

**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

Danielle Bloch, MPH<sup>1</sup>; John Zicker, MS<sup>1</sup>; Hannah Somhegyi, PhD<sup>1</sup>; Patrick Philips, n/a<sup>1</sup>; Inder Singh, n/a<sup>1</sup>; Amy Daitch, PhD<sup>1</sup>; <sup>1</sup>Kinsa Health, San Francisco, California

**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 ( $\rho=0.84$ ,  $p<0.001$ ). Secondary transmission was 40% more likely to occur in households where the index case's initial temperature was  $\geq 39.1^\circ\text{C}$ . 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 ( $\rho=0.86$ ,  $p<0.001$ ). 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.

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

Alexander Hrycko, MD<sup>1</sup>; Benjamin Eckhardt, MD, MS<sup>2</sup>; Pedro Mateu-Gelabert, PhD<sup>3</sup>; Courtney Cierwo, BA<sup>4</sup>; <sup>1</sup>NYU School of Medicine, New York, New York; <sup>2</sup>NYU School of Medicine/Bellevue Hospital, New York, NY; <sup>3</sup>CUNY School of Public Health, New York, New York; <sup>4</sup>CUNY, New York, New York

**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)  $\geq 18$  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)

Andrew Walkty, MD<sup>1</sup>; James Karlowsky, PhD<sup>1</sup>; Philippe Lagace-Wiens, MD<sup>1</sup>; Alyssa Golden, PhD<sup>2</sup>; Melanie Baxter, MSc<sup>2</sup>; Andrew Denisuik, MD<sup>2</sup>; Melissa McCracken, MSc<sup>3</sup>; Michael Mulvey, PhD<sup>4</sup>; Heather Adam, PhD<sup>1</sup>; George Zhanel, PhD<sup>2</sup>; <sup>1</sup>Shared Health, Winnipeg, Manitoba, Canada; <sup>2</sup>University of Manitoba, Winnipeg, Manitoba, Canada; <sup>3</sup>Public Health Agency of Canada, Winnipeg, Manitoba, Canada; <sup>4</sup>National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, MB, Canada

**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<sub>50</sub> and MIC<sub>90</sub> values were 8  $\mu\text{g}/\text{mL}$  and 32  $\mu\text{g}/\text{mL}$  for isolates that possessed the OXA-1 enzyme versus 2  $\mu\text{g}/\text{mL}$  and 8  $\mu\text{g}/\text{mL}$  for those that did not. The percentage of ESBL-producing *E. coli* isolates that were inhibited by a piperacillin-tazobactam MIC of  $\leq 8 \mu\text{g}/\text{mL}$  was 68.5% for isolates that were OXA-1 positive and 93.8% for isolates that were OXA-1 negative.

**Conclusion.** The MIC<sub>50</sub> and MIC<sub>90</sub> 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

Leandro Cardinal, PharmD, PhD<sup>1</sup>; Cicera P. Marcelino, n/a<sup>1</sup>; Aline Okuma, n/a<sup>2</sup>; Gustavo Mizuno, PharmD<sup>2</sup>; Felipe Tuon, PhD<sup>3</sup>; Ana C. Gales, MD<sup>4</sup>; Ana C. Gales, MD<sup>4</sup>; Marina Della Negra, Medical Doctor<sup>5</sup>; Thales Polis, Medical Doctor<sup>3</sup>; Elisa Beirao, Medical Doctor<sup>3</sup>; <sup>1</sup>MSD in Brazil, São Paulo - SP - Brazil, New Jersey; <sup>2</sup>MSD Brazil, Sao Paulo, Sao Paulo, Brazil; <sup>3</sup>Pontifical Catholic University of Parana, Department of Medicine, Curitiba, Parana, Brazil; <sup>4</sup>Universidade Federal de São Paulo, Sao Paulo, Sao Paulo, Brazil; <sup>5</sup>MSD, São Paulo, Sao Paulo, Brazil; <sup>6</sup>Hospital Mandaqui, São Paulo, Sao Paulo, Brazil

**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.  $\beta$ -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%