

Submission Type	Breakout/Quick/Lightning/Poster
ID	11414
Abstract Type	Breakout
Abstract Title	An Outbreak of Human Adenovirus Type 7 in a Pediatric Long-Term Care Facility, New Jersey, 2018.

Abstract

BACKGROUND: The New Jersey Department of Health (NJDOH) received a report of an outbreak of human adenovirus (HAdV) in a pediatric long-term care facility housing children with severe congenital and/or acquired disabilities in October 2018. The facility consists of two adult and two pediatric floors. The outbreak occurred in the first floor pediatric wing that housed 67 children, majority of who were ventilator and/or trach dependent. HAdV typing was conducted at the Centers for Disease Control and Prevention (CDC) and revealed the outbreak was associated with human adenovirus type 7 (HAdV7). HAdV7 are known to cause outbreaks and are often associated with increased morbidity and mortality, particularly among medically compromised individuals. We investigated to characterize the epidemiologic and clinical characteristics of this outbreak.

METHODS: An Epidemiologic investigation, including daily clinical reports, chart reviews, staff interviews and observations, was conducted. A confirmed case was identified as a resident with a respiratory illness residing in the facility during the outbreak period who tested positive for adenovirus. A suspect case was identified as a resident with a respiratory illness during the outbreak period for which testing for HAdV was not performed. Public health control measures included increased surveillance for illness with cohorting based on test results, exclusion of symptomatic staff, competency-based training and assessment with emphasis on hand hygiene, donning and doffing of PPE, cleaning and disinfection, and respiratory etiquette. Daily on-site presence of NJDOH staff ensured support in implementing control measures and foster outbreak communications.

RESULTS: During an 11-week period in late 2018, 35 residents (19 female and 16 male), and one staff tested positive for HAdV. Predominant symptoms included fever ($>100^{\circ}\text{C}$), increased in tracheal secretions or tracheal bleed, and difficulty breathing. There were 33 hospitalizations and 11 deaths (case fatality rate = 31%, 11/35) associated with this outbreak. The average length from illness onset to death was 8.9 days. Nine specimens tested at CDC were positive for HAdV7.

CONCLUSIONS: HAdV7 may cause outbreaks in institutional settings, causing vulnerable populations to develop life-threatening disease. This investigation indicates that adenoviral outbreaks, although rare, can cause high mortality in medically fragile children. Providers should have a high level of suspicion for HAdV when dealing with respiratory outbreaks in such facilities. Facilities should also consider utilizing Infection Preventionists and Infectious Disease specialists for clinical consultation and to ensure appropriate infection control processes tailored to the facility are in place and are appropriately followed.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Special/Vulnerable Populations; Infection Control
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Assessment of Viral Shedding after a Human Adenovirus Type 7 Outbreak in a Pediatric Long-Term Care Facility, New Jersey, 2018

Abstract

BACKGROUND: The New Jersey Department of Health (NJDOH) received a report of an outbreak of human adenovirus (HAdV) in a pediatric long-term care facility in October 2018; infection prevention and control precautions (standard, contact, droplet) were recommended at the time of outbreak notification. This outbreak, lasting approximately two months, resulted in 34 residents testing positive for HAdV type 7 (HAdV7) and 11 deaths among 67 residents in the pediatric respiratory assistance unit. Individuals infected with HAdV7 can shed virus in respiratory secretions and stool for lengthy periods of time. However, the time interval for when shedding stops is not well-characterized thus posing challenges for infection control recommendations. NJDOH recommended serial testing of all residents in the outbreak-affected unit to assess viral shedding and to guide lifting of infection prevention and control precautions.

METHODS: Two nasopharyngeal (NP) swabs were collected 72 hours apart from each other on 25 residents who had not been previously tested or who had previously tested negative for HAdV but resided on the outbreak-affected unit; swabs were tested at a commercial laboratory using a HAdV specific PCR. Two NP swabs and two rectal swabs were collected 72 hours apart on 21 residents who were confirmed to have HAdV and tested using the same methodology. A positive result triggered repeat testing until two successive negative results were obtained.

