

SubmissionType	Breakout/Quick/Lightning/Poster
ID	14315
Abstract Type	Poster
Abstract Title	Association between Resistance to Ciprofloxacin in Enterobacterales Species and Ciprofloxacin Use in Tennessee Acute Care Hospitals Using NHSN Data
Submitted in 2020	Yes
Presentation Format Abstract	Any of the above formats

BACKGROUND: The threat of antibiotic resistant Enterobacterales is on the rise and poses a global public health challenge. Antibiotic overuse has been previously linked with increased antibiotic resistance. Ciprofloxacin, one of the most commonly used antibiotics to treat enterobacteriaceae infections, is often overprescribed within inpatient settings. The National Healthcare Safety Network (NHSN) offers a platform for hospitals to report and track their antibiotic use and resistance data through its Antibiotic Use and Resistance (AUR) module. We aimed to determine the correlation between ciprofloxacin use and resistance in enterobacterales in TN.

METHODS: Data from the NHSN Antibiotic Use (AU) and Antibiotic Resistance (AR) options were collected from January 1st, 2018 through December 31st, 2019. Facility-wide inpatient data from acute care hospitals (ACHs) that reported into both options during that time period were included in the study. Antibiotic resistance rate was defined as the number of enterobacterales reported as resistant to ciprofloxacin divided by the total number of enterobacterales tested against ciprofloxacin. Each hospital's antibiotic use rate was estimated by dividing the total days of therapy (DOT) of ciprofloxacin by total days present (DP). Pearson correlation coefficient was calculated and a multiple negative binomial regression was used to assess the relationship between resistance and antibiotic use.

RESULTS: A total of 21 ACHs reported into both options. *Escherichia coli* was the most represented enterobacterales (49.8%) followed by *Klebsiella pneumoniae* (20.7%). The average percent of isolates resistant to ciprofloxacin was 22.8% [0–54.1] while the average ciprofloxacin use rate was 8.2 DOT per 1000 days present [0–25]. The Pearson correlation coefficient for resistance percentage and ciprofloxacin use rate was 0.46 (p-value=0.03). After accounting for teaching status, hospital size and number of months facilities have reported AU data, the odds of resistance increases by 2.9% as ciprofloxacin use rate increases by one DOT per 1000 DP (p-value <0.001).

CONCLUSIONS: We identified a moderate correlation between ciprofloxacin resistance in enterobacterales and its use in inpatients in the same facility. Addressing antibiotic resistance requires a better understanding of the driving factors, which in turn requires the implementation of more tailored antibiotic stewardship interventions. With the small percentage of statewide hospitals represented in the study, more data is needed to better assess the correlation between fluoroquinolone use and their resistance in enterobacteriaceae species.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Epidemiology
Consider for Different Presentation?	Yes
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SubmissionType Breakout/Quick/Lightning/Poster
ID 13950
Abstract Type Poster
Abstract Title Outbreak of COVID-19 Among Professional Baseball Players

Submitted in 2020 No
Presentation Format Any of the above formats
Abstract

BACKGROUND: Mass gatherings have resulted in transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus which causes coronavirus disease 2019 (COVID-19). In response, many sporting events have been restricted or canceled. For the 2020 season, Major League Baseball (MLB) implemented health and safety protocols to resume play; however, an outbreak occurred infecting players and staff on two teams (Teams A and B). We investigated this outbreak to identify mitigation strategies that likely limited COVID-19 transmission.

METHODS: The Philadelphia Department of Public Health (PDPH) initiated an outbreak investigation after the first Team A member with laboratory-confirmed COVID-19. The PDPH reviewed outbreak-related MLB health and safety protocols, testing results, contact tracing procedures, and duration of on-field interactions for the three teams exposed during the outbreak (Teams A, B, and C). Players and staff were cohorted to limit exposures, required to wear masks and maintain social distance when not practicing or playing, and underwent daily symptom evaluations and routine testing. Saliva samples were collected and tested for SARS-CoV-2 using real time reverse transcription-polymerase chain reaction as part of repetitive testing for all MLB teams. Whole genome sequencing was conducted on residual positive samples.

