST203 (4%), or ST117 (3%). Five other STs accounted for the remaining 3% of our isolates. The majority of these isolates are not represented by the global *E. faecium* VLK clusters trained on 1,656 primarily hospital-derived isolates. Of the 262 total isolates, 238 (86%) from the four aforementioned STs were assigned to novel local VLK clusters: pp39 (120 isolates), pp41 (32 isolates), pp42 (13 isolates), pp40 (63 isolates), pp43 (9 isolates), pp9 (11 isolates), and pp49 (1 isolate). We observed the following distribution of Vancomycin resistance types in our most prevalent STs: ST80 (66%) VanB, (31%) VanA, (0.5%) VanD, not detected (n.d.) (0.5%); ST17 (97%) VanA, (1.5%) VanB, (1.5%) n.d.; ST203 (100%) VanA, and ST117 (100%) VanA.

CONCLUSION: WGS reveals the local VREfm population is unique compared to a global database of hospital-acquired isolates and consists of a large phylogenetically related group from ST80 harbouring primarily VanB-type resistance. Characterizing our local VREfm via WGS complements ongoing infection control measures and outbreak investigation.

P112

Test performance of the FungiXpert *Cryptococcus* antigen (CrAg) lateral flow assay (LFA) against the IMMY CrAg LFA: A retrospective and prospective study across five Canadian laboratory sites

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OBJECTIVE: Cryptococcosis is a disease caused by yeast species in the *Cryptococcus neoformans* and *C. gattii* complexes. Cryptococcal antigen (CrAg) lateral flow assay (LFA) enables the rapid and sensitive detection of cryptococcal infection. The FungiXpert CrAg LFA (Genobio Pharmaceutical) is a recently Health Canada–licensed product that lacks comprehensive evaluation in the North American setting.

METHOD: This retrospective and prospective study across five Canadian laboratories aimed to evaluate the test performance of the FungiXpert CrAg LFA compared to the IMMY CrAg LFA for serum and cerebrospinal fluid (CSF) samples. Positive and negative percent agreement, precision, and cross-reactivity were assessed. In addition, a subset of samples were evaluated against latex agglutination (LA) testing. Retrospective data review was performed for demographics, clinical data, and additional diagnostic testing results.

RESULTS: A total of 141 serum samples and 83 CSF samples from 192 individuals with and without HIV infection were included. In the overall retrospective cohort, the FungiXpert CrAg LFA demonstrated qualitative detection positive percent agreement (PPA) of 90.2% (95% confidence interval [95% CI] 87.3–93.1) and a negative percent agreement (NPA) of 100% (95% CI 97.7–100). By sample type, the CSF PPA was 93.9% (95% CI 79.8–99.3), and the serum PPA was 90.7% (95% CI 79.7–96.9). Overall, 55.6% of FungiXpert titres were within one doubling dilution of the original IMMY result. The prospective cohort consisted of 58 samples including 2 serum samples that were positive; of these, 1 was low titre (1:1) and missed by FungiXpert. Both the FungiXpert and IMMY CrAg LFAs showed cross-reactivity with *Trichosporon* species.

CONCLUSION: These findings support similar performance of the FungiXpert CrAg LFA on cerebrospinal fluid samples but lower sensitivity on serum samples and greater lot-to-lot variation compared to the IMMY CrAg LFA, which should be considered in clinical implementation decision-making.

P113

Development and evaluation of a standardized procedure for assessing sterility of compounding procedures using closed system transfer device to extend beyond-use-date of oncology medications

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OBJECTIVE: In accordance with National Association of Pharmacy Regulatory Authorities (NAPRA) standards for compounding hazardous sterile preparations, single-dose vials must be used or discarded within 6 hours of first access unless sterility can be demonstrated. To reduce medication wastage, we developed a standardized procedure for routinely evaluating sterility using the PhaSeal™ closed system transfer device (CSTD) to extend the beyond-use-date (BUD) from 6 hours to 7 days.

METHOD: Tryptic soy broth (TSB) and fluid thioglycollate medium (FTM) vials served as surrogates for chemotherapy and biologic drug vials. At two pharmacy sites, technicians used the PhaSeal™ CSTD and aseptic hazardous drug compounding techniques to withdraw 1-mL aliquots daily over 7 days. Vials were incubated for 5 days in ambient air or at 35°C and inspected daily for growth. TSB and FTM vials underwent terminal subcultures on chocolate agar (aerobic) and brucella agar (anaerobic) for FTM vials only, which were read at 48 and 72 hours. Control TSB and FTM vials were held unaccessed to confirm media sterility throughout the 15-day study. At the terminal step, one set of TSB/FTM vials was inoculated with standard microbiology organisms to confirm media integrity.

RESULTS: No microbial growth was observed in sample or control vials after 7 days of compounding with the PhaSeal™ CSTD. Subsequent incubation and daily observations confirmed no contamination. Positive control vials inoculated with quality control organisms demonstrated growth, validating media integrity.

CONCLUSION: This study demonstrates a simple, standardized method for evaluating the sterility of compounded oncology medications using a CSTD, supporting an extension of the BUD from 6 hours to 7 days. Semi-annual implementation of this protocol would reduce medication waste, ensure sterility, and improve supply sustainability during shortages.

P114

Paediatric community-acquired pneumonia in the COVID-19 era prior to the introduction of expanded-valency pneumococcal conjugate vaccines: A prospective cohort study

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OBJECTIVE: To explore the epidemiology, microbiology, management, and outcomes of paediatric community-acquired pneumonia (CAP) in the COVID-19 era prior to the widespread implementation of 15- and 20-valent pneumococcal conjugate vaccines in Canada.

METHOD: This was a single-centre prospective observational cohort study enrolling children aged >3 months clinically diagnosed with CAP. Data were collected relating to demographics, clinical signs/symptoms, imaging, lab testing, and clinical outcomes. Participants were followed for 30 days.

