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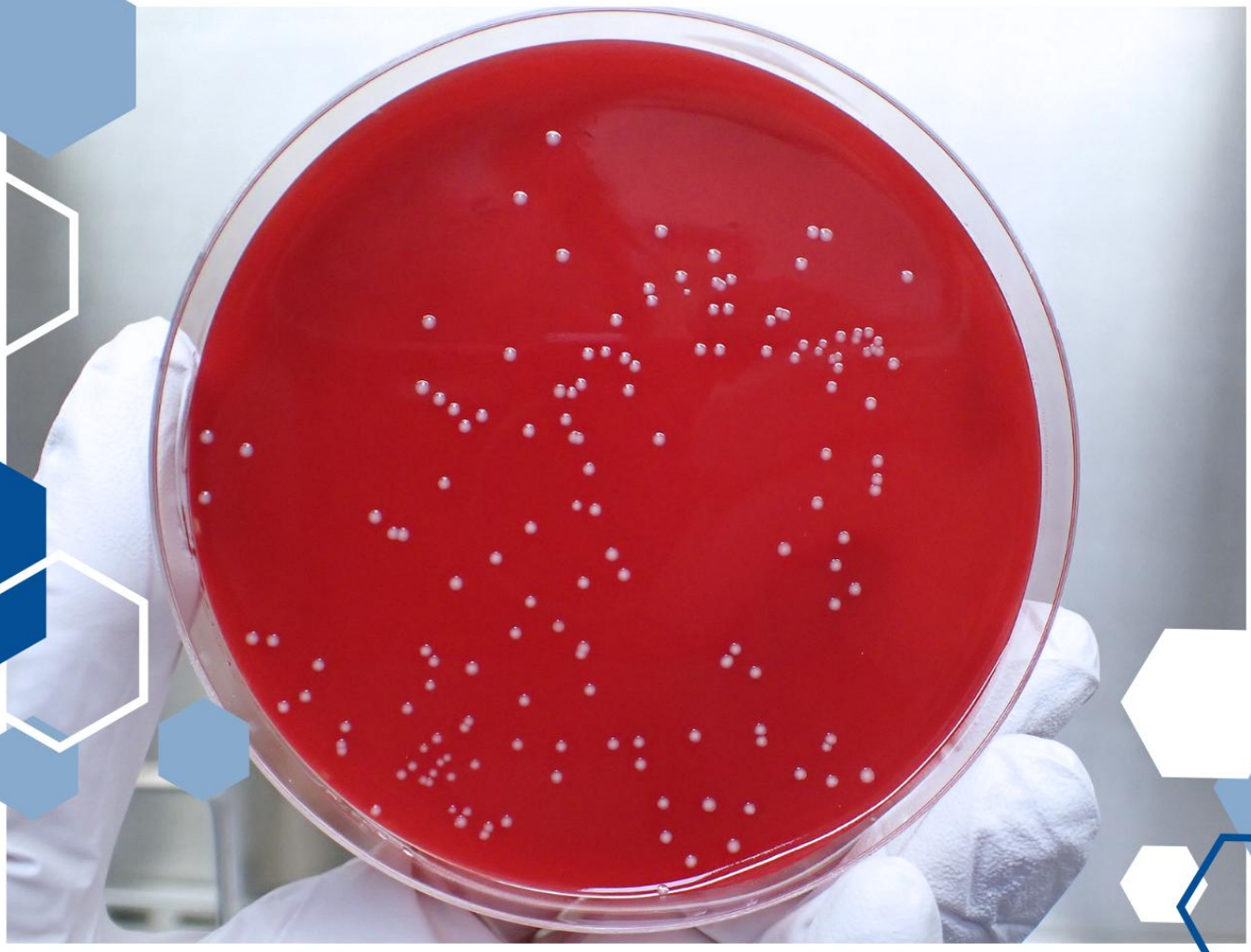

INFECTIOUS DISEASES RESEARCH DAY & CANADIAN CENTER FOR VACCINOLOGY SYMPOSIUM

HANDBOOK

March 31, 2026

CO-DEVELOPED BY

Canadian Center for Vaccinology (CCfV)

Dalhousie University Division of Infectious Diseases, Department of Pediatrics, and Department of Medicine

Nova Scotia Health Division of Infectious Diseases

ACCREDITATIONS

This activity meets the certification criteria of the **College of Family Physicians of Canada** and has been certified by Dalhousie University Continuing Professional Development and Medical Education for up to **5.5 Mainpro+** ® Certified Activity credits.

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Educationally approved by *Dalhousie University Continuing Professional Development and Dalhousie University Medical Education.*

Front Cover: *B. pertussis on blood agar (2025). Canadian Center for Vaccinology Lab Team.*

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Glenn Patriquin

MD, MSc, FRCP

Associate Professor, Dalhousie University
Microbiology and Infectious Diseases, Nova Scotia Health

Scott Halperin

MD, FRCPC

Director, Canadian Center for Vaccinology
Professor, Dalhousie University

Welcome to the Infectious Diseases Research Day and CCfV Symposium for 2026.

This annual event provides a unique learning opportunity for researchers, trainees, public health professionals, healthcare providers, and community members featuring experienced presenters, and inspiring research trainees. We are excited to learn from our invited speakers, and to showcase some of the incredible work done by local researchers and clinicians in the fields of infectious diseases, vaccinology, and beyond. Our aim is to identify our research strengths and to foster research collaborations.

We acknowledge that we are in Mi'kma'ki, the ancestral and unceded territory of the Mi'kmaq People. We have considered Equity, Diversity, Inclusivity, and Accessibility (EDIA) as an important aspect of our event's program.

Welcome and thank you for joining us!

The Infectious Diseases Research Day/CCfV Symposium is an important annual platform that allows local researchers to present their work and learn about the work of their colleagues. We encourage everyone to take part in this one-day event that will feature interesting topics surrounding infectious diseases. One of the great aspects of this event is that it gives researchers at different stages in their careers the opportunity to learn about the work of their colleagues, and I encourage everyone to make the most of this educational experience.

I would like to offer my sincerest thanks to our planning committee and the financial support from our corporate sponsors. This event would not be possible without the dedicated work and continued support from these individuals.

31st Annual Infectious Diseases Research Day & 18th Annual Canadian Center for Vaccinology Symposium

Tuesday, March 31st, 2026 | Lord Nelson Hotel, Halifax

7:15-8:00am	**Registration**	
7:30-8:00am	**Continental Breakfast**	
8:00-9:00am	**Introduction** – Dr. Paul Bonnar **TJ Marrie Lecture** – Dr. John Kim *Testing is easy – relationship building is the hard part: Dried Blood Spot (DBS) testing in Canada* **Q&A session (10-15 min)**	Imperial Ballroom/Zoom
9:00-9:15am	**Opening remarks, Introductions** – Drs. Patriquin, Bonnar, Halperin	Imperial Ballroom
9:15–10:30pm	**Oral Presentations (5)** **Q&A Session (5 min/presentation, 25 min total)**	Imperial Ballroom
10:30-10:45	**Nutrition Break**	
10:45–12:00pm	**Oral Presentations (5)** **Q&A session (5 min/presentation, 25 min total)**	Imperial Ballroom
12:00–1:00pm	**Lunch**	
1:00–2:00pm	**Poster judging** *(posters available for viewing 8:00am – 4:00pm)*	Regency Ballroom

2:00–3:00pm	**Introduction** – Dr. Tobi Kollmann IWK Plenary Speaker **Presentation** – Dr. Kyla Hildebrand *Precision Host Defense: Inborn Errors of Immunity in Invasive Pneumococcal Disease* **Q&A session (10-15 min)**	Imperial Ballroom
3:00-3:15	**Nutrition Break**	
3:15–3:45pm	**Introduction** – Dr. Craig McCormick **Presentation** – Dr. Amy Gillgrass *Investigating immune responses in infectious disease and vaccination using next-generation humanized mouse models* **Q&A session (10-15 min)**	Imperial Ballroom
3:45-4:15pm	**Introduction** – Shannen Grandy **Presentation** – Dr. Karen Lithgow *The Vaginal Microbiome in Health & Disease* **Q&A session (10-15 min)**	Imperial Ballroom
4:15-4:45pm	**Awards Presentations** **Closing Remarks** – Dr. Glenn Patriquin	Imperial Ballroom

After this program, participants will be able to:

Review and discuss local research findings in microbiology, immunology, infectious diseases, and vaccinology. *(CanMEDS roles: scholar, medical expert, professional)*

Collaborate with the other departments and disciplines by being introduced to local areas of expertise. *(CanMEDS roles: medical expert, collaborator, health advocate)*

Educationally approved by Dalhousie University Continuing Professional Development and Medical Education (CPDME).

2026 Speakers

TJ Marrie Lecturer

Dr. John Kim

Dr. John Kim is Chief of the NML's National HIV/AIDS Laboratories located at the JC Wilt Infectious Diseases Center in Winnipeg, MB. Their work involves national reference testing for HIV and HTLV, quality management, and novel technologies to expand access to testing such as Dried Blood Spot (DBS) testing in Indigenous communities. Dr. Kim and his team have applied DBS technology for serology testing to determine past infections to diseases such as the virus that causes COVID-19. The team has also participated in multiple studies measuring antibodies in populations such as people in long-term care homes, teachers, correctional services, 2SLGBTQ+ populations and pregnant persons.

Keynote Speaker

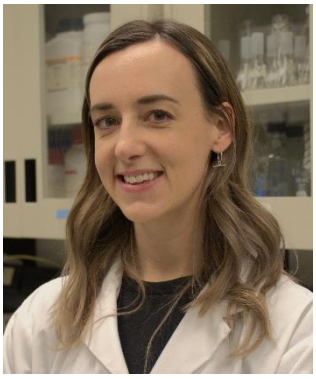
Dr. Kyla Hildebrand

Dr. Kyla Hildebrand is a Pediatric Clinical Immunology and Allergy specialist, Clinical Associate Professor and clinician educator at BC Children's Hospital, Department of Pediatrics, University of British Columbia in Vancouver, Canada. She is a clinical investigator at the BC Children's Hospital Research Institute and the Head of the Division of Immunology. Dr. Hildebrand's scholarly work focuses on the areas of immunization including adverse events following immunization, inborn errors of immunity and implementation of intrinsic CanMEDS roles in postgraduate medical education. She is a voting member on the National Advisory Committee for Immunization since 2018 and the Chair of the NACI Pneumococcal Vaccine Working Groups. Dr. Hildebrand has been recognized for excellence in teaching and medical education with several national awards including the Canadian Association for Medical Education Award of Merit and the Royal College of Physicians and Surgeons of Canada AMS Donald Richards Wilson Award for CanMEDS Integration.

Local Speakers

Dr. Amy Gillgrass

Since 2025, Dr. Amy Gillgrass has been an Assistant Professor in the Department of Microbiology and Immunology at Dalhousie University. She came to Halifax from McMaster University. Dr. Gillgrass' research is focused on utilizing next-generation humanized mouse models to investigate infectious disease and cancer. Using these mice, Dr. Gillgrass' lab has established models of HIV, TB and HIV/TB co-infection to explore pathogenesis, therapeutics and vaccination in the context of human immune cells. In addition, they are using these mice to test novel cancer immunotherapeutics. Based on the innovative nature of her program, Dr. Gillgrass has received the E.J. Moran Campbell Early Research Award and the Bhagirath Singh Early Career Award in Infection and Immunity from CIHR.



Dr. Karen Lithgow

Dr. Karen Lithgow is an Assistant Professor in the Dept of Microbiology & Immunology at Dalhousie University. Dr. Lithgow completed her PhD studying syphilis pathogenesis at the University of Victoria and conducted a postdoctoral fellowship at the University of Calgary investigating the vaginal microbiome. Dr. Lithgow's research program investigates host-microbe interactions in the female genital tract with a specific focus on the molecular mechanisms used by bacteria to trigger pregnancy complications and increase endocervical susceptibility to sexually transmitted infections (STIs).

PRESENTATION NOTES

Dr. John Kim

Presentation Title

Testing is easy, relationship building is the hard part: Dried Blood Spot (DBS) testing in Canada

Presentation Objectives

At the conclusion of this activity, participants will be able to:

1. **Describe** DBS as it compares to traditional blood testing *(CanMEDS roles: health advocate)*
2. **Summarize** the applications of DBS in Canada *(CanMEDS roles: leader, scholar)*
3. **Describe** the status of DBS in Canada *(CanMEDS roles: medical expert, health advocate)*

Notes

Please take the time to provide feedback on this presentation at the end of the day at ***bit.ly/IDDayEval2026***

PRESENTATION NOTES

Dr. Kyla Hildebrand

Presentation Title

Precision Host Defense: Inborn Errors of Immunity in Invasive Pneumococcal Disease

Presentation Objectives

At the conclusion of this activity, participants will be able to:

1. **Summarize** the prevalence and types of inborn errors of immunity identified in patients with invasive pneumococcal disease *(CanMEDS roles: medical expert, communicator)*
2. **Select** appropriate immunologic investigations for patients presenting with IPD to detect underlying immune defects *(CanMEDS roles: medical expert, health advocate)*
3. **Implement** immunization strategies tailored to individuals with inborn errors of immunity *(CanMEDS roles: medical expert, health advocate)*

Notes

Please take the time to provide feedback on this presentation at the end of the day at ***bit.ly/IDDayEval2026***

PRESENTATION NOTES

Dr. Amy Gillgrass

Presentation Title

Investigating immune responses in infectious disease and vaccination using next-generation humanized mouse models

Presentation Objectives

At the conclusion of this activity, participants will be able to:

1. **Express** what a humanized immune system mouse is and how it can translation of basic research to the clinic *(CanMEDS roles: scholar)*
2. **Recognize** the complex interactions of HIV and TB and their effects on immune responses in the lungs *(CanMEDS roles: scholar, medical expert)*
3. **Recognize** how humanized mice can inform vaccine research and the benefits of mucosal immunization *(CanMEDS roles: collaborator, scholar)*

Notes

Please take the time to provide feedback on this presentation at the end of the day at ***bit.ly/IDDayEval2026***

PRESENTATION NOTES

Dr. Karen Lithgow

Presentation Title

The Vaginal Microbiome in Health & Disease

Presentation Objectives

At the conclusion of this activity, participants will be able to:

1. **Recognize** how the vaginal microbiome influences sexual and reproductive health *(CanMEDS roles: collaborator, scholar)*
2. **Summarize** the mechanisms used by diverse vaginal microbiota to dysregulate the female genital tract *(CanMEDS roles: medical expert, scholar)*
3. **Describe** the role of bacterial proteases in dysregulating the cervicovaginal environment and contributing to adverse health outcomes *(CanMEDS roles: medical expert, scholar)*

Notes

Please take the time to provide feedback on this presentation at the end of the day at ***bit.ly/IDDayEval2026***

Oral Presentation Schedule

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1: STI CARE NOW: SERVICE USER ACCEPTABILITY OF STI SELF-TESTING AND VIRTUAL TREATMENT ASSESSMENT

Authors: **T.D. Ramsey[1,2],** M. d'Entremont-Harris[1], C. MacAulay[1], A. Joy[1], K. Merrick[1], A. Keenan[1], T. Matheson[1], C. Heinstein[1], S.A. McNeil[1,2], T. F. Hatchette[1,2] (on behalf of the NSH Emerging and Re-emerging Infections Network)

Affiliation: [1]Nova Scotia Health, [2]Dalhousie University

Introduction: Chlamydia and gonorrhea are the two most prevalent bacterial sexually transmitted infections (STIs) in Nova Scotia (NS), and new human immunodeficiency virus (HIV) infections are diagnosed every year. Accessible and acceptable prevention, testing, and treatment services are essential to prevent transmission and manage infections. STI Care Now is a centralized NS Health service that offers chlamydia and gonorrhea self-testing and treatment, and HIV self-screening. Testing is requested through an online webform, and kits are mailed out or picked up at participating high schools or community-based organizations.

Methods: STI Care Now service users were invited to complete a questionnaire about their experiences. Questions focused on satisfaction, including Likert-style questions with optional fields for free-text responses. Data were collected from September 20, 2024 to February 13, 2026. Descriptive statistics were used to quantify satisfaction and supporting quotes were drawn from free-text fields.

Results: Of the 3229 individuals who received results, 2377 responded to one or more survey questions, representing a 55% response rate. Overall, 97% of respondents reported satisfaction with self-testing for chlamydia, gonorrhea, and/or HIV, and would recommend STI Care Now to a friend. Most did not face stigma or discrimination when accessing the service (92%), did not fear that using the service would damage their relationship with other health care providers (92%), and found the time from testing to result receipt was acceptable (94%).

One hundred and nine-six respondents (8%) had a virtual treatment assessment with a pharmacist. Of those, upwards of 95% felt satisfied with the assessment, the care was accessible, and the availability of virtual assessments helps their community. One service user indicated: "The pharmacist during my phone assessment was amazing. The stress of discussing such personal details disappeared as I was so at ease and it was a comforting and normal conversation without any stigma."

Conclusions: Overall, respondents were very satisfied with their experience accessing services from STI Care Now. Future evaluation to understand STI Care Now service user experience with HIV self-testing and prophylactic assessments and opportunities for improvement is warranted.

2: NK CELL MEMORY-LIKE FUNCTIONAL ACTIVITY PREDICTS PROTECTION AGAINST BORDETELLA PERTUSSIS CHALLENGE IN A CONTROLLED HUMAN INFECTION MODEL

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Introduction: Despite high vaccine coverage, pertussis (whooping cough) remains a significant public health concern worldwide. Understanding the complex interactions between Bordetella pertussis, the causative agent of this disease, and human immunity is essential for advancing disease prevention strategies. Controlled human infection models (CHIMs) offer a powerful platform to dissect disease pathogenesis and characterize immune responses, findings that may facilitate the rational design of improved vaccines.