RESULTS: This COVID-19 outbreak among MLB players and staff occurred over 11 days. Twenty-one players and staff tested positive for SARS-CoV-2 (20 on Team A, one on Team B). Overall, 146 individuals were exposed; attack rates for Teams A, B, and C were 29% (20/68), 3% (1/31), and 0% (0/38), respectively. Symptoms developed in 90% (19/21) of persons testing positive, occurring an average of 2.3 days (0-7 days) after testing. Whole genome sequencing indicated a single introduction and spreading event. Potentially infectious players and staff had cumulative on-field time of 40 hours 23 minutes. The Team B individual with COVID-19 worked indoors with Team A and not with Teams B or C. Following the outbreak, MLB health and safety protocols were revised to address prevention gaps including off-field activities.

CONCLUSIONS: All but one infection occurred within Team A, despite extended outdoor exposure of two additional opposing teams. Interactions outside of on-field play may have been the source of exposure, highlighting the need for prevention activities off the field. Adherence to mitigation strategies, including social distancing, mask wearing, and rapid testing, may have limited COVID-19 transmission across teams. Adoption of multilayered approaches to COVID-19 prevention may provide baseball teams and similar sports with a safer environment during game play.

Committee Infectious Disease
Topic Emerging & Miscellaneous Infectious Diseases (including other mycotic/fungal disease, bacterial disease, and AFM)

Keywords Local Epidemiology; Outbreaks; COVID-19
Consider for Yes

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SubmissionType Breakout/Quick/Lightning/Poster
ID 14834
Abstract Type Poster
Abstract Title COVID-19 Outbreaks in Childcare Programs – Illinois, March 17th 2020-October 31st 2020
Submitted in 2020 No
Presentation Format Any of the above formats
Abstract

BACKGROUND: Following identification of community-transmitted COVID-19 in Illinois on 3/8/2020, an emergency rule was instituted closing all 12,774 childcare programs on 3/21/2020, except those serving children of essential workers. Beginning 5/29/2020, childcare programs could reopen with additional safety measures, including universal masking, limited class sizes, symptom screening of students and staff, and enhanced cleaning. This study describes outbreaks of COVID-19 in childcare programs in Illinois.

METHODS: Local health departments in Illinois are responsible for investigating and reporting all outbreaks of COVID-19 to the Illinois Outbreak Reporting System. Outbreaks linked to licensed and unlicensed childcare programs with an initial case onset before 10/31/2020 were included. Outbreaks were defined as two or more epidemiologically-linked, laboratory-confirmed cases of COVID-19 among program children and staff, who were not close contacts outside of the outbreak location. Age, race/ethnicity, and outcomes were abstracted from the Illinois National Electronic Disease Surveillance System.

RESULTS: There were 141 outbreaks and 616 cases identified, with a median of three cases per outbreak (range: 2-20). Among these cases, 12 (2%) were reported hospitalized; no deaths were reported. Outbreaks increased both in June following reopening and in early fall, consistent with statewide cases. Of 124 outbreaks with complete case information, 38 (31%) involved only staff, 76 (61%) involved children and staff, and 10 (8%) involved only children. The first reported case was a staff member in 76 (72%) of 105 outbreaks where chronology could be established. While a majority of cases occurred among staff (346, 59%), 28 (5%) occurred among infants (0-15 months of age), 139 (24%) occurred among toddlers and preschoolers (>15 mo. to 4 years of age), and 70 (12%) occurred among school age children (5-12 years of age). Three hundred and eighty-eight cases had race/ethnicity reported; 197 (51%) were non-Hispanic white, 119 (31%) were Hispanic or Latino, 48 (12%) were non-Hispanic Black, and 24 (6%) were multiracial or other. The most common response activities were isolation of symptomatic students and staff, environmental disinfection, and active case finding.