RESULTS: We enrolled 225 children between March 2023 and January 2025, including 5 with non-severe CAP (discharged home from the Emergency), 139 with severe CAP who required hospitalization on the ward, 30 with CAP complicated by effusion requiring procedural drainage, and 51 with critical CAP who required intensive care. The mean age of participants was 6.27 years (SD 4.59 years). Most (208/225; 92%) had nasopharyngeal testing; of those, 107/208 (51%) were positive for a viral pathogen (including 30 rhino/enterovirus, 22 RSV, 15 hMPV, and 7 influenza) and 19/208 were positive for *Mycoplasma* (9%). Most with complicated CAP (28/30; 93%) had pleural fluid tested. Almost all with pleural fluid testing (27/28; 96%) had a pathogen detected; there were 19 positives for *Streptococcus pneumoniae*, 6 positives for group A streptococcus, and 2 positives for Streptococcus *anginosus*. The median length of stay was 4 days (IQR 3–7 days) for severe CAP, 11.5 days (IQR 9–17 days) for complicated CAP, and 4 days (IQR 3–7 days) for critical CAP. There were 12 (5.3%) who were re-hospitalized within 30 days; 2 initially had non-severe

CAP, 8 initially had severe CAP, and 2 initially had critical CAP.

CONCLUSION: This is one of the largest prospective studies of paediatric CAP in Canada in the post-PCV13 era. Our study highlights the importance of viral infection in this population, the high yield of pleural fluid testing in complicated CAP, and the significant morbidity associated with this disease.

P115

Profile of children with active tuberculosis at a tertiary paediatric hospital

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OBJECTIVE: To describe the epidemiological, microbiological, and clinical characteristics of children diagnosed with tuberculosis at a tertiary care hospital.

METHOD: After approval from the ethics committee, we identified children that had a diagnosis of tuberculosis, combining cases identified through medical records (discharge diagnoses, International Classification of Diseases), laboratory information system (positive cultures and/or nucleic acid amplification tests [NAAT]), and clinical records from the outpatient clinic. Charts of children diagnosed and treated for tuberculosis disease from January 1, 2014 to December 31, 2023 were reviewed. Trained research assistants and the infectious disease fellow used a standardized case report form to extract data, which were then imported into Redcap. Descriptive statistics were used.

RESULTS: We identified 48 patients diagnosed and treated for tuberculosis disease: 23 males and 25 females, 50% born outside Canada, with a median age of 6.5 years (range 0.2–18). The index case was identified in 52.1%, essentially from close household contact, and none was a child. Overall, 81.3% were symptomatic, predominantly with pulmonary tuberculosis or intra-thoracic lymph nodes. Two patients had meningitis and one was miliary. Thirty-one patients (64.5%) had microbiologic confirmation through positive cultures (64.6%) or NAAT (43.8%), mostly from gastric aspirates (52.1%). Most strains were susceptible to first-line anti-tuberculosis drugs with less than 5% showing resistance to Isoniazid, Ethambutol, or Pyrazinamide. There was no resistance to Rifampicin. Limitations of the study include the retrospective design and possible incomplete data from records.

CONCLUSION: This cohort of children with tuberculosis was reviewed to improve our medical practice. We plan to use the case report form prospectively for new tuberculosis cases to have a standardized database and would hope to deploy to other paediatric centres to develop more accurate surveillance of tuberculosis paediatric cases in Canada.

P116

Risk factors for severe disease among children hospitalized with enterovirus/rhinovirus infections in 2022–2023

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OBJECTIVE: Enterovirus/rhinovirus infections are common in children, but their clinical course and outcomes remain poorly studied. This study aimed to describe hospitalized children with enterovirus/rhinovirus infections and identify risk factors for severe disease.

METHOD: We reviewed a cohort of 585 children aged 0–18 years hospitalized with acute respiratory illness caused by microbiologically confirmed enterovirus/rhinovirus at two Canadian paediatric hospitals between July 1, 2022 and June 30, 2023. Demographic, clinical, and laboratory data were retrospectively extracted from medical records. Severe

disease required mechanical ventilation, renal replacement therapy, or ECMO or caused cardiac arrest or death. Predictive models were developed using multivariable logistic regression, random forest, and XGBoost classifiers. Data were split into 80/20 training and testing sets. Models were evaluated using fivefold cross-validation to avoid overfitting. Model performance was assessed using receiver operating characteristic area under the curve (ROC AUC), precision, recall, and F1 score.

RESULTS: Among children admitted at one study site (multicentre analyses underway), median age was 3.1 years (IQR 1.1–6.6), and 67.3% had chronic comorbid conditions, most commonly neurological and gastrointestinal, as well as those qualifying for complex care. Children with severe disease were more likely to be under 2 years old and have neurologic, cardiac, and gastrointestinal comorbidities. Logistic regression identified young age (adjusted OR 0.93, $p < .001$), male sex (OR 1.41, $p = .014$), and increased work of breathing (OR 2.02, $p < .001$) as significant predictors of severe disease. Logistic regression (ROC AUC 0.76) outperformed random forest (0.61) and XGBoost (0.64).

CONCLUSION: Though often thought of as mild infections, enterovirus/rhinovirus may cause severe disease, as demonstrated by the results of this study. Key risk factors in our cohort include young age, male sex, and presence of comorbidities. These data may improve parental counselling, guide clinical management, and improve understanding of paediatric viral diseases.

P117

Fewer hands, faster diagnosis: Improving efficiency with simultaneous enteric protozoan NAAT implementation and discontinuation of permanent stain microscopy

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OBJECTIVE: Enteric protozoan molecular diagnosis has been increasingly used in Québec over the past decade. The main reported challenge has been variable success in switching completely to molecular testing from permanent stain microscopic examination, mainly because of pre-analytical complexities. In June 2023, routine enteric protozoan diagnosis by traditional microscopy was fully replaced with enteric protozoan nucleic acid amplification tests (NAAT) at the Centre Hospitalier Universitaire de Sherbrooke (CHUS), the server laboratory for the Eastern Townships region of Québec. Iron hematoxylin stain has been discontinued, and microscopy is maintained solely for helminth recovery and for coccidia not included in NAAT, based on clinical indications. The main objectives of this study are to evaluate the impact of the new algorithm on turnaround time (TAT), associated human resource allocation, and overall costs.

