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 among participants in the National COVID-19 Community Research Partnership (CCRP) who were initially receptive or hesitant to receive a COVID-19 vaccine.

Methods. The COVID-19 Community 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%, and 2% answered yes, unsure, and no, respectively.

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.

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

| Vaccine Intent | Vaccinated (N=17,461, % row) | Non-vaccinated (N=4,113, % row) | Overall (N=18,874, %) |
|----------------|-------------------------------|--------------------------------|-----------------------|
| Yes            | 14,582 (86.5%)                | 226 (1.5%)                     | 14,808 (78.5%)        |
| Unsure         | 1,929 (80.3%)                 | 474 (17.9%)                    | 2,403 (12.7%)         |
| No             | 715 (52.7%)                   | 643 (47.3%)                    | 1,358 (7.2%)          |
| Prefer not to answer | 225 (7.7%)                 | 66 (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 infection control 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 and identified risk factors for secondary transmission.

Methods. We conducted a retrospective cohort study among 396,096 febrile illness index cases recorded from August 1, 2016 to January 2021 in households with two or more individuals in all 50 states. FEVER was 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 of SAR with HI 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 IIL from reported with CDC (p=0.84, p<0.001). Secondary transmission was 40% more likely to occur in households where index case's initial temperature of 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 (p=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 IIL and COVID-19 cases. Primary or secondary 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
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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% were reporting homelessness 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 receiving a new drug source in the past 30 days; 75% reused cookers, 65% used poppers, and 34% used a crack pipe. 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 Pipercillin-Tazobactam MIC Values Among ESBL-producing Enterobacteriaceae 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 Enterobacteriaceae.

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-lactam resistance 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%, 418/667), CTX-M-27 (13.9%, 93/671), and CTX-M-14 (13.1%, 90/717) 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 against OXA-1 enzymes were 1 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 MICo and MICe 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/REI; 82.5% S)