CONCLUSIONS: While the number of outbreaks was low relative to the number of childcare programs in Illinois, outbreaks of COVID-19 do occur in childcare programs. Staff comprise a majority of cases, and a majority of outbreaks begin with a reported case in a staff member; however, this may be due in part to differential case ascertainment. Robust contact tracing and engagement with childcare providers was essential to outbreak identification and response.

Committee Infectious Disease
Topic Emerging & Miscellaneous Infectious Diseases (including other mycotic/fungal disease, bacterial disease, and AFM)
Keywords COVID-19; Infectious Diseases; Outbreaks
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SubmissionType	Breakout/Quick/Lightning/Poster
ID	14936
Abstract Type	Poster
Abstract Title	Using Characteristics of Infections with Common Salmonella Specimen Sources to Prioritize Interview Follow-up in Georgia, 2009-2019
Submitted in 2020	No
Presentation Format	Any of the above formats
Abstract	

BACKGROUND: More than 2,200 *Salmonella* infections are reported annually to the Georgia Department of Public Health (GDPH). Stool, urine, and blood specimens are the most commonly reported specimen sources submitted for *Salmonella* testing. GDPH utilizes a random selection scheme to prioritize 60% of *Salmonella* case-patients for interview. We examined whether certain specimen sources are associated with specific demographics, serotypes, or outcomes to better prioritize our interviews and to learn more about cases with severe outcomes.

METHODS: GDPH collects *Salmonella* case-patient demographic, outcome, and laboratory data in the State Electronic Notifiable Disease Surveillance System (SendSS). *Salmonella* case-patient data from 2009 through 2019 were analyzed for specimen source as it relates to: outcome, demographics, and serotype results. Descriptive statistics and other analysis were conducted in Microsoft Excel.

RESULTS: From 2009 through 2019, 27,633 *Salmonella* infections with the three most common specimen sources were reported including: stool (90.0%), urine (6.0%), and blood (3.9%). The median age of case-patients was 14 years; those with stool specimens had a median age of 10 years, lower than the median ages for those with blood specimens (50 years) or urine specimens (56 years). Among case-patients with known gender (27,519), 14,172 (50.5%) were female. Case-patients with urine specimens were significantly more likely to be female than male (86.1%, $p<.01$) while case-patients with blood specimens were significantly more likely to be male than female (60.2%, $p<.01$). Among case-patients with known hospitalization status (26,875) or death status (26,591), those with blood specimens were significantly more likely to have been hospitalized (79.5%, $p<.01$) or died (5.8%, $p<.01$) compared to those with stool specimens (27.5% hospitalized; 0.4% died) or urine specimens (21.8% hospitalized; 1.0% died). Among case-patients with reported race (24,849), 17,579 (70.7%) were white, 5,530 (22.2%) were black, and 1,243 (5.0%) were other/multiracial. Case-patients with blood specimens were significantly more likely to report black race (45.4%, $p<.01$) than those with urine specimens (19.4%) or stool specimens (21.4%). Among case-patients with known serotype results (22,780), 2,685 (11.8%) were infected with *S. Enteritidis*. Case-patients with blood specimens were significantly more likely to be infected with *S. Enteritidis* (24.3%, $p<.01$) than those with urine specimens (7.9%) or stool specimens (9.0%).

CONCLUSIONS: Demographics, outcome, and serotype results vary significantly among *Salmonella* case-patients with different specimen sources. Tracking these differences and changes over time can inform interview prioritization. Targeting education messages, including risk reduction measures, to case-patients with specimen sources with higher proportions of hospitalization could prevent future serious illness.

