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Session: P-71. Public Health

Background. Community-acquired pneumonia (CAP) causes substantial morbidity and mortality. There is a lack of data on the comprehensive burden of CAP across the life span in Canada. We estimated the incidence of all-cause CAP in all age groups in Ontario and British Columbia (BC), Canada.

Methods. We identified hospitalized and outpatient CAP episodes from the Discharge Abstract Database (DAD) and physician billing claims databases (Ontario Health Insurance Plan in Ontario and Medical Services Plan in BC) in both provinces. The National Ambulatory Care Reporting System was used to identify CAP episodes from emergency department visits in Ontario. CAP recorded with a primary or secondary diagnosis was identified using International Classification of Diseases 9 (480–486, 510, 513) and 10 (J10.0, J11.0, J12–J18, J86.9, J85.1) codes. We estimated the age and sex adjusted annual incidence of CAP overall, and by age groups (0–4, 5–17, 18–39, 40–64, 65–74, 75–84 and ≥85 years) according to routine childhood pneumococcal conjugate vaccine (PCV) immunization periods from 2005–2018 in Ontario and from 2002–2018 in BC. Poisson regression models were fitted with population denominators from Statistics Canada to estimate the incidence rates.

Results. Ontario had 3,607,186 CAP episodes from 2005–2015 with a mean annual incidence of 2,801 (95% confidence interval [CI]: 2,748, 2,854) per 100,000 population; incidence declined from 3,077/100,000 in 2005 to 2,604/100,000 in 2010 before increasing to 2,843/100,000 in 2018. BC had 1,146,172 CAP episodes from 2002–2008, with a mean annual incidence of 2,146 (95% CI: 2105, 2189); the incidence increased from 2,005 /100,000 in 2002 to 2,199/100,000 in 2018. A high incidence of CAP was observed in children aged 0–4 years and older adults, particularly in adults aged ≥85 years in both provinces across all PCV program periods (Figure 1).
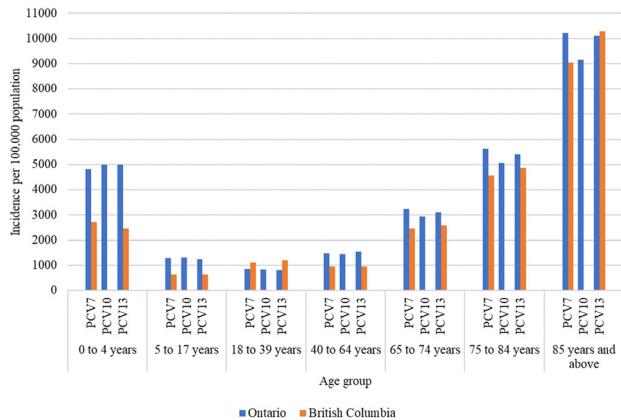

Figure 1: Age group-specific incidence of all-cause community-acquired pneumonia according to childhood pneumococcal conjugate vaccine (PCV) program periods in Ontario (PCV7 [1 Jan 2005–30 Sep 2009]), PCV10 [1 Oct 2009–31 Oct 2010] and PCV13 [1 Nov 2010–31 Dec 2018]) and British Columbia (PCV7 [1 Sep 2003–31 May 2010] and PCV13 [1 Jun 2010–31 Dec 2018]), Canada

Conclusion. CAP continues to be a public health burden in Canada despite publicly funded pneumococcal vaccination programs. Ontario seems to have higher CAP burden than British Columbia that warrants further investigation. The youngest cohort of children and older adults contribute significantly to the CAP burden.

1212. COVID-19 and the Importance of Institutional Trust to Public Health

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Session: P-71. Public Health

Background. Institutional trust is a key component of the public health system's effectiveness. However, the COVID-19 pandemic highlighted gaps in institutional trust and hesitation. Analysis was conducted to understand correlates of institutional trust to inform communication strategies for the ongoing pandemic and future public health crises.

Methods. The Roper Center for Public Opinion/ America's Voice Project Coronavirus Index conducted a US online survey February 22-April 5, 2021 and included questions about COVID-19 experiences, attitudes and behaviors. Respondents also indicated trust in each of four institutions to provide accurate information about COVID-19: federal government, state government, CDC and national public health officials. Scores were summed to create an Institutional Trust (IT) index: the top third was classified as "High IT," the middle third "Moderate IT" and the bottom third "Low IT." Data were analyzed using χ^2 tests, with z-tests for more granular between-group comparisons.