Methods: This open-label, phase 1, dose-escalation trial was conducted at the Canadian Center for Vaccinology (Nova Scotia, Canada). Healthy participants aged 18-40 years of age with different biological sex at birth and infant vaccination (wP vs aP) history were intranasally inoculated with escalating doses of the pertactin-producing B. pertussis isolate D420. Various biological specimens (blood, nasopharyngeal aspirate, and nasal wash) were collected the day before and at multiple time points after challenge.

Results: Despite a dose-dependent increase in the frequency of symptomatic participants, 20% participants were classified as non-infected. The non-infected status was defined by the absence of detectable bacterial colonization and clinic symptoms, displaying a lack of anti-pertussis antibody induction. B pertussis elicited distinct complement activation profiles, characterized by rapid engagement of the lectin pathway in non-infected participants and sustained activation of classic pathway in symptomatic individuals. B. pertussis also induced NK cell expansion in both non-infected and symptomatic groups; however, NK cells from non-infected participants displayed enhanced memory-like responses ex vivo, producing higher levels of perforin, granzyme B, and IFN-γ upon stimulation with heat-killed bacteria.

Conclusions: This study provides the first evidence that distinct innate immune signatures are directly link to clinical outcomes following B. pertussis challenge.

3: AN EXERCISE IN BALANCE: OPTIMIZATION OF PERSONAL PROTECTIVE EQUIPMENT USAGE AS PART OF A GREENING INITIATIVE ON AN INPATIENT HOSPITAL UNIT

Authors: **Katherine LeBlanc[1],** Nabha Shetty[1], Melissa Pettis[1], Mark Downing[1]

Affiliation: [1]Division of Infectious Diseases, Department of Medicine, Dalhousie University

Introduction: Healthcare activities represent 4.4% of global greenhouse gas emissions, and institutions are looking for ways to reduce their impact on climate change. The goal of this project is to reduce inappropriate PPE use without an increase in nosocomial infections. A local pilot project in 2023 trialed reuseable gowns but was discontinued due to concerns over contamination and barriers related to sourcing; disposable gowns have been used since.

Methods: An initial audit of current PPE use was performed on unit 8.2 at the HI to determine baseline use rates and adherence to correct donning and doffing procedure. A review of processes related to initiating and discontinuing additional precautions was also undertaken through interviews with frontline staff. The intervention will consist of enhanced audit, feedback, education and training with healthcare workers with involvement of IPAC staff. Reassessment with repeat audits will measure the effectiveness of interventions. Lead measures include proportion of staff adherence to appropriate PPE (with correct donning and doffing procedures), and correct duration and communication of precautions based on IPAC guidelines. Lag measure is the amount of PPE used, measured using purchasing data. Balancing measures are nosocomial transmission rates for MRSA, VRE, and CPO, and new and ongoing ARO outbreaks.

Results: The initial audit revealed opportunities to reduce inappropriate PPE use, particularly glove use where it was noted that 94% of healthcare workers wore gloves during interactions with patients regardless of whether they were indicated. There were also inconsistencies in procedures around communicating isolation precautions to staff, patients, and visitors, as well as systems level issues resulting in precautions remaining active for longer than necessary.

Conclusions: To date, the audit has revealed factors driving inappropriate PPE use that can be optimized. These include lack of EMR, inconsistent signage, and communication barriers between IPAC and patient care teams. Glove use is ubiquitous on the unit, and educating staff around a point of care risk assessment prior to donning gloves may help reduce glove usage. This pilot will help inform a provincial glove use reduction campaign being planned by the Nova Scotia Health IPAC program.

4: HIGH BURDEN OF PEDIATRIC MPOX HOSPITALIZATIONS DURING A MPOX VIRUS SUBCLADE IB OUTBREAK IN EASTERN DEMOCRATIC REPUBLIC OF THE CONGO.

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Introduction: Mpox is a public health concern in DR Congo as it causes substantial numbers of hospitalizations. Here, we aim to describe the clinical presentation of hospitalized participants infected with monkeypox virus (MPXV) subclade Ib/2023sh in Lwiro, DR Congo.

Methods: In this observational cohort study, patients admitted with suspect mpox infection were recruited if, during admission, they had skin lesions compatible with mpox. Patients without lesions that had contact with a suspect case of mpox infection in the last 21 days and had one of the symptoms: fever, cervical lymphadenopathy, or pharyngitis, were also recruited.

Results: MPXV subclade Ib/2023sh was detected in 494 (77%) of 643 participants with a median age of 9. A higher proportion of female (290 [59%]) participants tested positive for DNA presence of MPXV subclade Ib/2023sh and were older (median 16 years) than male participants (median age 4 years). 300 (61%) of 494 participants were aged ≤15 years. Fever (90%), skin lesion/rash (79%), and dysphagia (56%) were the most prevalent symptoms. 117 (24%) participants had lesions in the oral cavity. Oral swabs rendered detectable MPXV subclade Ib/2023sh DNA in the absence of assayable skin lesions.

Conclusions: Given the higher proportion of children and adolescents aged ≤15 years, we hypothesize a demographic shift in the target population that contributes to the community spread of mpox in the South Kivu region of DR Congo. Targeted public health measures should consider ways for reducing transmission among children and adolescents.

5: COMPARTMENT-SPECIFIC ALTERATIONS IN T-CELL COSTIMULATORY PHENOTYPES IN CYSTIC FIBROSIS

Authors: **Briley Hillyard**[1], Anjali Bhagirath[1]

Affiliation: [1]Dalhousie University

Introduction: Cystic fibrosis (CF) is characterized by chronic airway infection and sustained immune activation, providing a model of persistent antigen exposure. Chronic infection is known to drive differentiation of cytotoxic T-cell states, including loss of the costimulatory receptor CD28. However, how CD28-associated T-cell phenotypes are distributed across tissue and peripheral blood in CF remains incompletely characterized.

Methods: Multiplex OPAL TSA immunofluorescence was performed on lung and spleen tissues from 10-week-old CF and wild-type (WT) mice (n=3/genotype), staining for CD3, CD4, CD8, CD28, and DAPI. $CD3^+CD4^+CD28^+$ and $CD3^+CD8^+CD28^+$ cells were quantified using object-based colocalization across standardized regions of interest. In parallel, peripheral blood mononuclear cells from CF and healthy human donors were analyzed by flow cytometry to determine the proportion of $CD28^-$ cells within $CD4^+$ and $CD8^+$ T-cell compartments. Independent cohorts were analyzed descriptively.

Results: CF mouse lung and spleen tissues demonstrated increased lymphocyte presence with higher densities of CD28-expressing $CD4^+$ and $CD8^+$ T cells compared with WT controls. Quantitative imaging analysis showed increased counts of $CD3^+CD4^+CD28^+$ and $CD3^+CD8^+CD28^+$ cells in CF tissues. In peripheral blood, CF donors exhibited higher proportions of $CD28^-$ T cells relative to healthy controls, most prominently within the $CD8^+$ compartment. These patterns were observed across independent cohorts, including CF individuals receiving highly effective modulator therapy.

Conclusions: This proof-of-concept analysis identifies compartment-specific alterations in T-cell costimulatory phenotypes in CF, with accumulation of CD28-expressing T cells in tissue and expansion of $CD28^-$ subsets in circulation. These findings are consistent with chronic infection-associated T-cell remodeling and support further investigation of adaptive immune dysfunction in CF.

6: DEVELOPING A DIGITAL DASHBOARD FOR SURVEILLANCE OF ANTIMICROBIAL USE

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Introduction: Limited regional data on antimicrobial use (AMU) linked to indication is available to guide antimicrobial stewardship (AMS) initiatives in community settings. The objectives of this study are to 1) develop an efficient and sustainable antimicrobial surveillance dashboard that encourages appropriate use, 2) evaluate uptake and utility of the dashboard, and 3) to determine user preferences for visualization of antimicrobial use (AMU) data.

Methods: Development of the AMU dashboard used a participatory-design framework. Initial content and visualization were developed by a multidisciplinary team of clinicians, researchers, and patient partners through virtual meetings and an in-person workshop. Interactive visual analytics to display AMU data with ability to filter by region, indication, setting, and individual patient and prescriber characteristics were incorporated into the prototype. Interviews were then completed with additional key informants (clinicians and decision makers) in the province to validate design of the dashboard. Interview transcripts were coded and data was analyzed using thematic analysis.

Results: This study developed an interactive, public- and provider-facing dashboard with AMU data visualizations to highlight multiple dimensions of AMU in the province. Eight key informants with perspectives from infectious diseases, pharmacy, emergency medicine, primary care, and public health provided feedback between May – August 2025. “Building a culture of wise AMU” was a predominant theme with many comments on the value of the dashboard, particularly to inform future antimicrobial stewardship (AMS) initiatives. “Getting buy in and improving uptake” was also identified, suggesting improvements to increase use of the dashboard. Increased tailoring by user type and individual interest was extensively discussed. Interpretation of data, links to reputable resources, and embedded targets to guide appropriate prescribing were also suggested as opportunities to improve clinician uptake.

Conclusions: A digital dashboard reporting on AMU allows targeting improved community-based AMS efforts. The dashboard may also inform decisions on antimicrobial prescribing. After incorporating feedback from this qualitative study, the dashboard will be updated and undergo further usability studies.

7: BACTERIAL ACTIVATION OF PROTEINASE-ACTIVATED RECEPTORS (PARs) AS A TRIGGER OF INFECTION-INDUCED PRETERM LABOUR (PTL)

Authors: **Lauren Over[1],** Kristyna Blazkova[2], Matthew Bogyo[2], Karen V. Lithgow[1]

Affiliation: [1]Department of Microbiology & Immunology, Dalhousie University, [2]Departments of Pathology and Microbiology & Immunology, Stanford University, USA

Introduction: Preterm birth (<37 weeks) is the primary cause of neonatal mortality, affecting over 15 million pregnancies each year. Up to 60% of preterm labour (PTL) cases arise from uterine bacterial infection, often due to ascension

of dysbiotic vaginal microbiota including Prevotella bivia. However, the mechanisms by which these bacteria contribute to PTL initiation remain unknown. Labour pathways can be triggered by the activation of uterine proteinase-activated receptors (PARs). Select human proteases can cleave the PAR extracellular domain, exposing a tethered ligand that binds back to the receptor to initiate signaling pathways. In pregnancy, uterine PAR signaling can trigger inflammatory and contractile labour cascades. Our previous work shows P. bivia possesses proteolytic activity that degrades collagen and elastin; structural components of pregnancy tissues that are remodeled during labour. In this study, we investigate whether P. bivia proteases also contribute to labour initiation by activating human PARs.

Methods: PAR proteolysis was assessed with fluorometric protease assays using sequential fluorophore-quenched (FQ) peptides corresponding to the extracellular domain sequences of PAR1 and PAR2. Pooled FQ PAR peptides were incubated with P. bivia cell-free supernatants in kinetic assays to screen for secreted protease activity targeting PAR1 or PAR2. Protease inhibitors targeting metallo-, cysteine, and serine proteases were included in the assay to confirm the protease class conferring the observed activity.

Results: Cell-free supernatants from P. bivia proteolyzed the PAR1 and PAR2 FQ peptide pools, indicated by an increase in fluorescence over time. The metalloprotease inhibitor, 1,10-phenanthroline, abrogated PAR1 and PAR2 proteolyzing activity from P. bivia cell-free supernatants, confirming that secreted metalloproteases are conferring the PAR-proteolyzing activity.

Conclusions: Our findings reveal that P. bivia-secreted metalloproteases proteolyze peptides corresponding to the extracellular domains of PAR1 and PAR2. Bacterial targeting and activation of uterine PARs would be a novel mechanism by which dysbiotic vaginal bacteria could contribute to premature labour initiation.

8: IMPROVING CHILDHOOD VACCINE COVERAGE AMONG PRIORITY POPULATIONS IN NOVA SCOTIA

Authors: AL. Hart[1-2], S. Siddiqui[1-2], S. Brown[1-2], H. Choudhary[1-2], M. Eydt[1-2], J. Comeau[1-3], S. Deeks[1-2,4], J. Mannette[1-2], K. McIsaac[4], S. Halperin[1-2], SJ. Moss[1-2]

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Introduction: Canada's routine childhood vaccine coverage remains below national targets despite being essential to minimizing vaccine-preventable diseases. Understanding barriers to immunization among priority groups with low uptake, identified in partnership with communities and the Nova Scotia (NS) Department of Health & Wellness, is crucial to informing vaccine coverage interventions. As a first step to improve childhood vaccine access, confidence, and uptake, the current research focuses on adapting the Childhood National Immunization Coverage Survey (CNICS) for use in NS with priority populations to collect vaccine coverage data of 2- and 7-year-old children.

Methods: A Community Project Lead and four Community Research Partners (n=5 community-based staff in total) were hired to facilitate this mixed-methods community-based participatory study. The team engaged in an iterative feedback process, including facilitated workshops and item-by-item review, to adapt the CNICS. This entailed a mix of high-level edits to improve relevance and accessibility to equity-deserving populations in NS, and question-specific edits to promote cultural and psychological safety.

Results: Iterative feedback yielded five key CNICS adaptations: (1) enhanced demographic detail, expanding sex and gender, and cultural identity options; (2) inclusion of access and stability factors, with new items on primary care access and housing; (3) expanded barrier and influence assessment to include structural and cultural factors; (4) improved methodological flow and logic; and (5) strengthened privacy protections and psychologically safe wording.

Conclusions: The adaptations to the CNICS improved cultural safety, and the ability to identify barriers among priority populations of under-immunized children from equity deserving communities across NS. Community engagement highlighted the need for a culturally safe tool, relevant to the populations and contexts it is meant to serve. Community partnerships are vital to identifying barriers and informing equitable immunization programs. Next steps include piloting the adapted CNICS with 30 participants from priority populations to assess feasibility, acceptability, and data completeness.

9: CONCOMITANT RISE OF HYPERVIRULENT M1UK AND MACROLIDE-RESISTANT EMM92 EXPLAINS RECENT INCREASES IN INVASIVE GROUP A STREPTOCOCCI ACTIVITY IN NOVA SCOTIA

Authors: **Ariela Polsky[1],** Samuel F. Hatchette[1], Nicole Paterson[1], Gregory McCracken[2], Allana Loder[3], Janice Pettipas[3], Elizabeth Simms[2,4,5], Alyssa Golden[3], Irene Martin[3], Jason J. LeBlanc[2,5]

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Introduction: Invasive group A streptococci (iGAS) infections cause significant morbidity and mortality worldwide. Following the COVID-19 pandemic, iGAS activity increased and associations were made with the rise of a hypervirulent strain called M1UK. However, M1UK only partially explained the increased iGAS activity in Nova Scotia. As macrolide resistance also increased during the post-pandemic period, this study investigated whether antibiotic resistance could also have contributed to the increased iGAS activity.

Methods: Routine susceptibility testing was performed using erythromycin (15 µg), clindamycin (2 µg), and tetracycline (30 µg) disks. A D-test was used to assess macrolide efflux (M phenotype) or constitutive or inducible resistance to macrolide/lincosamide/streptogramin B (cMLSB and iMLSB, respectively) from erythromycin ribosomal methylases. Nova Scotia iGAS isolates from years 2012 to 2025 were subjected to whole genome sequencing for emm typing, and identification of genes encoding efflux (mefA/E) or ribosomal methylases (ermB, ermTR, or ermT) conferring the M, cMLSB and iMLSB phenotypes.

Results: Macrolide resistance rose from an average of 8.3% in years 2012-2019 to 40.4% in 2025. This rise was attributed primarily to emm92 harboring a plasmid-borne ermT, which was not seen in Nova Scotia prior to 2023. Smaller contributions to iMLSB resistance stemmed primarily from ermTR in emm83, emm77, and emm58, or from ermB-mediated cMLSB in emm11. All iMLSB cases were also tetracycline resistant from presence of tetM or tetO.

Conclusions: In recent years, increased iGAS cases in Nova Scotia were associated with hypervirulent M1UK and a concomitant rise in macrolide-resistant strains like emm92. The proportions of emm92 were much higher than seen nationally, possibly suggesting clonal expansion or co-selection of resistance macrolide and tetracycline resistance genes. Interestingly, Nova Scotia does have the highest rates of doxycycline prescriptions in Canada, likely due to treatment of diseases like Lyme. Further epidemiological studies are warranted to fully understand this epidemiology.

10: THE IMPACT OF AGE AND ROUTE ON BCG SYSTEMIC DISSEMINATION AND PROTECTION FROM NEONATAL SEPSIS

Authors: **Henok Andualem[1],** Mazhar Pasha[1], Nelly Amenyogbe[1], Tobias Kollmann[1]

Affiliation: [1]Dalhousie University

Introduction: Despite the known pathogen agnostic benefits of Bacille Calmette–Guérin (BCG) vaccination in preventing neonatal sepsis, critical knowledge gaps remain that must be addressed to optimize this approach for global benefit. Remarkably, despite Calmette's discovery of rapid-onset BCG bacteremia in human newborns after oral vaccination, whether systemic dissemination is a prerequisite for pathogen-agnostic protection has remained unanswered for ~100 years. This issue has regained prominence now that systemic dissemination of BCG in adults has been shown to be essential for protection from TB. This project will determine whether BCG's ability to enter the bloodstream underlies its protective efficacy in newborns. This project will focus on neonatal sepsis as a model.