Committee	Infectious Disease
Topic	Enteric Disease
Keywords	Foodborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
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SubmissionType	Breakout/Quick/Lightning/Poster
ID	14638
Abstract Type	Poster
Abstract Title	Evaluating Reasons for Admission Among Patients Readmitted to the Hospital for COVID-19 in Los Angeles County, July-October 2020
Submitted in 2020	No
Presentation Format Abstract	Hybrid

BACKGROUND: As the number of coronavirus disease 2019 (COVID-19) cases increase, healthcare systems may become overwhelmed. Hospital readmissions for COVID-19 may further strain limited hospital resources and subject patients to adverse health outcomes. Minimizing hospital readmissions for COVID-19 is critical to lessening the burden of COVID-19 on healthcare systems and optimizing patient outcomes. This study sought to characterize patients with COVID-19 infection who required repeat hospitalizations to identify those who might benefit from closer observation after discharge from the initial hospitalization.

METHODS: Clinical staff retrospectively reviewed medical records from a randomly selected sample of hospitalizations reported to Los Angeles County (LAC) with discharge dates between July and October 2020. Medical records were included if there was indication that the patient had a hospital readmission <60 days from previous discharge date, information for previous hospital dates were available, and patient had a documented positive severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) test within 10 days of readmission. Hospitalizations where SARS-CoV-2 was not a direct or contributing cause of hospitalization (e.g., motor vehicle accident, gunshot wound) were excluded from analysis. Reasons for admission were reviewed at index and subsequent hospitalization.

RESULTS: Of the 46,163 hospitalizations reported during our study period, 1,012 (2%) randomly selected medical records were reviewed. Of the 1,012 reviewed medical records, 29 (3%) were admitted for COVID-19 or acute illness that could be caused or exacerbated by COVID-19 at both hospitalizations and fit our inclusion criteria. Of those readmitted, 15 (52%) were Hispanic, 10 (34%) were White, 2 (7%) were Black, and 2 (7%) were Asian; the majority were male (n=17, 59%); median age was 64 years; and 5 (17%) died at readmission. Median length of days between discharge and readmission was 8 days (interquartile range: 24 days). Primary reasons for hospitalization was the same at initial and subsequent admission for 38% (n=11) of those readmitted. Twenty-one percent (n=6) of those readmitted had pneumonia as the primary reason for both hospitalization visits. A more severe prognosis at readmission (e.g., COVID-19 symptoms to pneumonia; urinary tract infection to sepsis) occurred in 28% of the sample.

CONCLUSIONS: Although our study is limited by a small sample size, it represents a longitudinal population-based sample. Our results indicate that COVID-19 patients diagnosed with pneumonia might need closer outpatient monitoring after being discharged from the hospital. Additional research regarding the adequacy of care coordination after discharge, including patient comprehension of self-care, is warranted.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Disease (including TB)
Keywords	Hospital Data; COVID-19
Consider for Different Presentation?	Yes
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SubmissionType	Breakout/Quick/Lightning/Poster
ID	14968
Abstract Type	Poster
Abstract Title	Trends in COVID-19 Deaths By Urban-Rural Classifications of GA Counties, 2020
Submitted in 2020	No
Presentation Format Abstract	Hybrid

BACKGROUND: The COVID-19 pandemic has contributed to >9,000 deaths in Georgia and >300,000 deaths in the United States during 2020. National trends have shown that although deaths were concentrated in urban areas in the first few months of the pandemic, there was a shift over time leading to more deaths in rural areas. To reduce COVID deaths and target areas most in need of resources for prevention and treatment of COVID-19, we compared the magnitude and trajectory of COVID-19 mortality rates among Georgia's metropolitan and nonmetropolitan counties during March-December 2020.

METHODS: Confirmed COVID-19 deaths were reported by healthcare providers or medical examiners/coroners, identified by death certificates, or there was evidence that COVID-19 contributed to the individual's death. The residential population projections by Georgia's Governor's Office of Planning and Budget, Series 2020 were used to estimate the population size of each Georgia county. Using the 2013 National Center for Health Statistics urban-rural classification scheme, we categorized the 159 Georgia counties as metropolitan (81%) or nonmetropolitan (17%). Crude death rates were plotted during March-December 2020 and monthly risk ratios (RR) were calculated.