METHOD: Ova and parasite (O&P) test TATs from June 2022 to June 2023 (PreNAAT) were compared with enteric protozoan NAAT and helminth eggs microscopy TATs from September 2023 to September 2024 (PostNAAT). Other indicators were also compared between the two periods, such as parasite recovery, costs, and required human resources.

RESULTS: During the PreNAAT period, 11,780 O&P pooled microscopic examinations were processed, compared with 8,217 enteric protozoan NAATs and 1,529 unpooled microscopy examinations PostNAAT. Preliminary results indicate a reduced mean TAT from 13 days for O&P to 3 days for NAAT and 7 days for microscopy. Additional data including comparative O&P recovery, labour time reduction, and costs are presented.

CONCLUSION: The implementation of enteric protozoan NAAT, coupled with the elimination of iron hematoxylin stain, has led to important reductions in TATs and necessary technical time. These findings are particularly relevant given the current challenges of labour shortages, where optimizing resources is critical. Several aspects of implementation were discussed, including lessons learned and caveats.

P118

A family-focused immunization clinic to improve protection against vaccine-preventable diseases: Public health in an acute paediatric hospital setting

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OBJECTIVE: The Family Immunization Clinic (FIC) has provided immunizations to patients and their families since October 2017 via a drop-in immunization clinic within an acute care paediatric setting. The objectives of this analysis were to describe the populations served by FIC and identify trends in immunizations and behaviours at the clinic over the first 7 years of its operation.

METHOD: Data were collected contemporaneously by clinic staff and entered into a clinic database, which was created for evaluation purposes. Data were extracted from this database and the hospital charts for encounters between October 1, 2017 and September 30, 2024. Trends in referral information, patient demographics, patient visit summary, and vaccines administered were described.

RESULTS: During the analysis period, FIC provided a total of 47,117 vaccines to 17,467 patients in a total of 32,045 visits. Of the total clinic attendees, 84% were patients from the paediatric hospital and adjacent women's hospital and their family members. Overall, 64% of clinic attendees were ≤19 years old. There was an increase in visits due to needle anxiety/phobia since the clinic opened, but this has remained similar in the past 3 years, with 5.3–5.9% of all patients in the clinic seen for this reason between 2021–2022 and 2023–2024, compared with 0.9% in 2017–2018. Medically high-risk children consisted of 12% of all children seen at the clinic since its opening. Specific coping strategies have been used in the clinic to facilitate immunizations in 19% of individuals, with tablet/cell phones and topical numbing spray being the most common.

CONCLUSION: This analysis identified key trends in immunizations at the clinic, including an increase in visits due to needle anxiety/phobia. Clinical encounters at FIC reflect the changing climate of medical complexity and models an innovative approach to strengthening paediatric health across the region.

P119 – WITHDRAWN

P120 Leveraging wastewater-based surveillance to analyze societal drivers of population-level antimicrobial resistance

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OBJECTIVE: While various societal factors such as socioeconomic status, immigration patterns, and industrial activity are known to influence antimicrobial resistance (AMR) distribution in humans, their impact remains poorly understood at the population level. Utilizing wastewater-based surveillance – an inclusive and comprehensive tool for monitoring infection occurrence/trends across population – we aimed to investigate societal drivers contributing to the heterogenous distribution of AMR genes (ARGs) across Alberta.

METHOD: Between March 2022 and March 2023, we collected monthly wastewater samples from 11 cities in Alberta ranging from 7,969 to 1,371,575 inhabitants and representing 35% of total provincial population. Using metagenomics and multivariate analysis, we identified AMR genes and examined their association with socioeconomic factors, including income, education, unemployment, immigration, and livestock-industrial parameters (ie, the numbers of farms, pigs, and cattle), utilizing publicly available data.

RESULTS: Multivariate analysis identified significant association between ARG abundance and various societal factors including immigration, cattle density, and income ($p < .005$). The analysis also revealed cross-correlation among societal factors, with cattle density and income being negatively associated. A meta-analysis of published cattle-origin metagenomes revealed that ARG abundances associated with cattle were lower in Alberta feedlots compared to urban sewage, suggesting that factors such as income, rather than cattle exposure alone, might be a more significant driver. Univariate analysis further confirmed these findings, indicating that through a total of 123 ARG spanning 14 different resistance classes were significantly associated with either income or immigration.

CONCLUSION: Heterogeneity in the distribution of ARG was observed across Albertan communities. Our findings suggest that AMR exposure from agricultural activity is not necessarily reflected in human urban populations and may be overshadowed by other factors, including income. Furthermore, the identification of income and immigration

as key societal determinants highlights the need for investment in health care resources that can address disparities along these gradient of such variables, thereby improving health equity.

P121

Leveraging LAMPREG through exploiting omics, clinical and computational approaches to predict the outcomes of malaria in pregnancy (MiP)

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BACKGROUND: Malaria in pregnancy (MiP) often leads to serious morbidity and mortality. In sub-Saharan Africa, anemia accounts for about 20% of all maternal deaths, and low fetal birth weight is thought to be the single most significant risk factor for neonatal and infant mortality. In many cases MiP is difficult to diagnose and hence is not treated, which affects the mother as well as the offspring.

OBJECTIVES: To leverage the LAMPERG diagnostic clinical trial and develop a predictive model using machine learning-based on metabolomics, lipidomics, and clinical data that could forecast the outcomes of MiP.

METHODS: In this study we stratified the MiP patients into high-risk and low-risk groups and evaluated the differential host–parasite response between malaria infected and non-infected pregnant woman. We analyzed whole blood samples from 70 MiP patients with targeted omics using the Biocrates MxP® Quant 500 kit on a liquid chromatography/mass spectrometry (LCMS/MS) platform.