Methods: To determine age-dependent BCG systemic dissemination (bacteremia), blood was collected at 6, 12, and 24 hours post-vaccination across neonatal, juvenile, and adult mice following skin administration. We also evaluated BCG dissemination following subcutaneous and intravenous routes in adults. BCG bacteremia was quantified using ddPCR and culture. Given that BCG seeding of the bone marrow drives granulocyte colony stimulating factor (G-CSF)-mediated emergency granulopoiesis and confers protection from neonatal sepsis, G-CSF levels were measured using ultrasensitive assays and correlated with bacteremia to elucidate the mechanistic link between systemic BCG dissemination and host immune activation.

Results: Subcutaneous BCG administration resulted in bacteremia at 6 hours post-vaccination in all neonates and juveniles, but not in adults. G-CSF induction followed a sequential rather than parallel trajectory, surging at 12 hours after bacteremia onset.

Conclusions: Following vaccination, BCG spreads into the bloodstream in an age-dependent manner, rapidly occurring in neonates but not in adults. Bacteremia precedes G-CSF induction. This is the first experimental confirmation of Calmette's startling discovery. The relationship of bacteremia to protection can now be assessed in this model, including contrast of age vs route.

Poster Abstracts

(Presenter's name in **blue**)

Poster 1A

Title: STREAMLINED CONFIRMATION OF VANCOMYCIN-RESISTANT ENTEROCOCCI (VRE) FROM CHROMOGENIC MEDIA USING MALDI-TOF AND EXTRACTION-FREE PCR

Authors: **J.J. LeBlanc[1,2],** C. Oliver[1,2], D. Sahota-Leask[1,2], G.R. McCracken[1,2], C. Heinstein[1,2], J. MacDonald[1,2], A. Russell-Tattrie[1,2], R.J. Davidson[1,2], G. Patriquin[1,2]

Affiliation: [1]Division of Microbiology, Department of Pathology and Laboratory Medicine, Nova Scotia Health (NSH) [2]Department of Pathology, Dalhousie University

Introduction: Commercial PCRs are available for vancomycin-resistant enterococci (VRE) detection but are cost-prohibitive for many hospital laboratories. Nova Scotia uses a 5-day process where suspect colonies from chromogenic VRE Brilliance agar are inoculated onto blood agar, brain heart infusion agar with vancomycin (BHIV), and VanA or VanB phenotype is confirmed using vancomycin and teicoplanin E-tests. Approximately 14.9% of the monthly 2200 tests have a positive initial screen. Workload is further complicated as 81.1% of these are eventually determined to be false positive. This study evaluated an alternative algorithm for VRE confirmation from chromogenic media using MALDI-ToF and a cost-sparing PCR.

Methods: Initially, to investigate reduction in breakthrough growth on screening plates, four different chromogenic media were evaluated. Rectal swabs (in liquid Amies) were plated onto Brillance agar. Specimens that grew false-positive colonies (i.e., blue colonies that failed to grow on BHIV) were replated onto Brilliance agar, as well as ChromID VRE, Colorex VRE Blue, and Colorex VRE. The proportion of breakthrough was recorded for each media. All suspect colonies were confirmed to be E. faecium or E. faecalis by MALDI-ToF and VRE was identified by extraction-free real-time PCR targeting vanA and vanB (with a pan-16S internal control). Validation was supplemented with 160 clinical or reference isolates including 46 VRE-positive Enterococcus faecalis or E. faecium (23 VanA and 23 VanB), and various susceptible organisms from all chromogenic breakthrough events.

Results: Of 94 breakthrough events from the chromogenic media validation, 75.8% events repeated on Brilliance agar, whereas lower rates were seen for ChromID (55.8%), Colorex Blue (25.3%), and Colorex VRE media (5.3%). Extraction-free PCR accurately detected all vanA and vanB-positive isolates, and the 16S control was positive in susceptible bacteria.

Conclusions: Colorex VRE media paired with MALDI-TOF and PCR confirmation was an efficient and cost-effective approach for VRE testing in Nova Scotia.

Poster 1B

Title: HIGH THROUGHPUT ANAPLASMA PHAGOCYTOPHILUM PCR TESTING IN SERA WITH THE COBAS 6800

Authors: **J.J. LeBlanc**[1,2], D. Sarty, C. Jackson[1,2], J. MacDonald[1,2], C. Heinstein[1,2], T.F. Hatchette[1,2]

Affiliation: [1]Department of Pathology, Dalhousie University, [2]Division of Microbiology, Department of Pathology and Laboratory Medicine, Nova Scotia Health (NSH)

Introduction: Anaplasma phagocytophilum, the causative agent of human granulocytic anaplasmosis is transmitted by the same Ixodes tick that carries Borrellia burdorferi (causing Lyme disease). In Nova Scotia, hundreds of anaplasmosis cases are reported annually due to reflex PCR testing on serum samples submitted for Lyme. However, the workload associated with nucleic acid extraction, PCR testing, and reporting has become challenging with the 31,000 tests performed annually. With access to A. phagocytophilum-positive sera, this study compared our in-house PCR to a commercial tick-borne PCR panel for the detection of A. phagocytophilum, Babesia spp., Ehrlichia spp., and Borrelia spp. designed for high throughput testing on a large, automated instrument.

Methods: Preliminary method comparison was performed using a panel of 20 A. phagocytophilum-positive and 10 negative sera. Each serum (200 µl) was subjected to nucleic acid extraction on a Roche Mag96 instrument, and 5 µl was used in a real-time PCR targeting msp2 using a Taqman Fast Virus 1-step kit and an ABI7500Fast instrument. In parallel, 200 µl of each serum was tested on the Roche 6800 instrument, using the UC-TIB-Tickborne-3 panel which contains primers/probes for A. phagocytophilum msp2). Intra- and inter-run variability was assessed using low-, moderate-, and high-positive samples tested in triplicate over three days. Analytical sensitivity comparisons were performed using 10-folds serial dilutions in triplicate of a positive clinical sample into pooled negative sera. The limit of detection (LoD) was estimated and quantified relative to a standard curve generated with plasmid DNA harboring the ms2 gene.

Results: 100% correlation was seen between methods. The intra- and inter-experimental coefficients of variation ranged between 0.45%-1.02% and 0.46-1.07%. The LoD of the in-house PCR and commercial PCR were equivalent at approximately 42 and 34 copies/ml, respectively.

Conclusions: The Roche tickborne-panel provides a suitable alternative to in-house PCR testing for A. phagocytophilum on sera.

Poster 2A

Title: IS VACCINE RESEARCH, CLINICAL PRACTICE, DECISION-MAKING, AND POLICY AGEIST?

Authors: **Melissa K Andrew**[1,2], Katrina Bouzanis[3], Shelley L. Deeks[4]

Affiliation: [1]Department of Medicine (Geriatrics), Dalhousie University, [2]Canadian Center for Vaccinology (Dalhousie University, IWK Health, Nova Scotia Health), [3]International Federation on Ageing, [4]Department of Community Health and Epidemiology, Dalhousie University

Introduction: Immunization programs have traditionally prioritized childhood vaccines despite strong evidence of clinical benefit and cost-effectiveness for the growing number of adult vaccines and immunization programs.

Objective: We reflect on whether ageism plays a role in vaccinology research, decision-making and practice.

Methods: We holistically examine the impact of ageism on vaccine development, clinical trial design and recruitment, evaluation methodology, Immunization Technical Advisory Group composition, vaccine program decision-making, program implementation, and delivery, as well as knowledge, attitudes and biases of decision-makers, providers, and the public.

Results: Potential ageism arises at every step. Vaccine development may not fully consider frailty and aging immune responses, and clinical trials often exclude older adults. Outcomes relevant to older people (e.g. functional independence) are not often considered in trials. It has been rare for regulatory and advisory decision making to include geriatrics expertise, and structured approaches to decision-making (e.g. GRADE) rely on presence of robust evidence which is often lacking for older adults. Economic evaluations tend to devalue older adults due to shorter remaining life expectancies and difficulty valuing post-retirement societal contributions. Publicly-funded immunization programs are more often tailored to children and youth, with longer implementation times and limitations on older adult programs. Amongst competing priorities and scant public resources, decision-makers and the public may prioritize younger versus older people in resource allocation.

Conclusions: Addressing ageism in vaccine clinical practice, public health and policy is important to ensure the health of populations, strong health systems functioning, and recognize the value of older people in society.

Poster 2B

HOW WELL IS MESSAGING ABOUT THE IMPORTANCE OF VACCINATION FOR PEOPLE LIVING WITH DEMENTIA BEING COMMUNICATED? A JURISDICTIONAL SCAN OF NATIONAL IMMUNIZATION TECHNICAL ADVISORY GROUPS AND DEMENTIA ADVOCACY ORGANIZATIONS

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Affiliation: [1]Department of Medicine (Geriatrics), Dalhousie University, [2]College of Pharmacy, Dalhousie University

Introduction: Vaccination is particularly important for people living with dementia (PLWD), who are at risk for meaningful declines in function and cognition following acute illnesses including vaccine-preventable infections. Even so, vaccine uptake remains suboptimal. Optimal tailoring of messaging relies on awareness in advisory, decision-making and advocacy settings.

Methods: A jurisdictional scan conduced in January 2025 aimed to investigate three questions: 1) inclusion of geriatrics expertise in a sample of eight National Immunization Technical Advisory Groups (NITAGs), 2) whether PLWD are included in high-risk groups in NITAG advice, and 3) whether dementia advocacy organizations recommend vaccination. Lists of NITAG voting members were reviewed for the following countries: Canada, USA, United Kingdom, Australia, Germany, France, Switzerland, and for the World Health Organization. Published recommendations from the eight NITAGs were reviewed for five adult vaccines (COVID-19, influenza, pneumococcal, RSV and Herpes Zoster) to determine whether dementia or related conditions specifically appeared on lists of people for whom vaccination is particularly recommended or whether universal age-based recommendations would likely include most people living with dementia. Websites for dementia advocacy organizations in each of the seven countries were searched for information relating to vaccines, and any specific recommendation on the importance of vaccination for PLWD.

Results: Four of the eight NITAGs (Canada, USA, France, Germany) included a geriatrician voting member. All jurisdictions had variations on age-based recommendations for adult vaccines. Some included specific mention of dementia as a high-risk condition. All but one of the dementia advocacy organizations made some mention of COVID vaccines. Only the USA and UK organizations mentioned any non-COVID vaccine. None discussed vaccination as a specific recommendation for living well with dementia.

Conclusions: Messaging about the importance for vaccination for PLWD represents a missed opportunity and an area for improvement given the benefits of vaccination for PLWD.

Poster 3A

Title: RESPIRATORY VIRUS SURVEILLANCE IN THE NOVA SCOTIA HEALTH EMERGING AND RE-EMERGING INFECTIONS NETWORK (ERIN): CONTRIBUTION TO THE GLOBAL INFLUENZA HOSPITAL SURVEILLANCE NETWORK

Authors: **Melissa K. Andrew,** Kevin Wilson, Jason LeBlanc, Todd Hatchette, May ElSherif, Angela Keenan, **Shelly A. McNeil** on behalf of the Serious Outcomes Surveillance (SOS) Network and the NSH Emerging and Re-emerging Infections Network (ERIN)

Affiliation: [1]Infectious Diseases, [2]ERIN Network, [3]Canadian Center for Vaccinology (Dalhousie University, IWK Health, Nova Scotia Health), [4]Geriatrics

Introduction: The Global Influenza Hospital Surveillance Network (GIHSN) was established in 2012 to conduct coordinated worldwide influenza surveillance. Canada has been contributing since 2017/18, initially through the CIRN SOS Network. Since the 2024/25 season Canada's contribution has been from Nova Scotia Health's Emerging and Re-emerging Infections Network (ERIN) which conducts routine respiratory virus surveillance to inform Public Health efforts and clinical services planning in Nova Scotia.

Methods: ERIN's year-round surveillance is conducted using a standardized data collection, from which data harmonized with the GIHSN standardized surveillance protocol are extracted and submitted to GIHSN on a bi-weekly basis. Influenza, COVID-19 and RSV infections are laboratory-confirmed with RT-PCR. Clinical characteristics and outcomes are extracted from medical records. To allow estimation of Vaccine Effectiveness, and to harmonize with GIHSN's protocol, all patients presenting with acute respiratory illness, regardless of test positivity, are included 3 days per week during respiratory season. Influenza positive NP swab samples with suitable CT values undergo whole genome sequencing (WGS) for submission to both GIHSN and GISAID.

Results: Between November 1 2024 and October 31 2025, 684 patients were included in the GIHSN reporting cohort, of whom 143(20.9%) had laboratory-confirmed influenza, 66(9.7%) had COVID-19, 32(4.7%) had RSV and 541(79.1%) were test-negative controls. 75 influenza samples had WGS. Mean age was 69.9(SD 0.61), 48.4% were female. 43.1%, 85.5%, 3.5% had been vaccinated for influenza, COVID and RSV respectively. 11.3% were admitted to ICU and mortality was 11%.

Conclusions: Nova Scotia's ERIN contributes a vital source of respiratory virus surveillance data to inform provincial public health efforts and clinical service planning, while also providing North American data to the GIHSN.

Poster 3B

Title: CLINICAL CHARACTERISTICS, RISK FACTORS AND OUTCOMES OF NOSOCOMIAL COVID IN NOVA SCOTIA

Authors: K. Wilson[1], A. Keenan[1], H. Kennedy[1], A. Day[1], M.K. Andrew[1,3], **S.A. McNeil[1,2]** on behalf of the NS Health Emerging and Re-emerging Infections Network

Affiliation: [1]Nova Scotia Health Emerging and Re-emerging Infections Network, Divisions of [2]Infectious Diseases and [3]Geriatric Medicine, Department of Medicine, Dalhousie University

Introduction: In the era of vaccination programs and antiviral therapies, COVID's morbidity and mortality impacts predominantly frail, older adults. Nosocomial transmission of COVID in acute care facilities is common and understanding the clinical characteristics, risk factors and outcomes of affected patients is critical to quantify impact on the acute care system and to reinforce the importance of strategies to mitigate transmission.

Methods: All patients with nosocomial COVID at NSH acute care facilities from 01NOV2024 to 31OCT2025 were included. Nosocomial infection was defined as a positive COVID PCR ≥7d post admission. Charts were reviewed and data collected on demographics, treatment and outcomes. Where possible, outcomes were compared to community-acquired cases and amongst vaccinated and unvaccinated patients.

Results: There were 1321 patients with COVID hospitalized in NSH facilities during the study period; 525 (39.7%) were nosocomially acquired. Overall, 92% of patients with nosocomial COVID had received a 2 does primary vaccine series and 56.2% were treated with antivirals. Patients with nosocomial COVID were older (median 79 years vs 76.5 years, $p<0.01$) and more frail (median Clinical Frailty Scale 5 vs 4, $p < 0.001$) than cases acquired in the community. Among patients with nosocomial COVID, the average time to acquisition of COVID was 28 days post admission and the average LOS following a COVID diagnosis was 28 days (IQR: 9 to 71 days); 10.7% required admission to an ICU, 7.6% required mechanical ventilation and 11.1% died. Nosocomial COVID cases accounted for 29,019 bed days during the study period and challenges with bed flow related to impacts on required Infection Prevention and Control (IPAC) measures were observed.

Conclusions: Nosocomial COVID largely impacts frail older adults, is associated with significant morbidity and mortality and contributes to significant bed utilization in hospitals already facing over- capacity issues. Ongoing strategies such as universal masking of healthcare staff and visitors, programs to optimize vaccine coverage amongst patients and staff, and IPAC strategies designed to detect and cohort COVID cases are critical to minimize the adverse impacts of nosocomial COVID on vulnerable patients and on resource/bed utilization in hospitals.

Poster 4A

Title: STI CARE NOW: INCREASING ACCESS TO SEXUALLY TRANSMITTED AND BLOOD-BORNE INFECTION TESTING AND TREATMENT AND HUMAN IMMUNODEFICIENCY VIRUS PRE-EXPOSURE PROPHYLAXIS IN NOVA SCOTIA

Authors: **T.D. Ramsey[1,2],** C. MacAulay[1], M. d'Entremont-Harris[1], D. Deyoung[1], A. Joy[1], K. Merrick[1], A. Keenan[1], C. Heinstein[1], S.A. McNeil[1,2], T. F. Hatchette[1,2] (on behalf of the NSH Emerging and Re-emerging Infections Network)

Affiliation: [1]Nova Scotia Health, [2]Dalhousie University

Introduction: Barriers to sexually transmitted and blood-borne infection (STBBI) services delay early diagnosis, treatment, and access to prevention. The Nova Scotia (NS) Health Sexually Transmitted Infection (STI) Care Now Initiative expands access to STBBI testing, prevention, and treatment services in NS. The initiative includes human immunodeficiency virus (HIV) and chlamydia/gonorrhea (CT/NG) self-testing, CT/NG treatment, and HIV pre-exposure prophylaxis (PrEP) services.

Methods: Individuals self-referred using an online webform for chlamydia/gonorrhea (CT/NG) self-testing as of July 2024. HIV self-testing and pre-exposure prophylaxis (PrEP) assessment were added in April 2025. Self-testing kits for CT/NG and HIV with prepaid return postage were mailed to participants or picked up at participating community-based organizations and high schools. CT/NG results were provided by email or phone and individuals with a CT/NG diagnosis were assessed by a pharmacist and treated or referred. Pharmacists also conducted HIV PrEP assessments and prescribing.

Results: The STI CN initiative received 7567 self-referrals from 5697 individuals between July 8, 2024 and February 12, 2026. 7180 testing kits were issued, including 2128 HIV self-tests. 746 individuals (33%) reported their HIV results, with 715 non-reactive, 159 invalid, and 1 reactive results. The kit return rate was 57% for CT/NG self-testing. 245 were positive for CT and 44 for NG, yielding a 7% positivity rate. All individuals with positive results were linked to care. 368 HIV PrEP appointments were completed for 189 patients. These appointments included 203 eligibility, 72 initial prescription, and 93 refill assessments. 165 HIV PrEP prescriptions were written, including 99% for emtricitabine/tenofovir disoproxil fumarate and 1% for emtricitabine/tenofovir alafenamide.