RESULTS: Throughout 2020, nonmetro counties had an overall average monthly death rate/100,000 population that was over two times greater than metro counties (RR=2.35; 95% CI, 2.24-2.46). This disparity in rural-urban mortality was the smallest in March when comparing metro counties (2.0 deaths/100,000 population) to nonmetro counties (1.4 deaths/100,000 population). After March, nonmetro counties surpassed metro counties in monthly death rates. The largest disparity occurred in September, metro counties had 5.3 deaths/100,000 population and nonmetro counties had 20.6 deaths/100,000 population (RR= 3.88; 95% CI, 3.35-4.41).

CONCLUSIONS: The more than double average monthly COVID-19 death rates found when comparing Georgia's nonmetro counties to metro counties indicated a critical need for more preventative measures to be implemented in rural counties. Partnerships between nonmetro and metro counties should form to prevent physician shortages, a lack of resources, deficiencies in available health services, or other challenges that may contribute to more deaths occurring in nonmetro counties. Additional prevention measures must be established in rural counties, such as more campaigns on preventing COVID-19 transmission and more rural clinics as sites for COVID-19 testing and vaccinations. Throughout the rest of the COVID-19 pandemic, the changing trajectory of death rates could be used to inform prevention measures in nonmetro counties.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Disease (including TB)
Keywords	COVID-19; Health Disparities; Surveillance
Consider for Different Presentation?	Yes
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SubmissionType	Breakout/Quick/Lightning/Poster
ID	14988
Abstract Type	Poster
Abstract Title	Prolonged Outbreak of Group a Streptococcal Infections at a Long Term Care Facility— Georgia, 2018-2019
Submitted in 2020	No
Presentation Format Abstract	Any of the above formats

BACKGROUND: Group A *Streptococcus* (GAS) can cause colonization, pharyngitis, and invasive infections. The Georgia Department of Public Health (GDPH) conducts active surveillance for invasive GAS (iGAS) and monitors iGAS among residents of long term care facilities (LTCFs). In May of 2018, 3 cases of iGAS from April 2018 were reported from the same LTCF, Facility A, including 2 deaths. The GDPH, North Central Health District, and the Georgia Public Health Laboratory (GPHL) screened staff and residents for carriage, and evaluated medical and laboratory records for potential non-invasive cases. Active surveillance revealed additional cases of iGAS in residents over several months, with cases from June 2018 to April 2019.

METHODS: Invasive cases were defined as iGAS infections among Facility A residents during April 2018 – August 2019; non-invasive cases as symptomatic residents with a positive rapid antigen test or culture from a non-sterile site, and carriers as a resident or staff member with GAS cultured from a non-sterile site with no GAS signs or symptoms. Descriptive epidemiology of case characteristics was obtained. An IP evaluation was completed. Pharyngeal and wound swabs were cultured. Positive isolates underwent WG-MLST. Colonized individuals were given antibiotic prophylaxis and re-screened to ensure clearance of GAS.

RESULTS: From April 2018 to April 2019, 12 cases were identified (8 invasive, 4 non-invasive) and 15 carriers (7 staff, 8 residents). The average age of the 20 residents was 80 (range 47-92), 100% male, 14 had wounds, and all had underlying conditions. Between June and December 2018, 10 isolates were classified as emm 4/MLST 39. Between February and April 2019, 5 isolates were classified as emm1/MLST 28. One staff member with an emm4/MLST 39 isolate had 0 SNP differences from an invasive case resident. An additional case was identified and subsequent targeted screening of contacts was performed, 1 staff GAS strain was found to be related by 6 SNP differences to an iGAS case from February 2019. IP evaluation identified poor access to hand hygiene resources, lack of audits for environmental cleaning, and lack of data on employee illnesses.