RESULTS: Our analysis for both small molecules and lipids demonstrated significant differences in 260 ($p < .05$), 130 ($p < .01$), 46 ($p < .001$), and 16 ($p < .0001$) analytes. Compounds previously reported to be implicated in MiP and that were different between the two groups included amino acids, hormones, cholesterol esters, glycosylceramides, fatty acids, sphingolipids, indoles dihydroceramides, bile acids, biogenic amines, diacyelglycerols, acylcarnitines, glycerophospholipids, vitamins and cofactors groups, choline, triacyglycerols, and ceramides. We have trained machine-learning algorithms to predict outcomes of MiP exploiting an ensemble learning method using Random Forest and SVM classifiers. Thus far, the model received the ROC of 93.7% in classifying the MiP patients into high- and low-risk groups.

CONCLUSIONS: We present the findings on our novel strategy that uses modern computational as well as biological/clinical datasets to predict the outcomes of MiP, which will be a step forward towards precision medicine.

P122

Comparison of pneumococcal conjugate vaccines PCV20 and PCV15 for administration to children in Canada: analysis from the SAVE study

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OBJECTIVE: The objective of this analysis was to assess the differences in vaccine coverage provided by PCV15 and PCV20, both recommended by NACI, in Canadian children.

METHOD: From 2011 to 2021, 1,846 IPD isolates were collected from children 0 to 17 years of age. Serotypes were determined by Quellung reaction. Antimicrobial susceptibility testing was performed by CLSI broth microdilution methods.

RESULTS: Table P122-1 details the differences in the proportion of isolates with serotypes included in PCV15 and PCV20 by demographic and antimicrobial resistance categories.

CONCLUSION: A significantly greater proportion of paediatric SAVE isolates were serotypes included in PCV20 compared to PCV15 overall, for each demographic group analyzed and for clarithromycin-NS and SXT-NS isolates. Serotypes included in PCV15 and PCV20 were 64.6% and 68.1% of MDR *S. pneumoniae*, respectively.

Table P122-1: Differences in proportion of isolates with serotypes included in PCV15 and PCV20.

Category (n)	Proportion of isolates with vaccine serotype, n (%)		*P*
	PCV15	PCV20	PCV15 versus PCV20
All paediatric *S. pneumoniae* (1846)	803 (43.5)	1,208 (65.4)	<.0001
Age group (years)			
0 to <1 (407)	166 (40.8)	257 (63.1)	<.0001
1 to <2 (432)	162 (37.5)	275 (63.7)	<.0001
2 to <6 (593)	277 (46.7)	397 (67.0)	<.0001
6 to <18 (414)	198 (47.8)	279 (67.4)	<.0001
Region[a]			
Western (441)	178 (40.4)	295 (66.9)	<.0001
Central (1249)	548 (43.9)	816 (65.3)	<.0001
Eastern (156)	77 (49.4)	97 (62.2)	.03
Biological sex[b]			
Female (725)	322 (44.4)	461 (63.6)	<.0001
Male (1031)	440 (42.7)	685 (66.4)	<.0001
Antimicrobial resistance			
Clarithromycin-NS (444)	269 (60.6)	354 (79.7)	<.0001
Penicillin[c]-NS (242)	88 (36.4)	103 (42.6)	–
SXT-NS (304)	151 (49.7)	219 (72.0)	<.0001
MDR (113)	73 (64.6)	77 (68.1)	–
XDR (42)	42 (100)	42 (100)	–

[a]Western: SK/MB, Central: ON/QC, Eastern: NL/NS/PEI/NB.
[b]Missing values ($n = 90$; 4.9%).
[c]Oral penicillin breakpoints.
NS, non-susceptible; MDR and XDR defined as resistance to three or more and five or more antimicrobial classes, respectively; -, non-significant.

P123 – WITHDRAWN

P124

Simple but not easy: Assessing and addressing the underlying systemic barriers to the hepatitis C (HCV) cascade of care

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OBJECTIVE: Our clinic serves people who are experiencing poverty, mental health issues, homelessness, and/or substance use. We actively engage in outreach to the harder-to-reach. People can self-refer. Despite simple HCV treatment regimens and prioritized wraparound care for the most structurally vulnerable, the path to HCV cure is not easy. HCV care cascades are presented as linear medical steps. In practice, the path to cure is often circuitous and involves accessing resources and social stabilization before those traditional medical steps can be completed. We developed a tool to assess these systemic and socioeconomic barriers.

METHOD: We reviewed our historical HCV cascade of care, exploring the barriers highlighted there. We then conducted a pilot prospective mini-evaluation of client characteristics associated with treatment update in 2024.

RESULTS: Between July 2022 and February 2024, 272 patients were seen. Of these, 51% were homeless or unstably housed and 20% were uninsured for HCV mediations. Only 64% in total and 88% of those with medication coverage started treatment. The average time between prescription issue and starting HCV medication was 90 days. During the pilot project period of May–September 2024, 32 people were interviewed with the new questionnaire. Of those who responded, 72% were using illicit substances (stimulants 62.5%, opioids 62.5%), 22% reported being unable to access addiction care, 81% lacked a primary care provider, and 53% lacked a cellphone.

CONCLUSION: Despite wraparound care, 36% of people with HCV who engaged with our clinic were not able to access curative treatment in a timely manner. We identified that lacking housing, being uninsured for medications, having no cellphone, having higher social needs, and being less connected to addiction care are common and associated with a lower likelihood of starting treatment. We will prospectively track this actionable information to address

and advocate for the social determinants of accessing the HCV cascade.

P125 – WITHDRAWN

P126
Trends in Parvovirus B19 prevalence in blood donations in Quebec

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OBJECTIVE: Parvovirus B19 (B19V) is a small, non-enveloped DNA virus within the Parvoviridae family (genus *Erythrovirus*), predominantly transmitted via the respiratory route. Additionally, B19V is known to be transmissible through blood transfusion. B19V is endemic worldwide, typically peaking from end of winter to early summer and recurring in outbreaks at multi-year intervals. Since late 2023, several European countries have reported a notable increase in B19V infections. This surge raises potential concerns regarding the safety of blood products intended for direct transfusion. Our aim was to describe changes in the prevalence of B19V in blood donations from 2021 to early 2025 (January 1–12) in the province of Quebec, Canada.