Conclusions: STI Care Now successfully supported access to CT/NG testing and care, HIV testing, HIV PrEP assessments, and has potential for future use with other STBBIs.

Poster 4B

Title: THE EVOLUTION OF THE NS HEALTH INFLUENZA TREATMENT TEAM 2024-2026

Authors: **E.K. Reid[1],** D. Mallia[1], K. Merrick[1], S.A. McNeil[1,2], T.D. Ramsey[1,2], on behalf of the NS Health Emerging and Re-emerging Infections Network

Affiliation: [1]Nova Scotia Health, [2]Dalhousie University

Introduction: The Nova Scotia (NS) Health Influenza Treatment Team (ITT) launched in 2024 in collaboration with the Emerging and Re-emerging Infections Network. Positive influenza PCR test results were referred from NS Health microbiology laboratories to a pharmacist-led team for phone-based patient assessment and antiviral prescribing. Initially focused on outpatients without a primary care provider or those discharged from NS Health emergency departments as a pilot program, the ITT expanded over three seasons to include inpatient treatment and prophylaxis.

Methods: Workflow metrics and clinical documentation were reviewed to characterize evolution of the ITT scope, populations served, and antiviral prescribing patterns, from program launch January 23, 2024 to February 19, 2026.

Results: Over the course of three seasons, the ITT performed initial assessments on 10076 patients and full assessments for 3310. During the 2023–24 influenza season, 924 outpatients were fully assessed, with oseltamivir prescribed in 17% of cases. Many assessed patients did not meet criteria for antiviral therapy due to a lack of risk factors for influenza complications. In 2024–25, workflow shifted to prioritize hospitalized patients through an additional inpatient pilot in Central Zone to provide treatment assessments and collaborate with Infection Prevention and Control (IPAC) in coordinating antiviral prophylaxis during inpatient influenza outbreaks and for close contacts. During this season, 1729 full assessments for treatment or prophylaxis were completed, with oseltamivir prescribed in 44% of cases. In the current 2025–26 season, the ITT scope has expanded to provide province-wide assessment of inpatients and outpatients. As of February 19, 2026, 657 full assessments have been completed with oseltamivir prescribing in 63%. Across the first two seasons, the average time from referral to oseltamivir prescribing was under 7 hours.

Conclusions: Over three influenza seasons, the ITT evolved from a targeted outpatient pilot to a province-wide, pharmacist-led influenza management service spanning inpatient and ambulatory settings. This adaptable practice model facilitated timely antiviral access in prioritized populations and may be applied to other stewardship or IPAC initiatives.

Poster 5A

Title: ASSESSING BIOSAFETY AND STABILITY OF CHLAMYDIA TRACHOMATIS AND NEISSERIA GONORRHOEAE COLLECTIONS IN APTIMA TRANSPORT MEDIA UNDER TRANSPORT CONDITIONS CONDUCIVE FOR CANADIAN HOME TESTING

Authors: J.J. LeBlanc, G.R. McCracken, **T.F. Hatchette**

Affiliation: [1]Division of Microbiology, Department of Pathology and Laboratory Medicine, Nova Scotia Health (NSH), [2]Department of Pathology, Dalhousie University [3]Department of Microbiology and Immunology, Dalhousie University, [4]Department of Medicine (Infectious Diseases), Dalhousie University

Introduction: STI Care Now is a Nova Scotian home-collection program for Chlamydia trachomatis (CT) and Neisseria gonorrhoeae (NG) testing. Mail-in self-collection kits include swab and urine collection devices for the Hologic Aptima Combo 2 assay. These devices are Health Canada-approved for self-collection, but not home-collection. The ability of the device transport media to inactivate CT and NG was evaluated to ensure transport regulations are met, and temperature analyses were performed to ensure CT and NG RNA stability following transport.

Methods: Pooled CT- or NG-positive specimens were serially diluted in Aptima Multitest Specimen Transport Media (STM) or Aptima Urine Specimen Transport Tubes (USTT) to determine the limits of detection (LoD). To mimic transport conditions, each sample inoculated with CT or NG at 10× and 100× LoD was incubated for 24, 48 or 72h at -20°C, 4°C, room temperature (RT), 37°C, 42°C, and 60°C. Repeat freeze (-20°C, 8h)/thaw (4°C, 16h) and heat (60°C, 8h)/cool (RT, 16h) cycles were also tested. For biosafety assessments, CT and GC were spiked into STM, USTT, or saline controls for 30 min and were cultured onto McCoy cells or Thayer-Martin agar, respectively.

Results: With exception of 60°C for 72h that was 10-fold less sensitive for CT and NG detection in both swab and urine transport media, other test conditions had no impact. No growth was observed for CT/NG following exposure to the transport media.

Conclusions: Aptima transport devices pose no biosafety risk and effectively stabilizes nucleic acids for CT/NG testing at temperature conditions conducive for home testing.

Poster 5B

Title: CLESROVIMAB SAFETY, PHARMACOKINETICS, AND RSV-ASSOCIATED DISEASE INCIDENCE OVER TWO RSV SEASONS AMONG INFANTS AT INCREASED RISK FOR SEVERE RSV DISEASE: PHASE 3 SMART TRIAL

Authors: Heather J. Zar[1], Louis J. Bont[2,3,4], et.al on behalf of the SMART (MK-1654-007) study group[5]

Presented by Steven Findlay[5]

Affiliation: [1]University of Cape Town, South Africa, [2]UMC Utrecht, Netherlands, [3]ReSViNET Foundation, Netherlands, [4]Yale University, USA, [5]Merck & Co., Inc., USA

Introduction: Clesrovimab RSV neutralizing antibody binds with high affinity to antigenic site IV of the RSV F. A Single, fixed IM doses of 105 mg for season 1 and 210 mg for season 2 which is indicated for the prevention of RSV lower respiratory tract disease in neonates and infants who are born during or entering their first RSV season as well as infants/children <2 years at increased risk of severe RSV entering season 2.

Methods: Phase 3, partially-blinded, randomized, palivizumab-controlled SMART trial in infants (birth to 1 year) entering their 1st RSV season AND recommended to receive palivizumab based on local guidelines. Primary objective was safety and tolerability of clesrovimab (105 mg) vs palivizumab in RSV season 1 as assessed by the proportions of participants experiencing adverse events (AEs). Secondary objectives were incidence of RSV-associated medically attended lower respiratory infection (MALRI) requiring ≥1 indicator of LRI or severity and of RSV-associated hospitalization through day 150.

Results: Safety outcomes RSV Season 1 and Season 2: The proportion of participants with AEs, including solicited AEs, drug-related AEs, and SAEs, were generally comparable between intervention groups. No anaphylaxis/hypersensitivity AESI were reported, and the proportion of participants with rash AESI were low (≤0.6%) in either intervention group – All events were nonserious and Grade 1. No deaths were considered related to study intervention by the investigator. Clesrovimab PK in infants and children at increased risk of severe RSV across two RSV seasons were similar and are generally comparable to healthy infants in the phase 2b/3 trial CLEVER

Conclusions: Clesrovimab was well-tolerated in infants at increased risk for severe RSV disease. In season 1 and 2, the safety profile of clesrovimab 105 mg and 210mg respectively were generally comparable to that of palivizumab. The exposure similarity between healthy infants in CLEVER and infants and children at increased risk of severe RSV disease across two seasons in this study is supportive of the extrapolation of efficacy to this population.

Poster 6A

Title: MRNA-1010, AN MRNA-BASED INFLUENZA VACCINE, IS SAFE AND EFFICACIOUS IN ADULTS AGED ≥50 YEARS

Authors: Elissa Malkin[1], Murdo Ferguson[2], Anita Kohli[3], Rebecca Clark[4], Isabel Leroux-Roels[5], Evelyn Du[1], Agi Buchanan[1], Bryony Hicks[1], Eleanor Wilson[1] **Presented by Lionel Budry[1]**

Affiliation: [1]Moderna Therapeutics, Inc, [2]Colchester Research Group, [3]The Institute for Liver Health Arizona, [4]Layton Medical Centre - General Practice, [5]Center for Vaccinology, Ghent University and Ghent University Hospital

Introduction: mRNA-1010, a novel mRNA-based influenza vaccine targeting vaccine-matched influenza A and B strains, has demonstrated superior immunogenicity compared to licensed standard-dose (SD) and high-dose comparators, as measured by hemagglutination inhibition assay. We present the safety and relative vaccine efficacy (rVE) from the end of influenza season analysis of the pivotal phase 3 trial comparing mRNA-1010 to SD influenza vaccination in adults aged ≥50 years.

Methods: This phase 3, randomized, double-blind, active-controlled, case-driven study (NCT06602024) enrolled participants (≥50 years) from 11 countries throughout the Northern Hemisphere. Participants were randomized 1:1 to receive a single dose of trivalent mRNA-1010 37.5 µg (12.5 µg µg HA mRNA per strain) or SD comparator (Fluarix 45 µg or Fluarix Tetra, Influsplit Tetra, or Alpharix Tetra 60 µg). The primary efficacy endpoint was rVE in the prevention of the first episode of RT-PCR–confirmed protocol-defined influenza-like illness (ILI) caused by influenza A or B strains beginning ≥14 days after study vaccination through end of the influenza season.

Results: In the 2024-2025 influenza season, 40,703 participants were randomized and received study vaccine (mRNA-1010, n=20,350; SD comparator, n=20,353). The median age was 64 years; 56.9% were female; 82.6% were White, 13.2% Black; and 10.4% Hispanic/Latino. Median follow-up was 181 (1-227) days. Solicited adverse reactions within 7 days of vaccination were more frequently reported in the mRNA-1010 than the SD comparator group; most reactions were mild/moderate, transient, and self-limiting. mRNA-1010 demonstrated an rVE of 26.6% (95% CI, 16.7-35.4%; 1-sided p=0.0005) against RT-PCR–confirmed protocol-defined ILI compared to SD comparator, meeting the prespecified superiority criteria (lower bound of the 95% CI >9.1%).

Conclusions: mRNA-1010 demonstrated superiority over SD comparator in the prevention of RT-PCR–confirmed protocol-defined influenza disease in adults ≥50 years, consistent with approved enhanced influenza vaccines. rVE was consistent across vaccine-included strains, including Influenza B strains.

Poster 6B

Title: MODELING THE PUBLIC HEALTH IMPACT OF RSV VACCINATION IN U.S. ADULTS ≥60 YEARS USING REAL-WORLD EFFECTIVENESS DATA

Authors: Hicks K[1], Xiao L[1], Zhang L[2], Wilker W[2], Clarke C[2], Ghaswalla P[2] **Presented by Lionel Budry[2]**

Affiliation: [1]RTI-HS, [2]Moderna Therapeutics, Inc;

Introduction: The US Advisory Committee on Immunization Practices (ACIP) recommends a single RSV vaccine dose for adults ≥75 years and for adults 60–74 at increased risk for severe RSV disease; eligibility was recently extended to include 50–59-year-olds at increased risk. Using CDC-reported VE, we estimated multi-season reductions in RSV burden under a single-dose strategy in older adults.

Methods: We modeled five respiratory seasons using a static decision-analytic cohort model of the ACIP-recommended U.S. adult population (all adults ≥75 years; adults 60–74 years at increased risk). A single-dose strategy was compared with no vaccination. Baseline RSV incidence and hospitalization rates were sourced from the literature. Time-varying VE, VE(t), was parameterized by fitting a nonlinear function to product-agnostic estimates from the CDC-supported VISION network (two seasons). VE(t) was extrapolated beyond the CDC/VISION network's ~19-month observation window to five years.

Results: The fitted VE(t) function indicated high initial protection with attenuation over time: 89.2% at 1 month, 52.5% at 12 months, 28.2% at 24 months, and 8.6% at 36 months. When applied in the model, the largest absolute reductions in RSV hospitalizations occurred in Years 1–2, with progressively smaller incremental reductions thereafter. Modeled RSV hospitalizations for "no vaccination" vs. "single-dose vaccination" were 174,000 vs. 119,000 in Year 1 (−55,000; −31.6%), 167,000 vs 136,000 in Year 2 (−31,000; −18.6%), 160,000 vs 146,000 in Year 3 (−14,000; −8.8%), 154,000 vs 152,000 in Year 4 (−2,000; −1.3%), and 148,000 vs 148,000 in Year 5 (~0%). Over five years, ~102,000 hospitalizations were averted (range: 71,000–136,000), with ~84% (74-93%) of benefits accruing in the first two years, consistent with the modeled VE over time.

Conclusions: A single-dose RSV vaccination program confers substantial public-health benefits in U.S. older adults, particularly in the early post-vaccination period. In projections based on real-world effectiveness data (CDC-supported VISION network), the incremental benefit decreases over successive seasons in the absence of revaccination. These results support the value of current programs and inform evaluation of evidence-based revaccination intervals, especially for higher-risk adults.

Poster 7A

ROLE OF THE INTEGRATED STRESS RESPONSE IN MODULATING THE HOST IMMUNE RESPONSE TO PSEUDOMONAS AERUGINOSA LUNG INFECTION

Authors: **Rhea Nickerson**[1], Michal Scur[1], Shannen Grandy[1], Zhenyu Cheng[1]

Affiliation: [1]Department of Microbiology & Immunology, Faculty of Medicine, Dalhousie University, Nova Scotia, Canada

Introduction: Pseudomonas aeruginosa is a highly adaptable environmental Gram-negative bacterium which causes diverse opportunistic infections in humans, particularly chronic lung infections in people with cystic fibrosis (pwCF), where it drives persistent inflammation leading to lung damage and respiratory failure. P. aeruginosa is highly antibiotic-resistant, and during its transition to chronicity adapts to exploit the lung niche and evade immune clearance, making it very difficult to treat. My project aims to deepen our understanding of this host-pathogen interaction and develop novel treatments by exploring the relationship between chronic P. aeruginosa infection and the host integrated stress response (ISR). The ISR is a highly conserved eukaryotic stress response mediated by phosphorylation of eIF2α leading to general translation inhibition and activation of transcription factor ATF4 to promote cellular stress adaptation and recovery, or cell death depending on stress intensity and duration.

Methods: Based on previous literature, our lab is developing and characterizing in vivo infection models using P. aeruginosa-embedded agar beads to model “extended” lung infection in C57BL/6 mice. In this extended infection model, we treated mice daily with specific ISR-inhibiting drugs (ISRIB and 2Bact) and assessed various parameters including immune populations (by flow cytometry), immune mediator production (by ELISA), clinical recovery, and bacterial burden over the course of 1-week post-infection to understand how inhibiting the ISR affects the course and outcomes of infection. We have paired this investigation with an in vitro murine macrophage (RAW264.7) P. aeruginosa infection model using the same ISR inhibiting drugs to gain a more molecular understanding of the roles of ISR signaling in infection.

Results: In our mouse extended lung infection model, we have been able to establish persistent infection for up to 1 week, with sustained production of inflammatory cytokines and neutrophil recruitment, recapitulating hallmark features of the persistent inflammation which drives lung damage in human chronic infection. In this model, treatment with the ISR inhibitor 2Bact significantly improved weight recovery and clinical symptoms beginning at 3 days post-infection. ISRIB, our other ISR inhibitor, resulted in an intermediate but non-significant phenotype. Interestingly, this protective effect of 2Bact was only seen in male mice. In our in vitro cell-based infection model, we have corroborated that P. aeruginosa infection activates the ISR in RAW264.7 cells, indicated by upregulation of downstream transcription factor ATF4 via western blot. Pre-treatment of cells with 2Bact strongly decreases this activation.

Conclusions: We have demonstrated in vitro that P. aeruginosa infection activates the ISR and that the use of ISR inhibiting drugs like 2Bact dampens this activation. In vivo, this ISR inhibition with 2Bact significantly improved the severity of P. aeruginosa infection in a mouse lung infection model as measured by weight recovery and clinical symptoms. We are continuing to characterize the impacts of and potential mechanisms driving this protective effect. Together, these observations position ISR inhibition as a potential novel strategy to modulate the host response to chronic P. aeruginosa lung infection and reduce infection-associated morbidity and mortality in pwCF and other chronic lung diseases.

Poster 7B

Title: WEAPONIZING LATERAL GENE TRANSFER: A NOVEL CAS9-BASED THERAPEUTIC AGAINST SHIGELLOSIS

Authors: **Maggie Hosmer**[1], Gregory Pellegrino[2], Ankit Pandeya[3], Isabella Rauch[3], David Edgell[2], and John Rohde[1]

Affiliation: [1]Department of Microbiology and Immunology, Dalhousie University, [2]Department of Biochemistry, University of Western Ontairo, [3]Department of Molecular Microbiology, Oregon Health Sciences University

Introduction: Shigellosis continues to inflict a huge burden on humanity and kills hundreds of thousands each year, predominantly in low-income countries. In high-income countries, including Canada, shigellosis is an emerging pathogen affecting people experiencing homelessness. There is no vaccine against shigellosis and multidrug resistant isolates of Shigella spp. (the causative agent of shigellosis) are becoming more prevalent. Shigella use a Type 3 Secretion System (T3SS) to inject “effector” proteins into the human cells that they infect. Among these effectors are a closely related family of proteins known as ipaHs. The twelve IpaH proteins share a C-terminus that is invariant. We have developed a Cas9-based therapeutic that targets the ipaH genes. This Cas9 platform is introduced into Shigella from E. coli via conjugation.