CONCLUSIONS: GDPH investigated a prolonged GAS outbreak in a LTCF. Multiple IP deficiencies were identified and interventions were implemented. WG-MLST not only identified likely transmission between staff and residents, but also an introduction of a new strain, with apparent eradication of a previous one. The outbreak was considered over in August 2019, after no new cases were identified among Facility A residents for 4 months.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Surveillance; Healthcare Associated Infections (HAI); Outbreaks
Consider for Different Presentation?	No
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SubmissionType Breakout/Quick/Lightning/Poster
ID 14405
Abstract Type Poster
Abstract Title Accidental Overdose Is the Leading Cause of Death Among Individuals with Hepatitis C in North Carolina, 2018-2019

Submitted in 2020 No
Presentation Format Abstract Virtual

BACKGROUND: In North Carolina it is estimated that 150,000 individuals are infected with hepatitis C (HCV), a liver disease transmitted through injection drug use with shared injection equipment. Little is known about causes of death for individuals with HCV. Although HCV electronic laboratory records are reportable by law in North Carolina, limited HCV risk data is collected. Utilizing HCV reporting data from 2018 and 2019, we analyzed ICD-10 codes from death certificates to determine the cause of death for individuals with HCV in North Carolina.

METHODS: Death certificates and HCV case records were matched using the Centers for Disease Control and Prevention (CDC) Link Plus cancer registry linkage program to identify cause of death among individuals with HCV in NC for the years of 2018 and 2019. Matching occurred through corresponding first/last names, date of birth, social security number, and race/ethnicity. Matches from Link Plus were merged with HCV cases in the North Carolina Electronic Surveillance System (NC EDSS) and analyzed using SAS 9.4 (Cary, NC) software.

RESULTS: We identified 1,638 individuals with matching death certificates from 2018 and 2019. The majority of deaths were among men (1,161/1,638, 70.9%) and the average age at death was 56.0 (range, 19-90 years). The most reported cause of death among individuals with HCV was “accidental poisoning and exposure to narcotics and psychodysleptics” (n=157, 9.6%) followed by “liver cell carcinoma” (n=106, 6.5%). Men had the highest overall proportion of deaths (114/157, 72.6%) in the drug exposure category, and majority of deaths occurred in the 35-39 age group for both sexes (30/157, 19.1%). A chi-square analysis was used to examine the association between sex and cause of death. An association was not found among those in the drug exposure category, however our analysis did show an association between sex and death due to liver cell carcinoma (= 15.6; p <0.0001) with three times the odds of death occurring among men compared to women in this category (= 3.1; 95% CI= 1.7, 5.6).

CONCLUSIONS: Through the matching of death certificates and HCV cases, we were able to successfully identify causes of death for individuals with HCV. Results highlight the impacts of North Carolina’s opioid epidemic with accidental overdose classified as the leading cause of death among individuals with HCV. This information can help improve the collection of HCV risk data and tailor public health efforts to best fit the needs of North Carolinians with HCV.

Committee Infectious Disease
Topic Hepatitis
Keywords Hepatitis; Substance Use; Surveillance
Consider for Different Presentation? Yes
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SubmissionType Breakout/Quick/Lightning/Poster
ID 14554
Abstract Type Poster
Abstract Title Controlled Substance Prescription Patterns Among Chronic Hepatitis C Patients, Pennsylvania 2018

Submitted in 2020 No
Presentation Format Abstract Hybrid

BACKGROUND: The abuse of prescription opioids can lead to eventual illicit drug usage. One major cause of chronic hepatitis c (HCV) is injection drug use. In 2016, nearly 1 million Americans reported using heroin. Therefore, looking at prescription drug monitoring program (PDMP) data is crucial in understanding whether certain prescribing patterns are related to opioid use disorder (OUD) in HCV patients. The objective of this project is to understand controlled substance prescribing patterns in patients diagnosed with HCV.

METHODS: Confirmed and probable HCV cases ages 18 to 40 years old reported in 2018 were linked to July 2016- December 2019 Pennsylvania Prescription Monitoring Database (PDMP). Match*Pro probabilistic data linkage software was used for the link process based on personal identifiable information: first, middle, last names, gender, date of birth, and zip code. Base SAS 9.4 was used for the analyses.