METHOD: This study included all blood donations collected during the period. Routine nucleic acid testing (NAT) for B19V DNA (B19V-NAT) was implemented at Héma-Québec in December 2020 using pools of 16 donations with a detection threshold of 10^4 IU/mL. Prevalence rates were estimated for each calendar year, with 95% Wilson confidence intervals.

RESULTS: Between 2021 and early 2025, 104 of 1,474,355 donations (7.05 per 100,000 donations) tested positive for B19V DNA. The annual prevalence of B19V DNA-positive donations per 100,000 donations was estimated at 0.27 (95% CI 0.05–1.58) in 2021, 0.60 (95% CI 0.16–2.18) in 2022, and 1.40 (95% CI 0.60–3.27) in 2023. A significant increase was observed in 2024, with the prevalence reaching 13.61 (95% CI 10.41–17.80) and further escalating to 99.75 per 100,000 donations (95% CI 52.49–189.50) during the first 2 weeks of 2025.

CONCLUSION: The prevalence of B19V DNA-positive donations in Quebec remained low from 2021 to 2023 but demonstrated a marked increase in 2024 and early 2025. This trend underscores the importance of monitoring of B19V prevalence in blood donations to mitigate potential risks associated with transfusion-transmitted infections.

P127
Babesia nucleic acid prevalence in blood donations in southern Quebec

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OBJECTIVE: *Babesia* is a red-cell parasite that can be transmitted by transfusion (TTB). Prior to 2021, babesiosis was the most common transfusion-transmitted infection in the United States, with over 250 cases reported. Ultrasensitive nucleic acid tests (NAT) amplifying parasite 18S ribosomal RNA are now available to screen blood donations, and the US Food and Drug Administration (FDA) recommended their use in 2019 with implementation in 14 endemic states plus the District of Columbia in 2020. This mitigation measure has been highly effective in eliminating TTB cases from screened blood. The aim of this study is to determine the prevalence of *babesia* nucleic acids among blood donations in southern Quebec during the 2024 summer season.

METHOD: Whole blood and platelet donations in southern Quebec were tested between June 1 and October 31, 2024 in real time with the FDA-approved Procleix Babesia Assay (Grifols Diagnostic Solutions) by the American Red Cross. Prevalence rate with 95% Wilson confidence intervals were reported.

RESULTS: A total of 28,800 donations from 12,900 male donors (mean age: 51;24 ± 16;17) and 11,158 female donors (mean age: 47;12 ± 16;82) were tested. Of those, 88% were from Caucasian donors. Male donors gave a mean of 1.41 (±0.32) donations and female donors gave 1.07 (±0.32). The highest represented regions were Montérégie (53%), Montréal (30%), and Estrie (12%). All donations tested negative for *Babesia* NAT.

CONCLUSION: While *Babesia* is known to be present in *Ixodes scapularis* ticks in southern Quebec, clinical cases of babesiosis in Quebec are extremely rare. Results from this study indicate that TTB risk in Quebec is less than 1:28,800 donations (95% CI: 0–1:7,481).

P128

Prevalence of *Streptococcus pneumoniae* colonization in unhoused populations in an urban Canadian setting

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OBJECTIVE: *Streptococcus pneumoniae* colonization in the upper respiratory tract is a common occurrence that can lead to severe invasive pneumococcal disease or meningitis. This study aims to assess the prevalence of *S. pneumoniae* colonization in unhoused populations within an urban Canadian centre and explore demographic factors associated with colonization rates.

METHOD: A retrospective analysis was conducted using 54 oral nasal swabs from unhoused adults (18 or older) across multiple shelters in a mid-sized urban centre. Samples were tested for *S. pneumoniae* via molecular detection of the *lytA* gene. A cycle threshold (CT) value of 40 defined positivity. Age and shelter gender designation were recorded. Fisher's Exact Test evaluated the association between gender and colonization while logistic regression assessed the combined effects of age and gender. Correlation analysis explored the relationship between age and bacterial load in positive cases.

RESULTS: Of the 54 samples analyzed, 19 (35%) tested positive for *S. pneumoniae*. The median age of participants was 44.3 years (range 18.8–78.5). The population consisted of 38 women (70%) and 16 men (30%). Colonization rates were significantly higher in men (69%) than in women (18%) ($p < .001$). The quantitation mean of bacterial load in positive cases was 6.36 Log10/mL. Logistic regression supported this disparity, with men having 9.8 times higher odds of colonization compared to women ($p < .001$). Age was not a significant predictor of colonization ($p = .93$). Correlation analysis revealed no significant relationship between age and bacterial load ($r = 0.12$, $p = .64$).

CONCLUSION: *S. pneumoniae* colonization is prevalent in unhoused populations in urban Canadian settings, with markedly higher colonization rates in men compared to women. These findings highlight the need for targeted public health interventions tailored to this high-risk group. Future analyses will focus on serotype identification via nanopore sequencing to inform vaccine development.

P129

Disseminated gonococcal infection in Manitoba: A descriptive study

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OBJECTIVE: The goal of this project was to characterise this changing epidemiology, describe symptomatology and clinical presentation, and outline the manner of diagnosis, treatments received, and short-term outcomes for identified cases of disseminated gonococcal infection (DGI) in Manitoba.

METHOD: Cases of DGI occurring between January 1, 2011 and December 31, 2021 were identified by isolation in culture from a non-mucosal site through data linkage with Cadham Provincial Laboratory, which processes all *N. gonorrhoeae* positive isolates in Manitoba. Chart review of both the paper and electronic medical records from Health Sciences Centre, St. Boniface Hospital, Grace Hospital as well as the Community Intravenous Program in Winnipeg, Manitoba was undertaken for extraction of demographic data, case presentation, risk factors, comorbidities, diagnostic testing performed, treatment received, and outcomes. Descriptive statistical analyses were performed using R statistical software.