Methods: We built transmissible plasmids, capable of conjugation from E. coli into Shigella. These plasmids express a Cas9 nuclease and a guide RNA that targets all twelve ipaH genes. We tested these plasmids for their ability to kill Shigella in vitro. We also tested these constructs for their ability to protect against Shigella infection in a newly developed mouse model of infection.

Results: We found that the Cas9-constructs are remarkably potent against strains of Shigella. These constructs are effective against Shigella strains commonly used in research as well as clinical isolates that are multi-drug resistant. We will present data that show that E. coli harboring the Cas9 constructs can protect NLRC4- mice from Shigella infection.

Conclusions: We propose that Cas9-based therapeutics that target highly conserved virulence factors of Shigella are a novel platform for antimicrobial therapy.

Poster 8A

Title: ROLE OF CHLAMYDIA-INDUCED IMMUNOSUPPRESSIVE MICROENVIRONMENT IN THE DEVELOPMENT OF HEREDITARY HIGH-GRADE SEROUS OVARIAN CANCER (HGSC)

Authors: **Hannah Burton[1],** Parnian Jahanbani[1], Jun Wang[1,2]

Affiliation: [1] Dalhousie University, [2]IWK Health Centre

Introduction: HGSC is an aggressive subtype of ovarian cancer with the highest mortality of any gynecological malignancy. While it is rare in the general population, 40-50% of HGSC cases have a significant hereditary component, including germline mutations in BRCA1/2 genes, or broader cancer predisposition syndromes such as Li-Fraumeni Syndrome. However, HGSC is far from ubiquitous among those with hereditary cancer-associated genetic mutations. Another emerging potential risk factor for HGSC is Chlamydia trachomatis (Ct) infection. Ct is the leading cause of bacterial STIs globally and has an annual incidence rate of approximately 4% among women. We hypothesize that the immunosuppressive microenvironment induced in the genital tract and peritoneal cavity during the infection resolution stage of Ct infection may contribute to future HGSC development in those with germline cancer-associated mutations.

Methods: To explore the effects of *Chlamydia* infection in the development of HGSC, we used a tamoxifen-induced, oviduct-specific Cre-lox system in a murine model called BPRN mice. In this model, intraperitoneal injection of tamoxifen leads to Cre-mediated deletion of four tumour suppressor genes in the mouse oviduct: *Brca1*, *Trp53*, *Rb1*, and *Nf1*. Subsequently, mice experience HGSC development and progression over a period of months to years, mimicking the human process. To model hereditary HGSC, where the gene deletions predispose *Ct* infection, BPRN mice receive tamoxifen-induced gene deletions during adolescence, shortly followed by intravaginal injections of *C. muridarum* (Cm). Cm is a murine pathogen that shares >90% of its genome with Ct and is well-established as a mouse model. After determining mortality between infected and uninfected groups, samples of the genital tracts, peritoneal wash fluid and any other visible tumours were collected at various timepoints post-infection or mock infection. Histological staining was used to look at HGSC incidence and characterize tumours, and flow cytometry was performed on the samples to look at immune cell populations.

Results: Cm-infected tamoxifen-induced mice had a higher incidence of ovarian cysts and HGSCs visible to the naked eye compared to uninfected tamoxifen-induced mice. Histological analysis of HGSCs is ongoing. As well, a greater number of uninfected mice remained healthy by the end of the study at one year post-tamoxifen injection compared to infected mice, with healthy defined as complete absence of ovarian cysts, ascites, and ovarian tumours. BPRN mice showed a typical acute response to Cm infection, with an upregulation of CD8+ and CD4+ T cells, NK cells, B2 cells and M1 macrophages in the spleen, iliac lymph nodes, peritoneal wash fluid and genital tract at day peak infection compared to uninfected mice. By day 90 post-infection, infected mice exhibited a pro-resolution, immunosuppressive microenvironment, particularly in the peritoneal cavity, showing increased CD206+ and Arg1+ M2-like macrophages and decreased pro-inflammatory cells compared to their uninfected counterparts.

Conclusions: *Chlamydia* infection may increase the risk of HGSC development in those with germline cancer-related genetic mutations by inducing an immunosuppressive microenvironment in the genital tract and peritoneal cavity during infection resolution, including skewing of macrophage populations toward M2-like phenotypes. These pro-resolution immune cells may curb anti-tumour immune mechanisms and promote uncontrolled cell growth.

Poster 8B

Title: THE NEONATAL GUT MICROBIOME FUNCTIONAL TRAJECTORY IN THE FIRST WEEK OF LIFE: DIVERGENCE IN HEALTH AND SEPSIS

Authors: **Bakary Sanyang**[1], Tobias Kollmann[1], Nelly Amenyogbe[1]

Affiliation: [1]Dalhousie University

Introduction: The neonatal gut microbiome undergoes rapid and dynamic changes in the immediate postnatal period, playing a critical role in immune programming, metabolic development, and protection against infection. Disruptions to this early colonization process have been implicated in adverse neonatal outcomes, including sepsis. While the taxonomic composition of the early neonatal microbiome has been characterized, its functional trajectory and how deviations from this trajectory relate to sepsis onset remain poorly understood. Using gut microbiome data from a well-defined human newborn cohort, we characterized gut microbiome functional trajectory in the first week of life between healthy and unhealthy (diagnosed with sepsis in first week of life) neonates.

Methods: We used stool microbiome data from the Expanded Program on Immunization Consortium (EPIC) study, a prospective observational cohort study which recruited 720 newborns from The Gambia. Each baby was sampled at birth and at a subsequent time point on day of life 1, 3, or 7. Shotgun metagenomic sequencing was performed on all samples. Functional profiling was carried out using SUPER-FOCUS, with metabolic pathway abundance analyzed to characterize the functional microbiome. We applied unsupervised clustering to identify distinct functional clusters and examined how these clusters are represented over the first week of life. We also developed a gut microbiome acceleration score based on functional changes over time and modeled this score on age for healthy and unhealthy babies using linear models.

Results: Out of the 720 neonates, 37 were diagnosed with sepsis (25 early onset, 12 late onset). Our results showed that healthy neonates follow a distinct gut microbiome functional trajectory in the first week of life, and that neonates who develop sepsis exhibit measurable divergence from this trajectory prior to or at clinical presentation.

Conclusions: The healthy neonatal gut microbiome follows a robust and predictable functional maturation trajectory in the first week of life. Neonates who develop sepsis diverge significantly from this trajectory from the earliest postnatal days, suggesting that functional microbiome disruption may precede or accompany sepsis pathogenesis.

Poster 9A

Title: PARTIAL DELETION OF THE OPG164 (A36R) TRANSMEMBRANE PHOSPHOPROTEIN IN MONKEYPOX VIRUS CLADE Ib/Sh2023 DISRUPTS THE ACTIVE REGION INVOLVING TYR140

Authors: **Anuj Kumar**[1,2,3,4], Gustavo Sganzerla Martinez[1,2,3,4,5,6], Mansi Dutt[1,2,3,4], Ali Toloue Ostadgavahi[1,2,3,4], Alyson Kelvin[6], David J Kelvin[1,2,3,4,5]

Affiliation: [1]Department of Microbiology and Immunology, Dalhousie University, [2]Canadian Center for Vaccinology, [3]Faculty of Medicine, Dalhousie University, [4]Laboratory of Immunity, Shantou University Medical College, China, [5]BioForge Canada Limited, [6]Faculty of Veterinary Medicine, University of Calgary

Introduction: The ongoing monkeypox virus clade Ib/sh2023 outbreak, propagated by human-to-human transmission, was declared a public health emergency of international concern by WHO on Aug 14, 2024. This novel, contagious virus is spreading globally. The deletion of OPG32, a complement control protein in monkeypox virus clade Ib/sh2023, is often cited as a possible contributing mutation for sustained human-to-human transmission.

Methods: A total of 536 MPXV Clade Ib/sh2023 MPXV genomes were downloaded from the EpiPox database of the Global Initiative on Sharing All Influenza Data (GISAID) with the identifier EPI_SET_250524qc. The downloaded Clade Ib/sh2023 MPXV genomes were annotated using the Prokka pipeline, utilizing NC_003310.1 as a reference genome of MPXV Clade I. Further, the IGV (Integrative Genomics Viewer) was employed to visualize the sequencing reads aligned in the sorted .bam file. Moreover, a phylogenetic tree and protein structure model was generated using the MAFFT (Multiple Alignment using Fast Fourier Transform) version 7 and AlphaFold2, respectively.

Results: Based on Prokka annotation, we observed a 48-bp deletion (145 110 to 145 157) corresponding to 16 residues (131–146 aa), including one of the phosphotyrosines (Tyr140) in OPG164, across 474 annotated genomes of clade Ib/sh2023. To validate our observations, we also re-examined the .bam files of early (hMpxV/DRC/CRSN-1/2023 to hMpxV/DRC/CRSN-4/2023) clade Ib/sh2023 sequences submitted to GISAID and visualised the aligned reads using the Integrative Genomics Viewer, confirming this deletion in clade Ib/sh2023. To further validate the deletion, we annotated the clade Ib/sh2023 sequences with Nextclade v3.15.1. Our Nextclade results showed the common deletion of 16 aa in all clade Ib/sh2023 sequences.

Conclusions: Deletion of the phosphorylated Tyr140 and neighbouring residues in clade Ib/sh2023 mpox might disrupt the activation of the host Arp2/3 complex, leading to no actin tail formation and decreased cell-to-cell pathogenicity, explaining in part the possible reduced human pathology of monkeypox virus clade Ib/sh2023 or sustained human-to-human transmission. Additional experimental studies are needed to find out the effects of this deletion on host actin dynamics and viral transmission. Detailed comparative genomics, as reported here, coupled with astute epidemiological and clinical investigations of emerging monkeypox virus outbreaks in humans, can help to build hypothesis-driven medical countermeasures based on molecular targets.

Poster 9B

Title: THE GLOBALIZATION OF THE MONKEYPOX CLADE IB: TRACKING THE PATH OF SUSTAINED HUMAN-TO-HUMAN TRANMISSION

Authors: **Anuj Kumar1**, Gustavo Sganzerla Martinez[1,2], Mansi Dutt[1], Ali Toloue Ostadgavahi[1], Alyson Kelvin[3], Luis Flores Girón[4], Kaleme Kiswele Prince[4], David J Kelvin[1,2]

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Introduction: Mpox, formerly known as monkeypox, is a viral infectious disease caused by the mpox virus (MPXV), a member of the Orthopoxvirus genus of the Poxviridae family. Due to a surge in the confirmed mpox cases and multiple outbreaks of the novel Clade Ib/sh2023 in the Democratic Republic of Congo (DRC) and neighboring African countries, mpox has been declared as a Public Health Emergency of International Concern (PHEIC) between 14 August 2024 and 05 September 2025.

Methods: Initially, we retrieved a total of 608 mpox Clade Ib/sh2023 MPXV genomes available on the Global Initiative on Sharing All Influenza Data (GISAID) up to 18 November 2025, with the GISAID Identifier: EPI_SET_251118wd. Prokka, a rapid prokaryotic genome annotation software, was employed to annotate the mpox Clade Ib/sh2023 viral genomes. To predict the genome-wide variants in the Clade Ib/sh2023 genomes, gtf2vep.pl script from the Ensembl-VEP was utilized to prepare the reference genome. Afterward, the MUMmer (Version 4.0+) program was employed to predict the changes in the genome. Moreover, a set of in-house bash scripts was applied to the annotated .vcf files of all 540 Clade Ib/sh2023 MPXV genomes to fetch nucleotide and amino acid changes in mpox genomes.

Results: Based on extensive investigations, we observed that among the analyzed genomes, some of the genes were found to have emerging mutations. The majority of MPXV sequences from Burundi, Congo, and Uganda were found to have some unique features, such as in-frame deletion, frameshift, and substitutions. Clade Ib/sh2023 mpox sequences from the DRC and Congo were predominantly characterized by APOBEC3-like mutations. Phylogenetic analysis demonstrated that most sequences from Uganda and Burundi formed two distinct clusters, indicating unique genomic features. Moreover, travel-associated cases showed grouping with multiple sub-lineages but had a close association with Uganda sequences when compared to others.

Conclusions: The occurrence of multiple sub-lineages may reflect that multiple Clade Ib strains are circulating from different locations in the environment, and multiple recombination events are possible. Screened emerging mutations in the present study may be considered for the development of vaccines and screening of small chemical molecules as potential therapeutics for an effective treatment against the deadlier mpox disease. There is a pressing demand for continued efforts to sequence the MPXV samples globally for more genomic insights, leading to the development of strategies to combat mpox significantly.

Poster 10A

Title: AVIDITY OF ANTI-PERTUSSIS TOXIN ANTIBODIES CORRELATES WITH SYMPTOMATIC BORDETELLA PERTUSSIS INFECTION IN A NOVEL CONTROLLED HUMAN INFECTION MODEL

Authors: **Carlos Espinosa-Vinals[1,2],** Hala Obeid[1,2], Kara Redden[1], May ElSherif[1,3], Scott Halperin[1,2,3], Bahaa Abu-Raya[1,2,3]

Affiliation: [1]Canadian Center for Vaccinology (Dalhousie University, IWK Health, Nova Scotia Health), [2]Department of Pediatrics, Dalhousie University, [3]Department of Microbiology and Immunology, Dalhousie University

Introduction: The interplay between antibody immune responses to Bordetella pertussis infection and the development of symptomatic disease remains unclear. Anti-B. pertussis antibody levels alone do not fully account for protection from disease, thus, qualitative features of antibodies may help identify correlates of immunity. A key antibody quality measure is avidity, which reflects the strength of antigen binding to its antibody.

Methods: Healthy adults were intranasally challenged with B. pertussis in a first in North America controlled human infection model. In this study, participants who received the human infectious dose that resulted in symptomatic infection in 70-90% of participants (10^7 CFU), one dose lower (5×10^6 CFU), or higher (5×10^7 CFU) were included. Sera collected from infected participants (n=30) at −1, 14, 28, 56, 180, and 365 days post-challenge were tested for anti-pertussis toxin (PT) IgG avidity. Ammonium thiocyanate served as the bond breaking agent to quantify low- to very high-avidity antibodies using a titration of chaotrope concentration (0.5–3 Molar). Avidity was compared between symptomatic and asymptomatic participants using Welch's t test. Linear regression models were used to determine associations between covariates and avidity, and high dimensional analyses were performed to integrate all data.

Results: Anti PT IgG avidity increased in both symptomatic (n=20) and asymptomatic (n=10) participants, peaking at day 56 before declining through day 365. Symptomatic participants developed significantly higher levels of very high avidity antibodies from day 28 onward. In multivariate models, symptomatic infection remained associated with higher avidity at days 180 and 365. Integrated analyses revealed distinct avidity profiles between groups beginning at day 28 consisting of high avidity antibodies in the symptomatic group, where asymptomatic infection was associated with a qualitatively weaker and faster-waning antibody response.

Conclusions: Avidity maturation differentiates individuals who develop symptoms from those who remain asymptomatic after controlled B. pertussis infection and may serve as a surrogate of disease outcome. These findings offer a promising lead in identifying a correlate of protection against B. pertussis and a potential benchmark for assessing next generation pertussis vaccines.

Poster 10B

Title: DELINEATING THE ROLE OF MOUSE LY49I^{+} ANTIGEN SPECIFIC NK CELLS IN ANTI-TUMOUR IMMUNITY

Authors: **Sayanti Dey[1],** Daniel Medina-Luna[1], Gayani S. Gamage[1], Andrew P. Makrigiannis[1]

Affiliation: [1]Department of Microbiology & Immunology, Dalhousie University

Introduction: Natural killer (NK) cells are known to contribute to immunological memory; however, the receptors involved and the broader mechanisms underlying this phenotype remain poorly understood. In our lab, we have observed that NK cells can provide antigen-specific, long-lasting anti-tumour protection in Rag1$^{-/-}$ mice lacking functional T and B cells. The protection is observed when the mice are vaccinated with a tumour antigen prior to tumour implantation. However, in the absence of Ly49C/I receptors, the protection is lost. Hence, my work is trying to unveil how these receptors are allowing NK cells to protect better against cancer.

Methods: The crucial role of Ly49C/I receptors in eliciting NK memory responses was validated using a Ly49C/I-deficient murine model. To capture the heterogeneity of tumor-associated NK cells, Rag1$^{-/-}$ mice were immunized with the MHC I-restricted tumor-associated antigen R9F, 16 days prior to tumor implantation. Forty-five days post-implantation, tumors were excised to harvest immune cells, and isolated CD45+ immune cells were sequenced. Comprehensive transcriptomic analysis was then performed to identify distinct NK cell subsets and assess their functional states.

Results: Transcriptomic analysis of tumour infiltrating CD45^{+} cells expressing NK cell-associated markers NK1.1 and NKp46, identified five distinct NK cell subsets and one ILC1 subset. Using differential gene expression, trajectory inference, and RNA velocity analyses, we identified populations of immature progenitor NK cells, mature cytotoxic NK cells, and differentiated ILC1 cells. Interestingly, NK cell subsets 3 and 4 exhibited distinct transcriptional profiles compared to other subsets characterized by enrichment of pro-inflammatory TNF pathway, lipid, and iron metabolism genes and expressed high levels of Ly49I receptor. These subsets were exclusively found in tumours from vaccinated mice but not in naïve mice. These findings indicate substantial heterogeneity of tumour-infiltrating NK cells and identify two potential NK memory populations with high Ly49I expression exhibiting antigen-specificity.