RESULTS: Of the 8,246 18 to 40-year-old 2018 HCV patients, 4141 (50%) had one or more controlled substance prescription in the PDMP database. Of those HCV patients, 59% patients were between the ages of 24-34 and 53% were males. Comparing pre-diagnosis to post-diagnosis HCV patient's prescription history revealed that 64% of pre-diagnosis prescriptions were buprenorphine, compared to 77% in the post- diagnosis. 14% of pre-diagnosis prescriptions were opioids compared to 7% in the post- diagnosis. The average Morphine Milligram Equivalent (MME) for HCV patients was 57 MME, compared to 49 MME for a similar demographic profile (non-HCV Males/Females 15-45).

CONCLUSIONS: Linking HCV surveillance with PDMP data enhances our understanding of prescribing patterns and informs education of both providers and patients. Identifying early risk factors and drug profiles can provide targeted prevention for vulnerable populations. Further analysis will include comparing pre-diagnosis HCV and post-diagnosis HCV prescribing patterns by using CDC risky prescribing metrics, such as: percent of patients with an average MME over 90, overlapping opioid/benzodiazepine prescriptions, and doctor shopping (5 prescribers and 5 dispensaries in one calendar year).

Committee Infectious Disease
Topic Hepatitis
Keywords Substance Use; Hepatitis; Mental Health
Consider for Different Presentation? Yes
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SubmissionType	Breakout/Quick/Lightning/Poster
ID	14135
Abstract Type	Poster
Abstract Title	Evaluation of National Dengue Surveillance in ArboNET, 2015–2019
Submitted in 2020	No
Presentation Format Abstract	In-Person

BACKGROUND: Dengue is caused by four distinct dengue virus (DENV) serotypes transmitted by *Aedes* species mosquitoes. Competent DENV vectors are present throughout most of the U.S., and dengue is a common disease in returning travelers from endemic areas. Given its epidemic potential, CSTE made it a nationally notifiable disease in 2010 and updated the case definition in 2015. We evaluated dengue reporting in ArboNET, the national arboviral surveillance system, to make recommendations regarding data quality and reporting simplicity.

METHODS: We assessed data quality by reviewing confirmed and probable dengue cases reported to ArboNET during 2015–2019. We calculated the proportion of cases with a response of “no” or “unknown” for fever, a required criterion for the case definition, as well as response rates for dengue-specific variables based on the clinical syndrome classification. We calculated the proportion of cases reporting a DENV serotype among confirmed cases. Lastly, we performed open-ended interviews with state stakeholders about case investigations, laboratory protocols, and their experience with electronic reporting.

RESULTS: Among 5,166 probable or confirmed cases classified as dengue-like illness, dengue, or severe dengue, 18% (n=939) reported fever as “no” or “unknown” decreasing from 31% in 2015 (n=290) to 3% (n=43) in 2019. A total of 5,051 cases were classified as dengue by at least one of 13 criteria. The highest response rate at the variable level was 59% for myalgias (n=3,018) and lowest was 14% (n=712) for positive tourniquet test. Among 69 severe dengue cases, the response rate was 58% for severe organ involvement (n=40), 45% for severe bleeding (n= 31), and 30% (n=21) for severe plasma leakage. Only 24% (n=701) of 2,982 confirmed cases reported a DENV serotype. State stakeholders reported variation in case investigation protocols, but all used a state-specific standardized form for collecting clinical variables. Strengths of the ArboNET system were high acceptability among state arboviral coordinators, stability over time, and timely reporting of national surveillance data with weekly dengue activity reports.

CONCLUSIONS: Dengue surveillance in ArboNET is effective in monitoring the incidence of symptomatic DENV infection among people presenting to a healthcare setting, but low response rates for all clinical variables could lead to misclassification error and bias towards underestimating severity. ArboNET stakeholders should identify and remove barriers to reporting clinical variables and DENV serotype, including creating a dengue reporting form with a clinical variable reference guide, automatic data quality reports, and reminders about the importance of reporting DENV serotypes.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Emerging Infections; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
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