RESULTS: Of the 102 isolates identified, chart information was available for 79 cases, with exclusions occurring secondary to duplicate isolates within one case or inaccessibility of data. Over 30% of cases had prior STBBI diagnoses, and half used substances including intravenous drugs. Humoral or cellular immunosuppression was not a commonly observed comorbidity. Most presented with septic arthritis. Endocarditis was an uncommon but serious clinical syndrome, associated with deaths in two of the three cases identified. A proportion of cases received surgical intervention, which did not appear to impact outcomes, including for cases of septic arthritis.

CONCLUSION: This descriptive study highlights the epidemiology of DGI in Manitoba, as well as clinical features and serious outcomes associated with DGI, which will contribute to the understanding of these infections and hypothesis generation for future study.

P130

Resurgence of syphilis: Unveiling epidemiological trends and rising cases in Alberta, Manitoba, Saskatchewan, and Canada

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OBJECTIVE: This study describes the epidemiology of new syphilis and congenital syphilis diagnosis and the control strategies in Alberta, Saskatchewan, and Manitoba compared to Canada, 1980–2022.

METHOD: This ecological study collected publicly available information related to syphilis and congenital syphilis released by the governments of Canada, Manitoba, Saskatchewan, and Alberta since 1980. We analyzed the trend of the incidence rate of infectious syphilis; the distribution of new cases by sex, age, and type of infection; and the number of congenital syphilis cases.

RESULTS: Since 1993, Canada's syphilis incidence fell below 1/100,000 population, but since 2002 it has increased, reaching 36.1/100,000 in 2022. Females accounted for 8% of infectious syphilis cases in 2016 and increased to 35% in 2022, with most cases among females aged 20–39 years. In Alberta, rates were stable until 2002, followed by a sharp increase, with the highest peak in 2022 (73.2/100,000). While syphilis has been more prevalent in males, females now account for 46.2%. In Manitoba, the number of cases has increased since 2013, reaching the highest rate in 2019 (143.2/100,000). Cases among females have risen since 2003, with females accounting for most cases over the past 2 years of review (51.9%, 2021; 56.0%, 2022). Saskatchewan's available data show a similar trend, increasing from 7.5/100,000 in 2016 to 164.2/100,000 in 2021. Congenital syphilis is rising across Canada and these provinces: in 2022, the rates per 100,000/live births were Canada—36.1; Saskatchewan—175.0; Manitoba—122.7; Alberta—69.3. Data on ethnicity, risk factors, and vulnerable populations remain unavailable. Changes in screening tools and algorithms reflect shifting epidemiology.

CONCLUSION: Canada and the three provinces are experiencing a syphilis outbreak, with unacceptable rates of congenital syphilis. Several strategies are underway. However, it is urgent to implement intersectoral and tailored strategies and actions from policymakers, public health authorities, health care professionals, and social support to mitigate this public health crisis comprehensively.

P131

Increased burden of hepatitis C (HCV) in Alberta, Saskatchewan, and Manitoba associated with syndemics of substance use, 1980–2023

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OBJECTIVE: To describe the prevalence and associated risk factors for hepatitis C infections in Alberta, Saskatchewan, and Manitoba compared to Canada between 1991 and 2023.

METHOD: This was an ecological study. Data were procured from publicly available reports from government of Alberta, Saskatchewan, Manitoba, and Canada from 1991 to 2023. Variables included the number of cases and rates of hepatitis C by year, proportions by sex (female/male), age groups, ethnicity, province, sexual orientation (gay and bisexual men who have sex with men, heterosexual), and risk factors (injection drug use, blood products, and history of incarceration).

RESULTS: The first incidence reports were in 1991 in Canada (3.3/100,000 people), 1984 in Alberta (0.6/100,000 people), 2000 in Saskatchewan, and 2002 in Manitoba. In 2021, Manitoba (42.3/100,000 people) and Saskatchewan (38.3/100,000 people) had higher rates compared to Alberta (14.7/100,000 people) and Canada (19.7/100,000 people). Males were overrepresented in HCV infections (Canada: 60.7% of infections in 2022); this trend was similar across the three provinces. From 1991 to 1995, the proportion of HCV cases was greater in individuals aged 30–39 years; from 1996 to 2022, there was a notable increase in cases among those aged 40–49 years for both sexes. Saskatchewan had the highest overall rates of hepatitis C (51.7/100,000 people), particularly among females aged 20–29 and males aged 30–39. In 2010–2013, 60% of the cases in Manitoba were in Winnipeg. In Alberta, First Nations had higher rates of HCV (126.8/100,000 people) than provincial rates (41.7/100,000 people). Injection drug use was the most common risk factor (Saskatchewan: 61% in 2012 and 54% in 2015).

CONCLUSION: HCV prevalence in Canada has declined over time. However, in Saskatchewan and Manitoba, the rates of HCV continue to be high as part of syndemics of substance use, unstable housing, and co-infections with other STBBIs. A collaborative effort in surveillance, testing, treatment, and prevention of HCV in the three provinces is necessary.

P132

Neisseria gonorrhoeae infection and antimicrobial resistance in Alberta, Saskatchewan, and Manitoba compared to Canada, 1980 to 2022

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OBJECTIVE: We aimed to describe the trends of *Neisseria gonorrhoeae (NG)* infection and antimicrobial resistance (AMR) in Alberta, Saskatchewan, and Manitoba compared to Canada from 1980 to 2022.

METHOD: This was an ecological study. Data were extracted from publicly available sexually transmitted infection reports published by the governments of Canada, Saskatchewan, Manitoba, and Alberta. Variables included the number of NG cases per year; rate per 100,000 population; proportion of diagnoses by sex, age, and ethnicity;

history of injection drug use; houselessness; and percentage of AMR strains where data were available.