RESULTS: Testing on residents who were not previously HAdV-confirmed revealed two residents that had PCR-detectable virus. Both residents had mild respiratory illness during the outbreak period but had not been tested at the beginning of the outbreak. Testing of the confirmed cases revealed eight residents with detectable virus, of which two tested positive on at least one NP swab; two tested positive on at least one rectal swab; and four tested positive on at least one NP and one rectal swab. Overall, the virus was detected an average of 47 days after the cases returned to clinical baseline status. Additional results on repeat testing of those found to be positive are pending.

CONCLUSIONS: Determining when residents can be removed from isolation precautions and return to normal activities after a severe HAdV7 outbreak with high mortality can be challenging. Standardized guidance for assessing HAdV shedding does not exist; however, in this outbreak NJDOH used serial testing for informed decision-making on public health recommendations. Serial testing provided valuable insight into the length of HAdV shedding and can potentially guide other outbreaks with similar challenges.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Outbreaks; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Forecasting Peak Activity of Seasonal Influenza Using Only One Surveillance Indicator — Colorado, 2013-2019

Abstract

BACKGROUND: Sustaining surveillance for seasonal influenza requires substantial effort from state and local public health agencies (PHAs). Numerous population-based indicators are used to describe the time course (beginning, peak, end) of seasonal influenza activity during September through May, which differ from indicators defining disease severity, burden, and circulating strains. PHAs share influenza surveillance data to promote vaccination and implement disease control measures. Tri-County Health Department (TCHD) sought to characterize a simplified approach to forecast peak influenza activity in Colorado and disseminate timely health alerts to augment disease control measures just prior to peak activity.

METHODS: We examined 12 routinely collected influenza surveillance indicators statewide or locally in TCHD's large 3-county jurisdiction around Denver, Colorado for 5 influenza seasons from 2013-2018. Number/rates of influenza-associated hospitalizations, proportion of outpatient influenza-like illness (ILI) visits, number of outbreaks, and number/percent positive of influenza testing from hospital laboratories were analyzed seasonally and tracked with peak influenza activity (MMWR week with the highest number and rate of hospitalizations). We explored patterns in each indicator's values that could potentially forecast peak influenza activity within 4 weeks, accounting for disease variability across influenza seasons. The most predictive indicators were monitored during the 2018-19 season to identify when TCHD should send prompt health alerts.

RESULTS: The 5 influenza seasons analyzed varied in time course, severity, and predominant circulating strains (H3N2 or H1N1); peak activity ranged between MMWR weeks 52 and 10. County-based hospitalization data, percent ILI, and outbreaks provided duplicative information to describe seasonal time course. We iteratively eliminated 8 redundant indicators and focused on 4 indicators per season to use for forecasting peak influenza activity, which included statewide hospitalizations, county percent ILI, statewide outbreaks, and hospital laboratory test percent positive (LPP). One indicator, LPP >10%, successfully forecasted peak activity within 4 weeks for four of five seasons, particularly when the slope of increase was >2.0. During the 2018-19 season, once LPP surpassed 10%, TCHD broadcasted alerts to healthcare systems about escalating influenza activity, anticipating the need to enhance infection control measures (measure vaccination status, visitation restrictions, antiviral treatment, outbreak reporting), then monitored timing to peak activity.

CONCLUSIONS: Public health is responsible for communicating trends in seasonal influenza. One indicator, LPP>10%, has potential for forecasting peak activity during each influenza season, thereby facilitating timely alerts to healthcare systems for stepped-up prevention efforts ahead of peak activity. PHAs should evaluate LPP as a forecasting tool in state and local jurisdictions.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Influenza Surveillance; Epidemiologic Methods; Indicators
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Investigation of an Outbreak of Respiratory Illness Associated with a National Conference in Michigan, August 2018

Abstract

BACKGROUND: In August of 2018, the Kent County Health Department (KCHD) investigated an outbreak of respiratory illness associated with a 5-day national conference hosted at a convention center in Grand Rapids, MI. Approximately 3,000-3,500 people attended the conference. Initial reports based on postings to the social media accounts of the host organization indicated that “hundreds” of attendees became ill with flu-like symptoms (fever, sore throat, runny nose, cough, muscle aches, nausea, vomiting, or diarrhea) after attending the conference.