Conclusions: This study identifies existing heterogeneity within the tumour infiltrated NK cells and allow us to understand how NK cells might be transitioning within the TME. It is also indicative of a potential NK memory population with high Ly49I expression exhibiting antigen-specificity, which is crucial for anti-tumour protection. Our findings highlight the protective role of NK cells against cancer and identify a surface molecule that is involved in this protection phenotype. These insights would advance our existing knowledge regarding our innate immune system and allow us to harness its potential and together with adaptive immunity, it will be instrumental for developing better immunotherapies against cancer.

Poster 11A

Title: DEVELOPMENT AND VALIDATION OF FUNCTIONAL ASSAYS FOR MEASURING NEUTRALIZING ANTIBODIES TO H5N1 INFLUENZA A VIRUS HEMAGGLUTININ AND NEURAMINIDASE IN A WIDE RANGE OF SPECIES AND SAMPLE TYPES.

Authors: **Abdulla Shuhait[1],** Eric S. Pringle[1], Ishraq Rahman[2], Susantha Gomis[3], JT McClure[4], Lisanework Ayalew[5], Lisa Barret[1], Andrew Lang[2], Craig McCormick[1], Denys A. Khaperskyy[1]

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Introduction: Highly pathogenic avian influenza (HPAI) H5N1 are zoonotic viruses circulating in birds that pose serious threat to mammals, including humans, due to sporadic cross-species transmission that is associated with severe disease. Influenza virus envelope has two major glycoproteins: hemagglutinin (HA) and neuraminidase (NA). HA mediates attachment to sialic acid on host cells and NA cleaves sialic acid during viral egress, making both glycoproteins key targets for vaccines and antiviral drugs. While seasonal H1N1 and HPAI H5N1 viruses share the N1 subtype of NA, HA remains immunodominant, and the lack of pre-existing H5-specific immunity in humans highlights the pandemic threat of H5N1. Developing serologic surveillance tools to monitor infection of animals and humans is essential for early detection and preparing for potential spread of this pathogen. Virus neutralization assays are the gold standard in assessing antibody-mediated protection. However, conducting these assays using the H5N1 HPAI virus requires high containment level 3 (CL3) facilities, which significantly raises the cost and limits throughput.

Methods: Using H5N1 pseudotyped lentivirus particles combined with enzyme-linked lectin assays we established a robust CL2 system for surveying and functionally assessing antibody-mediated immunity to H5 and N1 in a wide range of species and sample types (e.g. milk) acquired through immunization or prior infections.

Results: Using our assays, we characterized significant levels of cross-reactive anti-N1 antibodies in serum samples from wild waterfowl and mammals infected with different influenza virus subtypes and confirmed that measurable anti-H5 neutralizing antibodies are elicited only through prior exposure to H5 subtype virus infection or vaccination.

Conclusions: Developing CL2 serologic surveillance tools to monitor infection of animals and humans is essential for early detection, pandemic preparedness, and preparing for potential spread of current and emergent HPAI H5N1.

Poster 11B

Title: IMPAIRED HOST SHUTOFF IS A FITNESS COST ASSOCIATED WITH BALOXAVIR MARBOXIL RESISTANCE MUTATIONS IN INFLUENZA A VIRUS PA/PA-X NUCLEASE DOMAIN

Authors: **Jack R. Case**[1], Denys A. Khaperskyy[1]

Affiliation: [1]Department of Microbiology & Immunology, Dalhousie University

Introduction: The polymerase acidic (PA) protein is a subunit of the influenza A virus (IAV) RNA-dependent RNA polymerase and the direct target of the anti-influenza drug baloxavir marboxil (BXM). As with other direct-acting antivirals, treatment with BXM selects for viruses carrying resistance mutations. If these mutations have negligible fitness costs, resistant viruses can spread widely and render cap-snatching endonuclease inhibitors like BXM obsolete. Multiple BXM resistance mutations in the nuclease domain of PA have been identified, with I38T and I38M amino acid substitutions occurring frequently. These mutations have minimal to no effects on viral polymerase activity, virus replication, or transmission. However, for reasons that are not well understood, viruses with BXM resistance substitutions have not been able to compete with parental wild-type strains. The IAV genome segment encoding PA also encodes the host shutoff nuclease PA-X, which shares the endonuclease domain with PA but has a unique C-terminal domain generated by ribosomal frameshifting during translation. Unlike their effects on PA activity, the effects of BXM or the I38T/M substitutions on PA-X function remain uncharacterized.

Methods: To investigate this question, we used a combination of in-vitro overexpression models and authentic viral infections.

Results: In our work, for the first time, we directly examine the effects of baloxavir and I38T/M substitutions on PA-X activity. Most importantly, we demonstrate that the I38T/M resistance mutations significantly impair the host shutoff activity of PA-X proteins from different IAV strains of H1N1, H3N2, and H5N1 subtypes

Conclusions: Our work reveals that the deleterious effects of I38T/M on PA-X function may represent an important barrier to the spread of BXM-resistant viruses.

Poster 12A

Title: NON-INVASIVE PHYSIOLOGICAL PROFILING OF COLOSTRUM DEPRIVATION IN NEONATAL SEPSIS

Authors: **Autumn Sweeney[1],** Mariama Jammeh[1], Taylor Caddell[1], Tobias Kollmann[1], Nelly Amenyogbe[1]

Affiliation: [1]Dalhousie University

Introduction: Exclusive early breast milk (colostrum) feeding is the best-known prophylaxis against neonatal sepsis - a leading cause of neonatal mortality worldwide. However, the molecular mechanisms for colostrum's conferred protection are not understood. We deploy preclinical mouse models to investigate how colostrum deprivation impacts neonatal sepsis. Coupled with these models, non-invasive longitudinal assessment of vital organ function allows us to link early physiological perturbations to long-term clinical outcome. We thus aim to deploy a suite of non-invasive technologies called "NIMO" (non-invasive multi-omics) to enhance our understanding of disease course.

Methods: To model colostrum deprivation vs. physiological breast feeding, mouse pups are cross-fostered at birth to colostrum-producing or mature-milk producing dams. Pups are monitored until day of life 7, when they are challenged with different sepsis models: polymicrobial sepsis (cecal slurry), sterile bacterial inflammation (lipopolysaccharide), or sterile viral inflammation (poly I:C). Prior to challenge and continuing until clinical endpoint, pups will be non-invasively assessed via NIMO. This incorporates Indirect Calorimetry (IC) and Pulse Oximetry to track vital organ function and metabolic variables essential for determining overall trajectories that lead to immune resilience against infection.

Results: Preliminary findings reveal that colostrum-deprived pups are significantly more susceptible to all three models of sepsis, having more severe clinical scores and a higher degree of weight loss compared to control pups. Additionally, colostrum-deprived pups have a significantly reduced resting energetic expenditure (measured via IC) than colostrum-fed pups prior to challenge. Future studies will employ NIMO technologies early in the challenge course to identify the physiological drivers of sepsis susceptibility in colostrum-deprived animals.

Conclusions: The NIMO platform will enable us to bridge preclinical to clinical insight into how disruptions to early-life feeding impact homeostatic physiology. Hence, this research addresses a fundamental knowledge gap with direct translational potential and the potential to inform public health strategies to improve neonatal health.

Poster 12B

Title: CONCURRENT VERSUS SEQUENTIAL ADMINISTRATION OF TDAP AND RSV VACCINES IN PREGNANCY – A PILOT FEASIBILITY TRIAL (COSTAR).

Authors: **H. Obeid[1,2,3],** K. Salter[1,2,3], J. Breeze[1,2,3], T. Kollmann[1,2,3], S. Halperin[1,2,3], J. Langley[1,2,3], B. Abu-Raya[1,2,3].

Affiliation: [1]Dalhousie University, [2]IWK Health Centre, [3]Canadian Center for Vaccinology.

Introduction: To protect infants from Respiratory syncytial virus (RSV) and pertussis diseases, RSV (RSVpreF) and pertussis (Tdap) vaccines are advised in pregnancy. Non-pregnancy studies suggest that giving the 2 vaccines together may result in reduced antibody responses transferred to infants. Given the need for and complexity of coadministration pregnancy vaccine trials, we are seeking to determine feasibility of conducting this trial at Canadian institutions.

Methods: This is a multicenter, randomized, observer-blinded placebo-controlled phase 4 trial (NCT07097012). Intervention and visits: Concurrent group: Visit 1: Normal saline at 28-29+6 wks gestation (WG); Visit 2: Tdap and RSVpreF vaccines 4 wks later; Sequential group: Visit 1: Tdap at 28-29+6 WG, Visit 2: RSVpreF and placebo 4 wks later. Visit 3 is 4 wks after visit 2 and visit 4 is at delivery (mothers and newborns). Blood is collected during visits 1-4. Target is 30 participants/group. Outcomes: **Feasibility:** Screening, consent, randomization, retention, and protocol compliance rates; **Safety:** Adverse Event Following Immunization (AEFI), pregnancy and birth Adverse Events of Special Interest (AESI) and Serious Adverse Event (SAE) after vaccination; **Immunogenicity:** Seroconversion of anti-*B. pertussis* and RSV preF IgG 4 wks after vaccination; Anti- *B. pertussis*, RSV preF IgG levels at birth.

Results: As of 13 Feb 2026, the team at Canadian Center for Vaccinology, have screened 10, consented and randomized 9 (1 screen failure). The team at the Vaccine Evaluation Center, BC, has screened, consented and randomized 5. Screening visits are planned at the Ottawa Hospital Research institute, ON, and ethics approval is pending at CHU Sainte-Justine, QC. Current retention and compliance with trial protocol rates are 100%. No SAE (related to study product), AESI or AEFI has been reported. Challenges resolved: blinded Electronic Medical Records (EMR) product registration, IWK EMR trial setup.

Conclusions: A complex pregnancy vaccine trial is successfully underway at several Canadian institutions. Future work will test samples for RSV and pertussis antibodies levels and functions.

Poster 13A

Title: VACCINE UPTAKE IN OLDER ADULTS UNDERGOING COMPREHENSIVE GERIATRIC ASSESSMENT: A REPORT FROM THE EFI-CGA STUDY

Authors: **A. Huang[1],** B. Clarke[1], X. Song[1], O. Theou[1], J. Penwarden[1], K. Rockwood[1], M.K. Andrew[1]

Affiliation: [1]Dalhousie University

Introduction: Vaccine uptake among older adults remains suboptimal. Individuals with frailty or cognitive decline are at particularly increased risk for morbidity and mortality from vaccine-preventable diseases. We examined influenza, pneumococcus, tetanus, and zoster vaccination status in participants of the Electronic Frailty Index/Comprehensive Geriatric Assessment (eFI-CGA) study.

Methods: For 81 Nova Scotia eFI-CGA site participants, vaccination status was recorded on the geriatrician paper CGA as yes/no for being up-to-date with seasonal influenza and tetanus vaccinations, and as yes/no for prior pneumococcal or zoster vaccinations. Vaccine data were not part of the study's electronic Frailty Index data Quality Assurance process. Frailty was measured using the Clinical Frailty Scale.

Results: Mean age was 84.1 years (range 65–98). 58.0% were female. 40/81 (49%) had vaccination data; missingness not associated with sex, frailty, or cognition and was highest for tetanus (74%), followed by pneumococcus (54%), influenza (54%), and zoster (49%). 50% of respondents were vulnerable and 26% frail. 93% vaccinated for influenza, 57% for pneumococcus, 47% for tetanus, 46% for zoster. Non-frail individuals were more likely to be up-to-date with tetanus (p=0.039). There was no association of sex, frailty, or cognition with any other vaccine status.

Conclusions: Vaccination status may be frequently missing from clinical assessments even when included on standardized clinical tools such as CGA. Potential contributors include respondents/collateral not recalling vaccination history and providers placing a lower priority on asking about vaccination status. Electronic assessments may offer an opportunity to support collection of vaccination status by directly harvesting from provider logs, pharmacy records, and vaccine registries.

Poster 13B

Title: HYBRID UNIVERSAL AND RISK-BASED HOSPITAL ADMISSION SCREENING FOR CARBAPENEMASE-PRODUCING ENTEROBACTERALES IN HALIFAX: A QUALITY IMPROVEMENT INITIATIVE

Authors: **L. Tennenhouse[1],** G. Patriquin[1], I. Davis[1], J. Comeau[1], M. Downing[1]

Affiliation: [1]Dalhousie University

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Poster 14A

Title: ESCAPE FROM SARS-COV-2 NSP1-MEDIATED HOST SHUTOFF IS DETERMINED BY SEQUENCE FEATURES 10-18 NUCLEOTIDES FROM THE 5' END OF MRNA

Authors: **Madeleine Stolz**[1], Caleb Galbraith[1], Scott Tersteeg[2], Emily Andrews[1], Trushar R. Patel[2], and Denys A. Khaperskyy[1]

Affiliation: [1]Dalhousie University, [2]University of Lethbridge

Introduction: Host shutoff is a process by which viruses suppress host gene expression. Non-structural protein 1 (Nsp1) of SARS-CoV-2 binds the ribosome and drives host shutoff by blocking mRNA access to the ribosome's RNA entry channel and by degrading host transcripts. At the same time, Nsp1 shutoff is selective and permits translation of viral transcripts and select host mRNAs, such as the stress granule-binding TIA1-related protein (TIAR), and many host mRNAs containing terminal oligopyrimidine (TOP) motifs. In SARS-CoV-2, the 5' leader sequence shared between all viral transcripts confers Nsp1 resistance, however the mechanism whereby viral or select host transcripts escape Nsp1 shutoff is poorly understood.

Methods: We used mScarlet reporter assays and fluorescence microscopy to measure expression of mScarlet under the control of select 5' untranslated regions (UTRs) in the presence of Nsp1. We furthermore performed 5' rapid amplification of cDNA ends (RACE) to determine at which nucleotide position in the 5'UTRs reporter translation is initiated.

Results: We examined the features of TIAR mRNA that allow it to resist Nsp1 shutoff and showed that the absence of guanosines (Gs) from a window 10-18 nucleotides downstream from the 5' end of both TIAR mRNA and viral mRNAs is sufficient and necessary to confer Nsp1 resistance. We also showed that removal of Gs from the 10-18 nucleotide window in the 5'UTR of a susceptible control mRNA similarly conferred Nsp1 resistance. The TOP motif-containing transcript encoding eukaryotic elongation factor 2 (EEF2), however, displayed Nsp1 resistance despite lacking a G-less window in its 5' UTR, suggesting that transcripts can escape Nsp1 shutoff by multiple mechanisms.

Conclusions: We provide evidence that a G-less window in the first 10-18 nucleotides of the TIAR 5'UTR and viral 5'UTRs confers Nsp1 resistance. Our findings are consistent with a model that argues that the Nsp1 escape is not determined by the secondary structure, but by sequence features of mRNA 5'UTRs.

Poster 14B

Title: PUBLIC VIEWS ON A SHARED COST FUNDING MODEL TO ADDRESS BARRIERS FOR RECOMMENDED BUT UNFUNDED VACCINES IN COMMUNITY PHARMACIES: A CANADIAN IMMUNIZATION RESEARCH NETWORK (CIRN) STUDY

Authors: **C. Zuniga[1],** S. Mizen[1], K. Slayter[1,2], T. Ramsey[1,3], J.E. Isenor[1], F. Lalji[4], J. Kaczorowski[5], N.M. Waite[6], D. Halperin[1,7], S. Halperin[1], E. Black[1]

Affiliation: [1]Dalhousie University (Canadian Center for Vaccinology), [2]IWK Health, [3]Nova Scotia Health, [4]University of British Columbia, [5]University of Montreal, [6]University of Waterloo, [7]St. Francis Xavier University

Introduction: Some vaccines recommended by the National Advisory Committee on Immunization lack public funding, requiring out-of-pocket payment or private insurance coverage. Evidence suggests that unfunded vaccines are often perceived as less important by the public and healthcare providers, and prescribers may hesitate to recommend them due to affordability concerns. This study explored public perspectives on a shared cost funding model (i.e., patients initially pay more out-of-pocket while the government gradually assumes a larger share) as a potential solution to cost-related barriers for recommended but unfunded vaccines (RUVs), focusing on implementation in community pharmacies.

Methods: Virtual focus groups were conducted with members of the public from December 2024 to January 2025. Thematic analysis, informed by the Theoretical Framework of Acceptability, was used to identify patterns in the data.

Results: Eight focus groups, with 35 participants, were completed. Participants represented a broad range of ages, income levels, and urban and rural residences. Five key insights were identified: 1) Something is better than nothing, reflecting acceptance of the model's partial coverage over no funding for RUVs; 2) Limited affordability, highlighting that partial funding remains ineffectual for individuals with low or no disposable income; 3) Equality does not address equity, underscoring how a “one-size-fits-all" approach overlooks income disparities and vulnerability factors; 4) Operational barriers to shared cost vaccine delivery, including challenges with remote pharmacy access, inconsistent vaccine supply, and inadequate infrastructure; and 5) Clear information drives model engagement, emphasizing transparent details of the model and increased vaccine education to bridge information gaps and promote vaccine uptake.

Conclusions: Participants recognized the potential of shared-cost models to reduce cost-related barriers to RUV access, but consistently emphasized that uniform application would be insufficient. Equity-informed affordability mechanisms that account for income and vulnerability, combined with transparent communication and comprehensive vaccine education, were identified as essential components for improving RUV uptake.