RESULTS: Gonorrhea rates decreased from 1980 until the early 2000s (lowest rates of 20.0/100,000 population for Canada and Alberta and 45.0/100,000 for Manitoba and Saskatchewan). Since the 2000s, the highest rates have been reported in the 2019–2022 period (Canada: 94.31/100,000, Alberta: 122.0/100,000, Saskatchewan: 271.9/100,000, and Manitoba: 272.7/100,000). Manitoba and Saskatchewan reported the highest rates in Canada over time. Males account for 60% of cases in Canada and approximately 50% in Alberta. However, in Saskatchewan and Manitoba, females represented 60% of cases. Province-specific data by age and ethnicity were not usually reported. AMR data were scarce in provincial reports, but Alberta and Manitoba participate in national surveillance. National reports found 0.61% of isolates exhibited decreased susceptibility to ceftriaxone in 2021, decreasing since the early 2010s. In contrast, the percentage of isolates with azithromycin MIC at the susceptibility breakpoint (1 mg/L) rose to 28.1% in 2021.

CONCLUSION: Since the early 2000s, NG diagnoses have increased four- to sixfold in Alberta, Saskatchewan, and Manitoba. Key sex differences exist between the prairie provinces and the rest of Canada. NG-AMR also varied across Canada and by province. The lack of standardized data collection and reporting limits the ability to adjust management guidelines based on local resistance rates and the ability to tailor public health strategies for key populations with the highest rates of infection.

P133

Trends in the incidence of Chlamydia in Alberta, Saskatchewan, and Manitoba compared to Canada, 1991–2022

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OBJECTIVE: To identify the trends in *Chlamydia trachomatis* infection in Alberta, Saskatchewan, and Manitoba compared to Canada from 1991 to 2022, and provincial variations over time.

METHOD: This was an ecological study. Data were procured from publicly available Chlamydia reports published by the governments of Alberta, Saskatchewan, Manitoba, and Canada from the first reported Chlamydia diagnoses to the latest available information. Variables included the rate per 100,000 inhabitants, proportion of diagnoses by sex (female/male), age, and ethnicity, by province. We report Chlamydia incidence by sex, age, and ethnicity annually where data are available.

RESULTS: Chlamydia became a nationally notifiable infection in 1990. The first Canadian report was published in 1991 (164.0 cases/100,000 population). The national Chlamydia rate dropped through the 1990s, reaching a low in 1997 (112.7 cases/100,000 population), but has shown increasing trends over time, with the highest rates from 2013 to 2019 (Canada: 335.1/100,000, Saskatchewan: 534.6/100,000, Manitoba: 402.7/100,000, Alberta: 399.9/100,000). Canada and the three provinces reported similar distribution by sex, with the highest proportion in females (60%) compared to males (40%). Over the past 20 years, Canada has reported the highest proportion of Chlamydia cases among individuals aged 20–29 years (54.4%). Data for Alberta, Saskatchewan, and Manitoba were not consistently reported by age. In Manitoba and Alberta during 2002–2003, Chlamydia was more frequently reported among non-Indigenous people (Manitoba: 69.7%, Alberta: 79.1%), while in Canada and Saskatchewan there are no reports available.

CONCLUSION: Chlamydia incidence steadily increased over the past decade, with Saskatchewan and Manitoba reporting the highest rates in Canada. Reports describe minimal information. The lack of standardized data

collection and reporting limits the ability to tailor public health measures to key populations with the highest burden of disease but does underscore the urgent need for intensified public health responses among females and young people (most affected groups) from national and provincial governments to halt the rising Chlamydia incidence.

P134

M. genitalium infections and associated antimicrobial resistance in six Canadian provinces, 1980–2022

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OBJECTIVE: To describe the trends in *M. genitalium* (*M. gen*) prevalence and associated resistance in six Canadian provinces between 1980 and 2022.

METHOD: This was an ecological study combined with a scoping review. Data sources included publicly available data published by the governments of Alberta, Saskatchewan, Manitoba, Quebec, British Columbia, and Ontario, as well as Medline database and grey literature using the search ("mycoplasma genitalium" AND (Canada). Variables included prevalence, age, sex, gender, symptoms, coinfections, samples used for diagnosis, and resistance rate to macrolides and fluoroquinolones. Where available, the prevalence of *M. gen* was provided over time by described variables.

RESULTS: We identified no Canadian national or provincial surveillance system. A literature search identified seven studies on *M. gen* epidemiology in Canada. The overall *M. gen* prevalence ranged from 4.4% to 30.0% with variation by provinces: Alberta (6.2%–7.4%), Saskatchewan (9.6%–20%), Manitoba (16%), Quebec (3%), British Columbia (11%–15.3%), and Ontario (4%–30%). Females' age range was 15–46 years, and for males it was 9–74 years. Two studies, including men who have sex with men, reported a higher prevalence than in heterosexual men (6.6%–7% versus 4.7%, respectively). Approximately half of the patients reported symptoms. Co-infection with *Chlamydia trachomatis* was higher than with *Neisseria gonorrhoeae* (4%–19.4% versus 5%–8%, respectively). The rate of ML resistance mutations was higher than FQ resistance (up to 82% versus up to 29%, respectively). The most collected specimens were urine, followed by cervical and urethral swabs.

CONCLUSION: *M. gen* prevalence and resistance profiles vary across Canada, differing by geographic area, tested population, and a high proportion of cases reporting ML and FQ resistance. Canadian guidelines recommend testing for *M. gen* only when concurrent infection with gonorrhea and chlamydia has been ruled out and continue to recommend ML as first-line therapy for suspected *M. gen* infections. In the absence of routine surveillance, incomplete data hinder understanding the bacterium's natural history, its impact on some key groups, the geographical tracking of resistance strains, and treatment patterns in Canada.

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Preliminary evaluation of decentralized rapid syphilis and HIV testing at seven acute care facilities in a western Canadian province after 14 months of implementation

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OBJECTIVE: To determine test volumes, performance, and result turnaround time (TAT) after implementation of on-site rapid syphilis and HIV testing (RSHT) at seven acute care facilities in a western Canadian province, serving populations with high rates of infectious syphilis infections.