Results. Those with Low IT were significantly more likely than those with Moderate or High IT to be white, male, rural, politically conservative, married, and live with children under age 18. Low IT individuals were less likely to have been tested for COVID-19 themselves and less likely to know someone who had tested positive for COVID-19. However, Low IT respondents were more likely to have tested positive for COVID-19, even when controlling for their lower propensity to be tested. Low IT individuals were significantly more likely to have visited restaurants and stores in the past week and feel these activities posed no health risk; they also wore masks less often. Despite greater risk-taking, Low IT respondents were over five times more likely than High IT respondents to refuse the COVID-19 vaccine.

Conclusion. Low IT was associated with higher COVID-19 vaccine hesitancy as well as behavior that, at the time data was collected, put people at higher risk of contracting COVID-19. Public health officials should prioritize the development of more effective communications towards Low IT populations. Traditional methods of establishing message credibility may require modification in order to encourage Low IT individuals to participate in behaviors that enhance public health.

1213. Vaccine Uptake Amongst Participants in the North Carolina COVID-19 Community Research Partnership Who Were Initially Receptive or Hesitant to Receive a COVID-19 Vaccine

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Session: P-71. Public Health

Background. Public health officials are concerned that adults may refuse to be vaccinated with an approved COVID-19 vaccine thereby limiting the community health benefit. Here, we studied the self-reported intent to be vaccinated of persons in North Carolina (NC) and then measured whether they did or did not get vaccinated.

Methods. The Community COVID-19 Research Partnership (CCRP) is a large prospective study exploring COVID-19 epidemiology and sequelae in participants of several mid-Atlantic and Southern States. All participants complete an online daily survey where they are asked questions about COVID-like symptoms, infections, and their vaccination status. In addition to the daily survey, in December 2020, we implemented a short online cross-sectional survey questioning NC participants on whether they intended to be vaccinated. After completing the cross-sectional survey, we used daily survey data through 15 May 2021 to see if participants reported receiving vaccine. Unvaccinated participants who did not complete the daily survey 30 days or more prior to 15 May 2021 were excluded.

Results. 18,874 participants completed the cross-sectional survey and reported vaccination status. Of these participants, 90% were white, 68% were female, 26% were healthcare workers, and 2% self-reported COVID-19 diagnosis The median age was 54 years (IQR: 41 – 65). 79%, 13%, 9%, and 2% answered yes, unsure, no, and prefer not to answer, respectively, about intention to be vaccinated (Table). 99% of the participants who intended to receive the COVID-19 vaccine reporting being vaccinated. Those who were unsure or intended not to get vaccinated had vaccination rates of 80% and 53%, respectively. 78% of the participants who preferred not to answer were vaccinated.

Table. Vaccine intent versus vaccine status – COVID-19 Community Research Partnership, North Carolina, December 2020 – May 2021

	Vaccinated (N=17,461, % row)	Non-vaccinated (N=1,413, % row)	Overall (N=18,874, %)
Vaccine Intent			
Yes	14,582 (98.5%)	228 (1.5%)	14,810 (78.5%)
Unsure	1,929 (80.3%)	474 (19.7%)	2,403 (12.7%)
No	715 (52.7%)	643 (47.3%)	1,358 (7.2%)
Prefer not to answer	235 (77.6%)	68 (22.4%)	303 (1.6%)

Conclusion. More than three-quarters of NC participants intended to get vaccinated and by mid-May 2021, the vast majority had received at least one dose. Similarly, those who were unsure or preferred not to say were mostly vaccinated. Even among those who reported they would not get vaccine in January, more than half had received vaccine by May. The nature of our sample makes it difficult to generalize results to the population of NC; nevertheless, further investigation as to the causes of the shift in attitudes is warranted.