Poster 15A

Title: ALTERNATIVE QUADRUPLEX REAL-TIME PCR REACTIONS FOR DETECTION AND DISCRIMINATION OF STREPTOCOCCUS PNEUMONIAE SEROTYPES WITHIN SEROGROUP 6

Authors: S.F. Hatchette, N. Paterson, A. Polsky, P. Robertson, G.R. McCracken, Z. Cheng, J.J. LeBlanc

Affiliation: [1]Department of Microbiology and Immunology, Dalhousie University, [2]Division of Microbiology, Department of Pathology and Laboratory Medicine, Nova Scotia Health (NSH), [3]Department of Pathology, Dalhousie University

Introduction: Streptococcus pneumoniae causes significant morbidity and mortality worldwide, and serotyping is important to assess the burden of disease that is vaccine preventable. For serotyping, the Centers for Disease Control and Prevention (CDC) use a series of 12 quadruplex real-time PCRs; however, reaction 5 (i.e., for detection/discrimination of serotypes 6A, 6B, 6C, and 6D) often failed. This study investigated the cause of the PCR failure and provided alternative PCRs to resolve this issue.

Methods: Streptococcus pneumoniae causes significant morbidity and mortality worldwide, and serotyping is important to assess the burden of disease that is vaccine preventable. For serotyping, the Centers for Disease Control and Prevention (CDC) use a series of 12 quadruplex real-time PCRs; however, reaction 5 (i.e., for detection/discrimination of serotypes 6A, 6B, 6C, and 6D) often failed. This study investigated the cause of the PCR failure and provided alternative PCRs to resolve this issue.

Results: Failure of the quadruplex PCR reaction 5 was associated with overlapping 6ABCD and 6BD targets. The separation of 6ABCD and 6BD targets in the alternative quadruplex PCRs A1 and A2 allowed sensitive and specific detection of serotypes 6A, 6B, 6C, and 6D, without impacting detection of serotypes 10F, 11BC, 18CFBA, and 37.

Conclusions: This study highlights the importance of rigorous author and peer-review to avoid manuscript errors and unintended consequences. By explaining what caused PCR failure, and proposing alternative quadruplex PCRs, this study demonstrates the value of scientific collaboration to ensure molecular assays best serve the scientific community.

Poster 15B

Title: A COST-SPARING EXTRACTION-FREE PCR FOR ANAPLASMA PHAGOCYTOPHILUM

Authors: **G.R. McCracken,** J.J. LeBlanc

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Introduction: The causative agent of human granulocytic anaplasmosis (Anaplasma phagocytophilum) is transmitted by the same Ixodes tick vector as Lyme disease. Nova Scotia is a well-recognized hotspot for Lyme disease, but awareness of anaplasmosis is limited despite hundreds of cases reported annually. To help identify anaplasmosis, Nova Scotia provides reflex PCR on all sera submitted for Lyme serology, which comes at a significant cost. This study assessed the feasibility of A. phagocytophilum PCR on sera without prior nucleic acid extraction (i.e., extraction-free PCR) as a cost- and time-sparing solution.

Methods: Sera from 40 previously positive specimens were compared using A. phagocytophilum PCR, with and without nucleic acid extraction. For DNA extraction, 200 µl of serum was processed using a Roche Mag96 instrument. Real-time PCR targeting A. phagocytophilum msp2 was performed with a Taqman Fast Virus 1-step kit on an ABI7500Fast thermocycler. Purified DNA (5 µl) was used as template and for extraction-free PCR, 5 µl sera was used instead. 10-fold serial dilutions of positive sera were also used to assess the limit of detection (LoD) and compare threshold (Ct) cycle values.

Results: While A. phagocytophilum was detected in all 40 sera with and without nucleic acid extraction, the Ct values were on average 3.6 Ct higher with the extraction-free PCR. Similar results were noted in the LoD analyses.

Conclusions: With Ct shifts observed with extraction-free PCR, this data suggests a small reduction in analytical sensitivity. While no impacts were seen with the specimens tested, A. phagocytophilum detection might be falsely negative in sera with low DNA concentration such as early or late disease. On the other hand, extraction-free PCR resulted saved approximately 1.5 hours of hand-on time and reduced PCR test costs from $15 to $3. This approach could be a time- and cost-sparing solution for epidemiological investigations.

Poster 16A

Title: CO-DESIGNING DIGITAL LITERACY INTERVENTIONS WITH HIGH SCHOOLS TO ADDRESS STUDENT VACCINE HESITANCY, HEALTH MISINFORMATION, AND LOW HEALTH LITERACY: A PILOT STUDY PROTOCOL

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Introduction: Vaccine hesitancy among adolescents is a growing public health concern, intensified by widespread exposure to health misinformation in digital environments and variable levels of health, media, and scientific literacy. Social media platforms commonly used by youth amplify scientific-sounding misinformation, which can undermine vaccine confidence and trust in science. Adolescence represents a critical window for intervention, as decision-making skills are actively forming. The objective of this pilot study is to co-design youth-centered interventions to strengthen scientific literacy and critical appraisal skills through intervention co-design and evaluation.

Methods: Using a community-based participatory research design, we will partner with high schools, Indigenous Knowledge Keepers, educators, and students in Nova Scotia. The Trust Erosion Framework will be used to guide intervention design and evaluation constructs. The study will include training of students in vaccine science, media literacy, and content creation (3-months); student-led co-creation and dissemination of the intervention through social media and school-based activities (3-months); and intervention evaluation (3-months). We will employ pre- and post-intervention surveys designed to assess inclusivity, accessibility, and improvement in students' vaccine confidence, scientific literacy, and misinformation appraisal skills.

Results: The intervention is expected to increase students' vaccine knowledge and confidence and ability to evaluate and identify misinformation. Pre- and post-intervention results will highlight changes in misinformation appraisal scores. Intervention and process evaluation will generate data on feasibility, acceptability, and reach.

Conclusions: This protocol is a youth-driven model for vaccine education that integrates digital literacy, co-design, and culturally respectful engagement. Findings will inform future vaccine confidence initiatives and provide evidence to support participatory, equity-oriented approaches to countering health misinformation and strengthening trust in science among youth. If evaluated as effective, the results of this pilot will be used to advocate for informed scale-up and dissemination across Nova Scotia.

Poster 16B

Title: PARTNERING WITH YOUNG MEN WHO HAVE SEX WITH MEN TO CO-DESIGN A DIGITAL HEALTH LITERACY TOOL TO SUPPORT HPV VACCINE DECISION-MAKING

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Introduction: Human papillomavirus (HPV) is a common, preventable infection that increases morbidity and mortality. Young men who have sex with men (YMSM) experience a disproportionate burden of HPV-related disease, yet vaccine uptake remains low. Key barriers include limited access to inclusive information, stigma, and mis- and disinformation. Digital health interventions offer a promising way to improve health literacy and support informed, autonomous vaccine decision-making. This study aims to co-design a user-centered digital health literacy tool with YMSM aged 18–26 years. The current study phase aims to 1) engage YMSM partners and a community engagement council (CEC) to co-define priorities; and 2) conduct a scoping review of digital health literacy tools relevant to YMSM.

Methods: This study uses a community-based participatory research design that emphasizes partnership and lived experience. Two YMSM research partners were onboarded and trained to co-lead study activities. Recruitment of up to six YMSM CEC members is ongoing. A scoping review search strategy was co-developed and applied across five databases (Embase, CINAHL, MEDLINE, Scopus, PsycINFO). Results were imported into Covidence and screened by trained reviewers in duplicate. Conflicts were discussed and resolved by the senior reviewer. Calibration activities were conducted prior to title and abstract screening and full text review.

Results: YMSM research partners identified key community organizations for CEC recruitment and co-created inclusive recruitment materials. The search strategy yielded 1,640 results for title and abstract screening following duplicate removal (n=406). As of February 2026, 109 articles were moved to full-text review. Data extraction is underway, and final results will be presented in narrative summaries and tabular formats.

Conclusions: By centering YMSM voices and lived experiences, this co-designed digital health literacy tool aims to support informed, value-aligned decision-making, and improve HPV vaccine confidence and uptake among YMSM. Next steps include a modified Delphi process with YMSM to collaboratively develop consensus statements to guide tool content and features, followed by prototype development and focus groups to support iterative refinement.

Poster 17A

Title: PUBLIC & HEALTHCARE PROVIDER PERSPECTIVES ON MENINGITIS B VACCINE AWARENESS AND COMMUNICATIONS IN CANADA

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Introduction: In Canada, Meningitis B (MenB) is the most common bacterial serogroup responsible for Invasive Meningococcal Disease (IMD); however, MenB vaccines are not routinely funded by provinces and territories, impacting awareness, access, and uptake. This study examined what healthcare providers (HCPs) and the public understand, need, or want to know about IMD, MenB, and vaccination.

Methods: We employed a mixed-methods design guided by the CFIR and i-PARIHS frameworks. Data were collected using a Canadian survey of HCPs (n=254) and online interviews with public participants with lived MenB experience (n=32). Frameworks supported integrated analysis across groups.

Results: Both groups identified challenges accessing clear and consistent information about MenB, vaccination schedules, eligibility, and costs. HCPs reported regular access to trusted government or research sources, but needed updated data on prevalence, indications, safety, effectiveness, and affordability. Public participants described learning about MenB mostly during outbreaks, relying on informal networks and online searches, and finding information too technical and contradictory. While HCPs viewed themselves as responsible for vaccine communication—and public participants trusted HCPs—both groups noted conversations about MenB were infrequent. HCPs included MenB less often than routine vaccines (19% vs. 49% “always included”). Cost and time were cited as key barriers; HCPs described affordability as also limiting discussions, while public participants perceived unfunded vaccines as less important. Both groups highlighted proactive awareness through plain-language digital communication, personal stories, and delivery at key opportunities (e.g., university orientation), identifying Public Health agencies as best positioned to lead consistent communications.

Conclusions: Integrating HCP and public perspectives highlights recognition of systemic challenges to MenB vaccination and the need for Public Health agencies to lead consistent, proactive communications. Equity-focused strategies supported by updated resources, plain-language messaging, digital outreach, and improved funding and access are needed to strengthen MenB literacy, support decision-making, and enhance vaccine uptake.

Poster 17B

Title: ADAPTING AN IMMUNIZATION ASSESSMENT TOOL FOR ADULTS IN A CANADIAN JURISDICTION: AN IMPLEMENTATION PILOT

Authors: **B. M. Selig[1-2],** J. Mannette[1-2], C. Zuniga Chacon[1-2], E. Bentley[3], S. Buchan[4], D. Halperin[1,5], S. Halperin[1-2], K. McIsaac[6], SJ. Moss[1-2], J. Parsons Leigh[1-2], K. Salter[1-2], J. Comeau[1-2,7] for the Canadian Immunization Research Network (CIRN) Investigators[8]

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Introduction: Immunization Assessment Tools (IATs) personalize vaccine recommendations by matching an individual's demographic and risk profile to local guidelines. IATs can improve vaccine awareness and uptake, and tool adoption can be maximized by involving end-users in the design process. For this study, we adapted a Prince Edward Island-developed IAT for use in Nova Scotia and generated implementation evidence to inform scale-up. The objectives of the current phase of this multiphase study were to co-draft the adapted-IAT with end-users (community members [CMs], healthcare providers [HCPs]), integrate their feedback into the tool, and pilot it with end-users.

Methods: Building on an environmental scan and interviews, we convened consultative discussion groups with end-users to refine content, design, and outputs of the adapted-IAT; feedback was iteratively integrated. The adapted-IAT was launched in January 2026 to be piloted with approximately 400 end-users. Implementation will be guided by the i-PARIHS framework and pre/post-IAT surveys will assess tool usability and acceptability, and explore changes in vaccine recommendation awareness, perceived risk of vaccine-preventable diseases, and vaccine-seeking intentions/behaviors.

Results: 13 participants (ages 18–54 years; HCPs n=4; CMs n=9) participated in consultative discussion groups. Feedback clustered into three areas: readability (plain language; embedded definitions), design (branding/visuals; accessibility features), and engagement/output (record retrieval guidance; where to book vaccines). Participants' perceived value of the adapted-IAT included the potential to save HCP's time, empower users to ask questions about vaccination, and privately address sensitive topics. IAT-NS pilot results will be analyzed and presented as summary statistics, frequency distributions, and descriptive statistics.

Conclusions: Early co-design indicates that successful IAT implementation depends not only on accurate recommendations, but also on readable content, accessible design, and actionable next steps that support users to move from recommendations to booking. Pilot findings will inform jurisdictional implementation planning and a targeted knowledge-translation webinar series in Spring 2026.

Poster 18A

Title: ENGAGING YOUTH RESEARCH PARTNERS TO IDENTIFY AND CLOSE GAPS IN STRUCTURAL DETERMINANTS OF HEALTH AND HEALTH EQUITY

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Introduction: Many influential determinants of youth health are structural, rooted in social, economic, and political contexts. Limited evidence exists on which structural factors most strongly affect youth health and how these differ from adult determinants. The overall study objective is to partner with youth aged 15-24 years to address health inequities through co-creation of evidence-based consensus statements to enhance youth engagement in structural determinants of youth health and health equity research. The objective of this first phase was to strengthen community-academic collaboration and develop a cross-sectional survey to assess youth knowledge and awareness of structural determinants of youth health and health equity.

Methods: Using a community-based participatory research design, we formed a community engagement council (CEC; n=6) to advise on study direction and hired youth research partners (YRPs; n=2) to co-lead study activities. Led by a YRP, survey development followed a theory-informed process: 1) defining constructs and domains using the IOM Health Literacy Framework and WHO Conceptual Framework for Action on the Social Determinants of Health; 2) developing survey objectives aligned with those constructs; and 3) generating survey items. The CEC provided pre-testing feedback to refine survey clarity and relevance.

Results: A Terms of Reference outlining CEC membership, roles, and responsibilities was co-developed with the CEC and research team. The survey will be refined through iterative rounds of CEC feedback. CEC survey feedback as of February 2026 includes suggestions such as adding a progress bar to track progress, dividing the survey into two halves (e.g., “Part A” and “Part B”) to encourage survey completion, and to further simplify the wording of the questions where possible.

Conclusions: By centering youth as co-designers of research rather than passive participants, this work offers a model for meaningful community-academic collaboration, laying the groundwork for youth-driven evidence on structural determinants of health. Next steps include finalizing and implementing the co-developed survey with a target sample of 400 youth in Nova Scotia in Spring 2026 to assess knowledge, awareness, and health literacy related to structural determinants of health.

Poster 18B

Title: TCEPVDB: ARTIFICIAL INTELLIGENCE-BASED PROTEOME-WIDE SCREENING OF ANTIGENS AND LINEAR T-CELL EPITOPES IN THE POXVIRUSES AND THE DEVELOPMENT OF A REPOSITORY

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Introduction: Poxviruses constitute a family of large dsDNA viruses that can infect a plethora of species including humans. Historically, poxviruses have caused a health burden in multiple outbreaks. The large genome of poxviruses favors reverse vaccinology approaches that can determine potential antigens and epitopes. Here, we propose the modeling of a user-friendly database containing the predicted antigens and epitopes of a large cohort of poxvirus proteomes using the existing PoxiPred method for reverse vaccinology of poxviruses.

Methods: In the present study, we obtained the whole proteomes of as many as 37 distinct poxviruses. We utilized each proteome to predict both antigenic proteins and T-cell epitopes of poxviruses with the aid of an Artificial Intelligence method, namely the PoxiPred method. PoxiPred was originally developed as an agnostic classification framework for predicting antigens and LTCEs in poxvirus protein datasets, functioning as an early data curation step. For the construction of TCEPVDB, we did not develop new models; instead, we employed the pre-trained Deep Learning Artificial Neural Network (DL-ANN) models for (i) antigen prediction and (ii) LTCE prediction. We implemented TCEPVDB as a web tool using the Django framework (version 4.2.4) for Python (version 3.11) web development.

Results: In total, we predicted 3966 proteins as potential antigen targets. Of note, we considered that this protein may exist in a set of proteoforms. Subsets of these proteins constituted a comprehensive repository of 54,291 linear T-cell epitopes. We combined the outcome of the predictions in the format of a web tool that delivers a database of antigens and epitopes of poxviruses. We also developed a comprehensive repository dedicated to providing access to end-users to obtain AI-based screened antigens and T-cell epitopes of poxviruses in a user-friendly manner. These antigens and epitopes can be utilized to design experiments for the development of effective vaccines against a plethora of poxviruses.

Conclusions: The developed TCEPVDB is devoted to providing a comprehensive catalog of a total of 3966 proteins as potential antigen targets and 54,291 linear T-cell epitopes from 37 distinct poxviruses. The antigen proteins and linear T-cell epitopes embedded in this database are predicted using the AI-based PoxiPred method.

TCEPVDB is a user-friendly database and can be freely accessed using the following URL: https://tcepvdb.microbiologyandimmunology.dal.ca/.

With further progress in genome sequencing and the AI-based screening of antigens and epitopes, we anticipate that the number of entries in TCEPVDB will eventually grow in the upcoming years. Taken together, the information available in TCEPVDB can be used in efforts of reverse vaccinology, facilitating the rapid development of effective vaccines to tackle poxviruses in a significant manner.

Poster 19A

Title: REAL-TIME MULTIPLEXED PCR FOLLOWED BY AMPLICON TILING AND NEXT-GENERATION SEQUENCING FOR ACCURATE RESOLUTION OF STREPTOCOCCUS PNEUMONIAE SEROTYPES

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Introduction: Streptococcus pneumoniae is a respiratory pathogen responsible for significant morbidity and mortality worldwide. Serotyping is important to establish the proportion of pneumococcal disease that is vaccine-preventable and inform vaccine policy. While traditional serotyping has merit, molecular methods have gained popularity as they do not require live organism and are amenable to automation. Real-time multiplex PCRs (rmPCRs) by the Centers for Disease Control and Prevention (CDC) can detect 64 serotypes, but some cannot be differentiated (e.g., 7F and 7A). Next-generation sequencing (NGS) can provide serotype-level resolution but lacks sensitivity unless performed on cultured isolates. This study aimed to resolve S. pneumoniae serotypes previously indistinguishable by rmPCRs using target-enriched NGS following amplicon tiling of cps loci targets conferring serotype specificity.