METHODS: An epidemiologic investigation was conducted to determine the cause of illness. KCHD nursing staff collected nasopharyngeal swabs from 3 in-state conference attendees and 2 of their household contacts. KCHD also worked with out of state hospitals to submit influenza specimens from hospitalized patients to the Michigan Department of Health and Human Services Bureau of Laboratories. Calls for cases related to the outbreak were distributed via the Michigan Health Alert Network (HAN) and the CDC’s Epidemic Exchange (Epi-X). To collect information regarding illness and exposures among conference attendees, KCHD distributed a HIPAA-compliant on-line survey via an e-mail sent by the national organization.

RESULTS: Three of the 5 specimens collected by KCHD nursing staff, 2 from out-of-state patients and one Michigan resident who was an employee of the convention center tested positive for Influenza A H1N1pdm09. Among 485 survey respondents, 308 (64%) reported flu-like symptoms and 98 self-reported that they were positive for influenza A by rapid testing. Flu-like symptoms were reported by attendees from 42 US states. Respondents reported attending conference events while symptomatic, with the earliest reported onset being the day prior to the start of the conference. Approximately 20% of those reporting illness experienced onset on conference days 4 and 5 (final day), while 50% reported becoming ill during the two days following the conclusion of the conference. Conference attendees responding to the survey reported a total of 76 household contacts who developed flu like symptoms.

CONCLUSIONS: The Kent County Health Department concluded that the outbreak of respiratory illness at the national conference was due to the early seasonal arrival of Influenza A H1N1pdm09. Transmission of influenza likely occurred among conference attendees that were in close contact with symptomatic or pre-symptomatic individuals for long periods of time. Illness among conference attendees likely caused spread across the United States through transmission to their household contacts.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Outbreaks; Influenza / Pandemic Influenza; Local Epidemiology
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Six Seasons of Forecasting Influenza in the United States, 2013–14 to 2018–19

Abstract

BACKGROUND: Seasonal influenza disease activity is associated with substantial health and economic burdens in the United States. The magnitude and timing of influenza activity varies from season to season. The U.S. Centers for Disease Control and Prevention (CDC) tracks influenza activity through the U.S. influenza surveillance system, which provides situational awareness and helps assess public health needs for the near future. However, this system is inherently retrospective and delayed, making the annual impact difficult to predict and giving no direct insight on what might happen next. Accurate and timely infectious disease forecasts are needed to help fill this gap and inform the basis of public health decisions and policy development during both influenza seasons and pandemics.

METHODS: For every influenza season since 2013–2014, CDC’s Epidemic Prediction Initiative has facilitated efforts to engage decision-makers and researchers through FluSight, an annual real-time influenza forecasting challenge. Support for these challenges includes the development of a web application for the submission of weekly forecasts; the coordination of guidance development for forecasting targets and evaluation; the creation of forecast communication products; and formal collaborations with the Council of State and Territorial Epidemiologists (CSTE) through a Forecasting Workgroup.

RESULTS: CDC has received forecasts for the timing, intensity, and short-term trajectory of influenza-like illness (ILI) activity in the United States and the 10 Health and Human Service Regions based on data from the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet). Pilot activities have also included forecasts at the state and territorial level for ILINet and forecasts at the national level for confirmed influenza hospitalizations based on data from the Influenza Hospitalization Surveillance Network (FluSurv-NET). Since the 2015–2016 influenza season, real-time influenza forecasts have been posted on <https://predict.cdc.gov/>. CDC and CSTE have hosted regular workgroup meetings to discuss forecasts, their interpretation and communication, and areas for continued improvement.