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1214. Household Transmission of Febrile Illness Measured by Smartphone-Connected Thermometers, United States, 2016-2021

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Session: P-71. Public Health

Background. Understanding household transmission dynamics of infectious diseases can help develop mitigation strategies. Traditional methods of population-level disease surveillance do not capture household transmission. Data collected from smartphone-connected thermometers that can differentiate among individuals in a household can be used to study these characteristics. Using this technology, we estimated the household secondary attack rate (SAR) of febrile illness, assessed its correlation with CDC-reported influenza-like illness (ILI) and COVID-19 case incidence, and identified risk factors for secondary transmission.

Methods. We conducted a retrospective cohort study among 596,096 febrile illness index cases recorded from August 1, 2016 to January 20, 2021 in households with two or more individuals in all 50 states. Fevers were measured using the Kinsa Smart Thermometer and mobile device app. Secondary cases were defined as household members who recorded a fever 1–10 days after an index case. We calculated SAR prior to and during the COVID-19 pandemic within the study period, and assessed correlation to ILI and COVID-19 case incidence using Spearman's rank correlation coefficient. Bivariate and multivariable mixed logistic regression models were used to identify risk factors for secondary transmission.

Results. SAR in the pre-COVID-19 period was 5.9% (95% CI: 5.8%–6.0%) during flu season (November to April), and 3.7% (95% CI: 3.6%–3.7%) in flu off-season, and weekly SAR was significantly correlated with ILI reported from CDC (ρ=0.84, $p<$ 0.001). Secondary transmission was 40% more likely to occur in households where the index case's initial temperature was ≥ 39.1°C. During the COVID-19 period, SAR was 3.3% (95% CI: 3.3%–3.4%), and daily SAR was significantly correlated with national daily COVID-19 incidence rates (ρ=0.86, $p<$ 0.001). Households in census tracts with >50% essential workforce were 50% more likely to experience secondary transmission.

Conclusion. Household SAR was highly correlated with ILI and COVID-19 cases. Capturing household transmission of febrile illness through routine public health surveillance may identify risk factors for infectious disease transmission, allowing for more targeted interventions.

Disclosures. **Danielle Bloch, MPH**, **Kinsa Health** (Employee, Shareholder) **John Zicker, MS**, **Kinsa Health** (Employee, Shareholder) **Hannah Somhegyi, PhD**, **Kinsa Health** (Employee, Shareholder) **Patrick Philips, n/a**, **Kinsa Health** (Employee, Shareholder) **Inder Singh, n/a**, **Kinsa Health** (Board Member, Employee, Shareholder) **Amy Daitch, PhD**, **Kinsa Health** (Employee, Shareholder)

1215. A Mixed Methods Study on Severe Bacterial Infections in People Who Inject Drugs

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Session: P-71. Public Health

Background. Severe bacterial infections (SBI) associated with intravenous drug use have been increasing in frequency in the U.S. over the last decade. This mixed methods study aims to identify the risk factors associated with SBI in hospitalized individuals with recent injection drug use.

Methods. We conducted 34 quantitative and 15 qualitative interviews between August 2020 and June 2021 at Bellevue Hospital in New York City. Eligible participants were (1) >/= 18 year of age, (2) admitted with a SBI, and (3) reported injection drug use within the 90 days prior to admission. Quantitative and qualitative data was obtained using a quantitative survey and in-depth, semi structured interviews of participants respectively. Analysis was performed to examine trends and explore common themes potentially contributing factors to SBI.

Results. Of the 34 participants included, the median age was 37.5, 85% were male, 53% white, and 65% reported being homeless within the past 3 months. Endocarditis was the most common primary diagnosis (65%). Median length of hospital stay was 24 days and 35% required ICU level care during admission. A causative microorganism was identified in 85% of participants and 50% had *Staphylococcus aureus* as the sole organism. Discharges against medical advice occurred in 35%. Daily injection drug use in prior 30 days was 95% with a median of 10 injections per day. In the 30 days prior to admission, 50% reported an increase in injection frequency, 80% reported reusing needles and/or syringes, 75% reused cookers, 65% reused cottons. Analysis of qualitative interview data revealed high risk injection behaviors. Participants were not practicing and unaware of strategies to reduce their risk of drug injection-related SBI. Prior hospitalizations for SBI did not impact on this knowledge deficit on what constitutes bacterial infection risk and how to prevent it.