Methods: Of the CDC rmPCRs reactions, 31 serotypes cannot be differentiated from closely related serotypes (e.g., 7F/A, 9NL, 9A/V, 11A/D/E/F, 11B/C, 12F/44, 15A/F, 15B/C, 18C/F/B/A, 24F/A/B, 28F/A, 33F/A, and 35F/47F). Reference genomes for serotypes of interest were retrieved from the Genbank database and genes associated to serotype specificity were targeted. PrimalScheme was used to design primers for two pools of overlapping amplicons for each cps target region. Following conventional PCR with DNA from previously characterized reference strains for each S. pneumoniae serotypes, the amplicon pools were subjected to NGS using Illumina technology. Paired isolates and PCR-positive nasopharyngeal swabs (n=188) collected from carriers of S. pneumoniae were also tested by the CDC rmPCRs and the NGS.

Results: Using reference strains, each serotype that previously could not be resolved with rmPCR-based serotyping was discriminated with a combination of rmPCR followed by target enriched NGS. When applied to 188 paired nasopharyngeal swabs and cultured S. pneumoniae isolates, each serotype was accurately resolved.

Conclusions: Target-enriched NGS following rmPCR can accurately identify S. pneumoniae serotypes, further enhancing the performance of epidemiological tools to assess pneumococcal disease.

Poster 19B

Title: STUDENT AND EXPERT PREFERENCE INTERSECTIONS TO INFORM MICROBIOLOGY CURRICULUM IN UNDERGRADUATE NURSING AND HEALTH SCIENCES

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Introduction: Microbiology is typically offered as a stand-alone course in the first year of undergraduate health programs; however, the delivery and curriculum may differ between programs. This inconsistency can cause variations in content taught across Bachelor of Science in Nursing (BScN) programs, which may impact the clinical knowledge students possess when beginning practice. In this study, we objectively assessed publicly available syllabi from Canadian BScN programs for microbiology topics and evaluated the opinions of relevant stakeholders about the microbiologic concepts considered core to BScN programs.

Methods: Using the Canadian Association of Schools of Nursing's (CASN) list of accredited nursing schools, an environmental scan was conducted in May 2024 to collect publicly available data on whether microbiology was included as a stand-alone course requirement for Canadian BScN programs. Additionally, publicly available course syllabi were reviewed. A survey was used to determine the microbiology topics relevant stakeholders considered core to BScN programs. Survey questions were derived from three sources, specifically, publicly available and personally communicated syllabi, the American Society for Microbiology (ASM) Undergraduate Curriculum Guidelines, and the ASM Guidelines for Microbiology in Nursing Education.

Results: Using a total of 55 CASN-accredited BScN institutions, publicly available data demonstrated that 37 (67.3%) institutions offered a stand-alone microbiology course. Average composite scores of importance and depth of coverage demonstrated six highly rated microbiology topics. When participants were categorized based on their role as either a student, health professional, or content expert, topic scores correlated well between groups with R2 values greater than 98% for all three permutations.

Conclusions: Our study demonstrates commonalities in microbiology topics that are thought to be important by three distinct groups: nursing students, practicing health professionals, and content experts. Opinions from these groups mostly align with overarching themes in prior guidelines. Future iterations of a microbiology for nursing curriculum should focus on emphasizing subjects of high importance and deemphasizing topics thought to be of little value.

Poster 20A

Title: THE RESACPE ASSAY AS AN ALTERNATIVE TO THE MODIFIED CARBAPENEM INHIBITION METHOD FOR THE DETECTION OF CARBAPENEMASE-PRODUCING ENTEROBACTERALES

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Introduction: The use of carbapenem antibiotics as a treatment for bacterial infections is threatened by the rise of carbapenemase producing Enterobacterales (CPE). This makes timely detection of CPEs in the clinical laboratory essential for appropriate antibacterial treatments and for infection prevention and control (IPAC) interventions. The modified carbapenem inhibition method (mCIM) is typically used to identify CPEs, however it requires a turnaround time of approximately 24 hours. We set out to to investigate the performance of a colourmetric assay, resaCPE in testing a variety of mCIM-positive (CPE) and mCIM-negative carbapenem-resistant bacterial isolates, assessing its ability to rapidly (within the same day) identify carbapenemase production among clinical bacterial isolates from multiple genera.

Methods: A panel of 64 carbapenem-resistant clinical bacterial isolates stored at the QEII Health Sciences Centre in Halifax NS, were used to validate the ResaCPE assay (51 mCIM-positive, 11 mCIM-negative, and 2 mCIM-indeterminate). Results of the resaCPE assay were used to determine sensitivity and specificity versus the reference method, mCIM. Polymerase chain reaction (PCR) was used to detect carbapenemase genes, and the enzyme was detected using a commercial lateral flow assay, Carba5 (NG Biotech), which identifies IMP, KPC, NDM, OXA-48, and VIM enzymes.

Results: The resaCPE assay had a sensitivity of 98% (when compared to the mCIM). The assay reliably detected plasmid-encoded KPC, NDM, OXA-48, and VIM enzymatic activity, as well as chromosomal NMC and SME enzymes. The assay specificity was 100% as all tested mCIM-negative isolates were also negative by resaCPE.

Conclusions: The ResaCPE assay provides an accurate and rapid alternative to mCIM detection of CPEs. Work is ongoing to test a larger panel of enzymes and organisms, and to use the resaCPE assay prospectively to assess its implementation into laboratory processes.

Poster 20B

Title: CULTURING AND MICROBIOME SEQUENCING OF NASAL WASH SAMPLES FROM ADULTS INTRANASALLY INOCULATED WITH BORDETELLA PERTUSSIS

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Introduction: Pertussis is a highly contagious respiratory illness caused by the bacterium Bordetella pertussis (B. pertussis). The nasal microbiome is understudied, particularly in disease states, and its stability during pertussis infection is of interest. In this study, we aimed to assess the viability of culturing and sequencing of B. pertussis and other resident bacteria from previously collected nasal wash (NW) samples.

Methods: NWs were obtained from the CCfV's D420 pertussis Controlled Human Infection Model (CHIM) study. A total of 120 samples were selected based on participants' clinical outcome (infected vs non-infected), dose category to which they were inoculated, and vaccine priming status (whole-cell pertussis vs acellular pertussis). NWs were thawed and plated on charcoal blood agar plates supplemented with 0.04 g/L cephalexin monohydrate to assess if the frozen storage of neat NWs impacts the recovery of viable B. pertussis. DNA and TNA extractions of the same samples were performed using the KingFisher Duo Prime magnetic particle processor: MagMAX™ Prime Viral/Pathogen NA Isolation Kit for TNA and MagMAX™DNA Multi-Sample Ultra 2.0 Kit. Full-length 16S rRNA gene sequencing was performed using the PacBio Vega system. Bioinformatics analysis was performed using QIIME-2, following the Microbiome Helper SOPs.

Results: Culturing was successful for some unidentified bacteria, but B. pertussis growth was not observed. Microbiome sequencing was successful, but TNA extractions yielded higher read depths. Microbiome profiles from the TNA extractions identified 50 - 148 unique bacterial taxa per sample from the phyla Proteobacteria, Firmicutes, Actinobacteria, Campylobacteria, and Fusobacteria. B. pertussis was also identified from the microbiome profiles and had varying relative abundance across the samples.

Conclusions: The culture results indicate that freezing neat NWs is insufficient to maintain B. pertussis viability. This finding is significant, as alternative preservation methods need to be explored if pertussis CHIM research is expanded to sites lacking culturing capacity. Despite B. pertussis viability weaning after neat frozen storage, B. pertussis was detected by sequencing these samples. This finding is supported by previous research showing that nucleic acid sequencing is highly sensitive for detecting pertussis.

Poster 21A

Title: ANTIMICROBIAL USE AMONG INPATIENTS WITH INFLUENZA

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Introduction: Oseltamivir reduces length of hospitalization and may reduce mortality in adults hospitalized with influenza. During the 2023-24 influenza season, the rate and timeliness of oseltamivir prescribing for influenza-positive inpatients at the QEll Health Sciences Centre was suboptimal. In response, interventions were implemented in 2024–25, including dissemination of educational resources by the Nova Scotia Health Antimicrobial Stewardship Program and the introduction of inpatient influenza assessments by the Influenza Treatment Team in collaboration with the Emerging and Re-emerging Infections Network. We aim to re-evaluate inpatient influenza antimicrobial management through retrospective chart review.

Methods: Identifiers were collected for all patients in the laboratory Information System (LIS) with positive documented influenza tests from the QEII, November 2024 to April 2025. From these, 120 patients were selected randomly using a weighted distribution according to positive tests identified each month. Charts for adult inpatients were retrospectively reviewed for relevant clinical details.

Results: The following are preliminary results based on 65 influenza-positive inpatients. Sixty-three of 65 (97%) patients were prescribed oseltamivir during their time in hospital, all of whom had risk factors for influenza complications. Two-thirds (44/65) required supplemental oxygen. The mean time from influenza test collection to oseltamivir administration was 22.0 hours, and from test reporting to administration was 11.6 hours. One quarter (16/65) of patients were prescribed oseltamivir empirically prior to test report. Two-thirds (43/65) were also prescribed an antibiotic for a respiratory indication during their influenza illness course, with an average total duration of 5 days. Of antibiotics prescribed within 48 hours of influenza assessment, 24% (8/34) were discontinued or narrowed after the return of the influenza test result.

Conclusions: The rate of antiviral prescribing amongst inpatients with influenza was appropriately high, though there is room for improvement in overall empiric prescribing. Future efforts toward reassessing and deprescribing of unnecessary antibiotics for viral respiratory illness should be prioritized.

Poster 21B

Title: ACTIVATION OF UTERINE CONTRACTILITY PATHWAYS BY VAGINAL MICROBIOTA AS A TRIGGER OF INFECTION-INDUCED PRETERM BIRTH

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Introduction: Preterm birth (PTB) affects 15 million pregnancies annually and is the leading cause of death and disability in children under five. Up to 60% of cases are associated with bacterial intrauterine infection, commonly resulting from ascension of dysbiotic vaginal bacteria. Proteolysis is a central feature of labour induction that leads to cervical dilation, water breaking, and uterine contractions. The human protease endothelin-converting enzyme (ECE1) contributes to labour onset by cleaving the precursor peptide big endothelin-1 (bET1) into bioactive endothelin-1 (ET1), which induces uterine contractions. The vaginal bacterium Prevotella bivia encodes a metalloprotease, PepO, with sequence and domain similarities to human ECE1. This study will examine whether P. bivia can proteolyze bET1 into the bioactive ET1, thereby mimicking human ECE1 and contributing to the initiation of uterine contractile signalling.

Methods: Degradation of bET1 was assessed using P. bivia cell suspensions, cell-free supernatants and recombinant proteases. Fluorophore-quenched protease substrate assays were used to quantify protease activity against a substrate specifically designed to measure human ECE1 activity. SDS-PAGE was used to visualize bET1 degradation over a time-course, while an ET1 immunoassay was used to assess whether P. bivia cleavage of the bET1 precursor resulted in conversion to ET1.

Results: Cell-free supernatants from P. bivia and recombinant P. bivia PepO were found to proteolyze an ECE1 fluorophore-quenched substrate. Notably, an active site mutant of P. bivia PepO (HAXXH) had no detectable protease activity against the ECE1 substrate. Cell suspensions of P. bivia resulted in degradation of bET1, which corresponded to detection of the bioactive breakdown product, ET1, via immunoassay.

Conclusions: These findings confirm that the P. bivia can mimic the activity of human ECE1 via its secreted metalloprotease PepO. This work suggests that P. bivia could actively contribute to PTB initiation by proteolytic production of the uterine contractile agonist ET1.

Poster 22A

Title: REAL-WORLD EXPERIENCE OF DALBAVANCIN FOR TREATMENT OF SERIOUS INJECTION-RELATED INFECTIONS (IRI) IN PEOPLE WHO INJECT DRUGS (PWID)

Authors: **Pritchard E[1],** Reid EK[2], Murphy V[2], Burgess S[3], Sampson C[3], Bonnar PE[3], Hughes JM[3,4]

Affiliation: [1]College of Pharmacy, Dalhousie University, [2]Department of Pharmacy, Nova Scotia Health, [3]Division of Infectious Diseases, Nova Scotia Health, [4]Dalhousie University Faculty of Medicine

Introduction: Severe bacterial injection-related infections (IRI) are a known complication of injection drug use, with increased morbidity and mortality often associated with challenges adhering to traditional antibiotic therapy recommendations. Dalbavancin is a long-acting intravenous lipoglycopeptide antibiotic with infrequent administration, which may improve clinical outcomes and reduce risks with direct vascular access particularly among PWID. Despite this, dalbavancin use is low across Canada. Within Nova Scotia Health, dalbavancin is a formulary medication with specific guidance for use since July 2023.

Methods: Convenience sampling identified PWID prescribed dalbavancin from late 2023 to the end of 2025. Electronic health records were retrospectively reviewed to determine the indication, dose, duration of therapy and patient outcomes 90 days after the last dose of dalbavancin.

Results: Sixty-seven patients were included with bone and joint infection (49%), bacteremia (16%), and endocarditis or vascular infection (13%) as the most common indications. Over 70% of patients had infections with Staphylococcus aureus, with methicillin-resistant (42%) more common than methicillin-susceptible S. aureus (30%). The number of prescribed doses ranged from 1 to 7, the most common prescribing interval was weekly, and the average cumulative dose prescribed was approximately 2500 mg. Over 80% of patients completed their prescribed therapy. At 90 days after the last dose, approximately two-thirds of patients recovered and there were two documented deaths. There were three treatment failures due to adverse drug reactions, including two severe cutaneous drug reactions.

Conclusions: Dalbavancin may be an option for treatment of serious IRI in PWID, or other individuals in whom standard antibiotic regimens may not be feasible. Information surrounding its use, safety, and positive outcome profile may provide valuable information for use in other provinces.

Poster 22B

Title: OUTPATIENT PARENTERAL ANTIMICROBIAL THERAPY IN NOVA SCOTIA

Authors: **Pritchard E[1],** Murphy V[2], Bonnar PE[3], Reid EK[2]

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Introduction: Outpatient parenteral antimicrobial therapy (OPAT) enables earlier hospital discharge and may improve quality of life for patients requiring prolonged intravenous antimicrobials. Nova Scotia (NS) lacks a formal program for OPAT oversight, and provincial data on utilization, safety, and outcomes are not routinely collected. We aimed to characterize OPAT utilization, prescribing practices, and patient outcomes across NS to identify opportunities for system-level improvement.

Methods: Consecutive patients referred for OPAT across all four NS Health zones were identified over a four-week period from late 2024 to early 2025. Electronic health records were retrospectively reviewed to collect demographic, clinical, and treatment data.

Results: A total of 127 OPAT referrals were received during the study period, and 114 patients were fully assessable. Of these, 79 (69%) were new OPAT initiations. The most common indications were bone and joint infections, skin and soft tissue infections, and abscesses. The most prescribed antimicrobials were ceftriaxone, cefazolin with or without oral probenecid, and ertapenem. The median OPAT duration was 24 days (IQR 9-42). Approximately two-thirds of patients received infectious diseases consultation. During OPAT, 38% of patients had at least one emergency department visit and 16% required hospitalization. Approximately half (51%) of patients routinely received recommended laboratory monitoring throughout therapy, highlighting gaps in safety surveillance.

Conclusions: OPAT is widely used in NS and is associated with frequent healthcare encounters and gaps in monitoring. Implementation of a structured provincial OPAT program with standardized monitoring and multidisciplinary oversight may reduce complications, optimize prescribing, and improve patient and system outcomes.

Poster 23A

Title: SOCIOECONOMIC INDICATORS AND SCHOOL-BASED HPV AND HBV VACCINATION COVERAGE ACROSS NOVA SCOTIA HEALTH ZONES: A CORRELATIONAL ANALYSIS

Authors: **Eric Schillinger** [1-2], Stephana Julia Moss [2-3]

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Introduction: While area-level socioeconomic indicators are broadly associated with vaccination coverage, it is not well described which area-level indicators are most strongly correlated with zone-level vaccination coverage in Nova Scotia.

Methods: This study employs an ecological correlational analysis to explore bivariate associations between school-based immunization data and six census-derived area-level socioeconomic indicators (e.g., median income, education, household size) using Pearson's correlations. HPV coverage was defined as receipt of one dose, while HBV coverage was defined as two doses if initiated at age 12, or three doses if age 11 or younger. Statistics Canada census populations were used as denominators for coverage rates. All correlations are purely exploratory and are interpreted cautiously. Scatterplots were inspected to assess linearity and influential observations, Spearman's correlation was used as a sensitivity analysis given the small sample size (n=8) and potential outliers. Data were stratified by age (13 and 17 years of age) as recorded in administrative data, yielding n=8 observations (4 zones 2 age cohorts). Zone-level sex-disaggregated data were not available; age-stratified results are exploratory and may reflect cohort/timing differences across socioeconomic context.

Results: Analyses are underway; preliminary results will be presented. Findings will describe patterns of regional disparities and highlight areas where coverage and indicators co-vary.

Conclusions: This exploratory and hypothesis-generating study provides a baseline for evaluating the reach of provincial immunization programs. Findings may inform targeted outreach for future vaccination programs and initiatives.

Thank you

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Evaluations

Feedback and evaluation is important, and your input is essential for our future planning. You will receive an evaluation form to give us your feedback to improve this learning event. You can fill it out on paper, or online at: **bit.ly/IDDayEval2026**

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