CONCLUSIONS: The FluSight activities have provided the scientific community experience in real-time forecasting; federal, state, and local public health officials experience in communicating and interpreting the results; and both groups the ability to evaluate forecast performance across different targets, seasons, and methods. CDC, CSTE, and researchers continue to work together to make further improvements in the accuracy and communication of forecasts to ensure they can be more fully integrated into public health decisions.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Influenza Surveillance; Respiratory Diseases; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Use of Mass Antimicrobial Prophylaxis to Stop a Group A <i>Streptococcus</i> Outbreak Among Unaccompanied Children in a Shelter — Maricopa County, Arizona, January–August 2018

Abstract

BACKGROUND: In January 2018, Maricopa County Department of Public Health (MCDPH) and the Office of Refugee Resettlement (ORR) were notified of a group A *Streptococcus* (GAS) pharyngitis outbreak at a shelter for unaccompanied children (UC). Transmission continued through July despite screenings, targeted treatments, and infection control interventions. We sought to characterize transmission sources, including whether cases were shelter-acquired and whether staff were affected, and stop transmission in this congregate setting.

METHODS: We reviewed the ORR surveillance system for confirmed cases (pharyngitis or lymphadenopathy with GAS isolation or a positive rapid test in a shelter-residing child); shelter-acquired infections had illness onset >5 days after arrival. To determine potential cases among ~500 shelter staff, we administered an anonymous survey regarding GAS symptoms during the previous 6 months. Staff reporting pharyngitis or lymphadenopathy had suspected cases. We requested all UC and staff to initiate antimicrobial therapy with cephalexin or azithromycin. Staff declining antibiotics were required to wear a surgical mask until the outbreak ended, defined as 2 incubation periods (10 days) after treatment completion and no new shelter-acquired cases reported among UC.

RESULTS: We identified 195 confirmed cases among UC occurring during January–July; 182 (93%) cases were shelter-acquired. Of 195 children, 142 (73%) were from Guatemala; median age was 16 years; 142 (73%) were male. Among 403 staff completing the survey, 144 (36%) had suspected GAS pharyngitis, of whom 100 (69%) also reported working while ill. On July 19 MCDPH dispensed 961 antibiotic courses (423 among UC and 538 among staff). The outbreak ended on August 7.

CONCLUSIONS: GAS transmission within a shelter persisting >6 months was successfully halted following mass antimicrobial prophylaxis of residents and staff. Staff who worked while ill likely contributed to sustained transmission. ORR continues to screen, and treat as needed, incoming minors for GAS.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Border Health; Infection Control; Special/Vulnerable Populations
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11214
Abstract Type	Lightning
Abstract Title	Comparison of Influenza-Associated Deaths Reported to Two State Surveillance Systems, Georgia, 2015-2018

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) estimates the number influenza-associated deaths throughout every influenza season. Specifically, CDC uses death certificates to approximate the number of influenza-associated deaths over 18 years of age. In contrast, all influenza-associated deaths are notifiable to the Georgia Department of Public Health (GDPH), and each one is manually reviewed and confirmed. We evaluated influenza-associated deaths reported to GDPH Epidemiology and state death certificate data collected over three consecutive influenza seasons to assess the completeness of both systems, separately and combined.

METHODS: GDPH is notified of potential influenza-associated deaths through Georgia's State Electronic Notifiable Disease Surveillance System (SendSS). Epidemiologists review patient medical record data to determine whether a death should be confirmed as influenza-associated; a confirmed influenza-associated death requires a positive influenza test and no period of complete recovery between illness onset and death. Death certificates with an influenza-specific ICD-10 code (J9-J11) listed as a cause of death were obtained from Vital Records. SendSS data and Vital Records data were compared for matching entries for three consecutive influenza seasons: October 4th, 2015 through September 29th, 2018.