METHOD: Commencing October 2023, RSHT was implemented at seven acute care sites using the INSTI Multiplex HIV-1/2 Syphilis test (bioLytical Laboratories). Specific ordering tools were built in Connect Care, a provincial health information system. Testing could only be ordered when there was no previous positive syphilis result. Two sera were collected, one for the RSHT performed at the onsite laboratory, the other for standard serologies referred to the Public Health Laboratory. Syphilis treatment was offered based on a positive syphilis rapid test.

RESULTS: After 14 months, 1,662 rapid tests and corresponding standard syphilis and HIV serologies were completed from 909 females (54.6%), of whom 329 (36.2%) were pregnant. Numbers of tests varied by site, one site performing 73% of all tests, attributable to the embedding of an STI nurse in the emergency department. Eighty-five rapid syphilis tests confirmed positive (5.1%), with eight (2.4%) from pregnant females. Eleven false-negative and three false-positive tests were later identified by standard syphilis serology. False-negative samples had either no RPR titre or titre of ≤1:2 dilutions. Sensitivity, specificity, PPV, and NPV were 88.5%, 99.8%, 96.6%, and 99.3%, respectively. Ten of 18 HIV-positive rapid tests were confirmed by standard serology yielding PPV (55.6%) and NPV (100%); one was a new HIV infection. Between 35% to 95% of all sites reported a RSHT result within 60 minutes, and by 90 minutes, 75% to 100% of results were reported.

CONCLUSION: On-site RSHT offers the opportunity for decentralized syphilis testing, creating opportunistic access to testing and treatment in key populations, especially pregnant persons.

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Preliminary data on the detection of rubella-memory T-cells: ELISpot assay versus flow cytometry

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OBJECTIVE: This work aims to determine the T-cell cellular-mediated immune (CMI) response in prenatal vaccinated population for rubella virus, thus validating and developing a CMI assay as the first step to achieve our main goal.

METHOD: Peripheral blood mononuclear cells (PBMC) were incubated with rubella virus (RuV) (1:10 viral dilution [VD]) for 24 hours. For flow cytometry ($n = 2$), CFSE-labelled memory CD4 and CD8 T-cells were mixed with infected PBMC, collected on days 4–8 post-infection, and analyzed by fluorescence-activated cell sorting (FACS). For ELISpot ($n = 1$), various conditions (neat, enriched, depleted CD4/CD8, and VDs 1:2–1:8) were assayed in quadruplicates at different cell concentrations (1×10^5–4×10^5 cells/100 μL) and enrichment percentages (10%–50%). Cells were infected and incubated for 4 days and subsequently added to the ELISpot plate. Plates were incubated and analyzed as per manufacturer instructions (CTL company, Fluorospot).

RESULTS: Our preliminary results show that by flow cytometry, one out of two vaccinated subjects showed a proliferative response, particularly in the CD8 T-cell population, prompting investigation of CD8 functionality (granzyme B [GrB] secretion). ELISpot analysis detected IFNγ, TNF-α, IL-2, and GrB, with polyfunctional T cells with different cytokine profiles (mainly IFNγ, TNF-α, and GrB) observed in multiple wells. The 1:2 RuV dilution outperformed the 1:10 dilution for cytokine detection and provided optimal cytokine detection. Both PBMCs and enriched conditions secreted similar cytokines, suggesting that enrichment may not be essential for assay success.

CONCLUSION: While flow cytometry detected some proliferation, it lacked sensitivity for reliably identifying rubella-memory T-cells and required a high PBMC count

($>10^6$ cells/mL). In contrast, ELISpot effectively detected rubella-specific memory T-cells and their functionality with fewer cells (10^5 cells/100 μL). However, further optimization is needed to confirm the assay's performance and establish optimal conditions across different donors.

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Acute human immunodeficiency virus confirmation using reflex viral load testing on sera

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OBJECTIVE: In Nova Scotia, HIV serology uses a fourth-generation chemiluminescent microparticle immunoassay (CMIA) for HIV-1 p24 antigen and HIV-1/2 antibody detection, followed by an HIV-1/2 immunoblot for antibody confirmation. In CMIA(+)/immunoblot(−) cases, p24 antigen testing is referred out to assess the possibility of acute HIV; results can take weeks. To expedite acute HIV detection, this study evaluated whether HIV RNA detection locally on serum could replace p24 testing.

METHOD: The ARCHITECT HIV Ag/Ab Combo and BioRad Geenius HIV-1/2 assay were used for CMIA and immunoblot. The National Laboratory for HIV Reference Services Testing performed p24 antigen testing. For RNA detection, the Roche cobas HIV-1 Quantitative Assay was used. Serum and plasma viral loads were initially compared in 44 CMIA(+)/immunoblot(+) patients. Then, sera showing CMIA(+)/immunoblot(−) or CMIA(+)/immunoblot-indeterminate results following routine diagnostic testing were subjected to p24 testing and serum viral loads. These results were compared to a paired plasma viral load and follow-up serology.

RESULTS: Paired serum and plasma viral loads in CMIA(+)/immunoblot(+) patients showed excellent correlation ($R^2 = 0.9956$) spanning 10^1 to 10^8 IU/ml. In routine diagnostic testing, nine CMIA(+)/immunoblot(−) cases had high-level RNA in both serum and plasma. Of these cases, eight were p24 antigen positive; all seroconverted. In the two CMIA+/immunoblot-indeterminate cases, neither were p24 positive. One patient eventually seroconverted, and both serum and plasma samples had low-level RNA at 343 and 61 IU/ml. In the second case, the patient never seroconverted, and the plasma viral load was negative; low-level RNA (64 IU/ml) was detected in the serum, which was deemed a false positive.

CONCLUSION: Reflex HIV-1 viral loads on sera is effective for rapid confirmation of acute HIV infection. However, low-level detections (<1000 IU/ml) should be confirmed with repeat serology and plasma viral loads to avoid false positives.