Conclusion. Study findings highlight the complexity of the injection drug use process and the potential social and physiological pathways leading to SBI. Multiple domains at the structural, network, and individual level that impact drug injection practices and provide context by which these factors predispose and lead to physiological tissue damage and the development of SBI among PWID.

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1216. Presence of the Narrow-Spectrum OXA-1 Beta-lactamase Enzyme Is Associated with Elevated Piperacillin-Tazobactam MIC Values Among ESBL-producing *Escherichia coli* Clinical Isolates (CANWARD, 2007-2018)

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Session: P-72. Resistance Mechanisms

Background. The clinical outcome of patients with bacteremia due to an extended-spectrum beta-lactamase (ESBL)-producing member of the family *Enterobacteriaceae* who are treated with piperacillin-tazobactam appears to depend, at least in part, on the piperacillin-tazobactam MIC. The purpose of this study was to determine whether there is any association between the MIC of piperacillin-tazobactam and presence of the narrow spectrum OXA-1 beta-lactamase enzyme among ESBL-producing *Escherichia coli.*

Methods. *E. coli* clinical isolates were obtained from patients evaluated at hospitals across Canada (January 2007 to December 2018) as part of an ongoing national surveillance study (CANWARD). ESBL production was confirmed using the Clinical and Laboratory Standards Institute phenotypic method. Susceptibility testing was carried out using custom broth microdilution panels, and all isolates underwent whole genome sequencing for beta-lactamase gene detection.

Results. In total, 671 ESBL-producing *E. coli* were identified as part of the CANWARD study. The majority of isolates (92.0%; 617/671) harbored a CTX-M ESBL enzyme. CTX-M-15 (62.3%; 418/671), CTX-M-27 (13.9%; 93/671), and CTX-M-14 (13.4%; 90/671) were the most common variants identified. The narrow spectrum OXA-1 beta-lactamase enzyme was present in 42.6% (286/671) of isolates. OXA-1 was detected in 66.3% (277/418) of isolates with a CTX-M-15 ESBL enzyme versus only 3.6% (9/253) of isolates with other ESBL enzyme types. The piperacillin-tazobactam MIC_{50} and MIC_{90} values were 8 μg/mL and 32 μg/mL for isolates that possessed the OXA-1 enzyme versus 2 μg/mL and 8 μg/mL for those that did not. The percentage of ESBL-producing *E. coli* isolates that were inhibited by a piperacillin-tazobactam MIC of ≤ 8 μg/mL was 68.5% for isolates that were OXA-1 positive and 93.8% for isolates that were OXA-1 negative.

Conclusion. The MIC_{50} and MIC_{90} values of piperacillin-tazobactam among ESBL-producing *E. coli* were higher for the subset of isolates that harbored a narrow spectrum OXA-1 beta-lactamase enzyme relative to the subset that did not. This association was primarily observed among ESBL-producers with the CTX-M-15 enzyme variant. OXA-1 was infrequently detected among isolates with other ESBL enzyme types.

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1217. Molecular Epidemiology of *Pseudomonas aeruginosa* in Latin America: Clinical Isolates From Respiratory Tract Infection

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Session: P-72. Resistance Mechanisms

Background. Respiratory Tract Infection (RTI) caused by *P. aeruginosa* is a common infection among hospitalized patients, with increased levels of morbidity and mortality. *This pathogen* exhibits multiple resistance mechanisms to antibiotics. We analyzed the molecular epidemiology and activity of the main therapeutic options against *P. aeruginosa* isolated from RTI in Latin America (LATAM).

Methods. Isolates were collected from 36 sites in 10 countries during 2017-2019. Non-duplicate samples were consecutively collected. MICs were determined by broth microdilution and interpreted by CLSI criteria. A subset of imipenem non-susceptible isolates was selected for characterization of carbapenemase encoding genes via multiplex PCR and DNA sequencing. β-lactamase genes encoding ESBLs, carbapenemases, and plasmid-mediated AmpCs were investigated.

Results. A total of 2,044 *P. aeruginosa* were collected from RTI. Overall C/T [87.8% susceptible (S)] was the most active antimicrobial tested against *P. aeruginosa* isolates followed by amikacin (85.8% S) and imipenem/relebactam (IMI/REL; 82.5%