RESULTS: During the 2015-2016, 2016-2017, and 2017-2018 influenza seasons, 60, 100, and 326 death certificates listed influenza as a cause of death, respectively. Of these, 6 (10%), 4 (4%), and 84 (25.8%) had also been confirmed as influenza-associated deaths via notifiable disease reporting. GDPH epidemiologists confirmed 7, 23, and 154 influenza-associated deaths during the three influenza seasons of interest. Of these, 6 (85.7%), 4 (17.4%), and 84 (54.5%) also had death certificates with influenza listed as a cause of death.

CONCLUSIONS: For the first time, GDPH epidemiologists have documented the disparity between influenza-associated deaths reported to SendSS versus death certificate data. The overlap between influenza-associated deaths reported to the two surveillance systems from 2015 to 2018 was low, ranging from approximately 4% to 25%. However, because there is no case definition requirement when reporting influenza as a cause of death on a death certificate, it is likely that the true number of influenza-associated deaths is overestimated. Limitations include the exclusion of death certificates with solely pneumonia, respiratory, or circulatory-specific ICD-10 codes and underreporting of potential influenza-associated deaths that don't meet GDPH case definition. This demonstrates the need for health care providers to report influenza-associated deaths to both GDPH and Vital Records. Furthermore, GDPH epidemiologists can review and confirm influenza-associated deaths reported only to Vital Records to improve surveillance in Georgia.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Epidemiology; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10744
Abstract Title	Lightning
Abstract Title	Comparison of the Timing of Influenza in a K-12 School Population with Medically Attended Cases in Surrounding Communities: Orchards/lisp (Wisconsin, September 2017—May 2018)

Abstract

BACKGROUND: The 2017/2018 influenza outbreak provided an excellent opportunity to compare the time courses of laboratory-confirmed influenza cases in a non-medically attended school population to medically attended influenza cases at five surveillance clinics in surrounding communities.

METHODS: As part of a school-based influenza study at the Oregon School District (OSD) in Wisconsin, parents of absent children with influenza-like illness (ILI) symptoms voluntarily called a study hotline; students were screened for ILI criteria, and, if eligible, received a home visit from a research team member for data and clinical sample collection. Naso/oropharyngeal (NP/OP) samples were tested for influenza by rRT-PCR (IVD CDC Human Influenza Virus RT-PCR Diagnostic Panel) at the Wisconsin State Laboratory of Hygiene. Surveillance of medically attended influenza (MAI) occurred in five primary care clinics in and adjoining the OSD as part of the Wisconsin Influenza Incidence Surveillance Project using the same laboratory testing. We compared mean dates of all influenza cases, and those of A(H3N2), A(H1N1) and B among the school and community sample using the t-test.

RESULTS: Influenza A(H3N2), A(H1N1) and B were detected in 109, 12, and 45 students (n=485) and in 198, 30 and 102 MAI patients (n=1046), respectively. The temporal patterns were markedly different, with the school population showing an initial wave and very rapid increase in A(H3N2) in early December 2018, well before MAI cases. The mean date of influenza for students was 1.8 weeks earlier than for MAI patients ($t=-3.85$; $p<0.001$). Although the mean date of A(H3N2) in the school population occurred 2.6 weeks earlier than for MAI ($t=-5.24$; $p<0.001$), no significant differences occurred for A(H1N1) ($p=0.143$) or for B ($p=0.908$).

CONCLUSIONS: A school population demonstrated a significantly earlier arrival and peak of influenza A(H3N2) during the 2017/2018 outbreak as compared to MAI within the same community. School populations may provide early warning for significant outbreaks of influenza, which is particularly important during pandemics for timely deployment of mitigation measures. Further research will help evaluate if this pattern is consistent across different influenza seasons and locales.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Influenza & Other Respiratory Diseases
Consider for Different Presentation?	Infectious Diseases; Influenza / Pandemic Influenza; Influenza Surveillance
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11849
Abstract Type	Lightning
Abstract Title	Influenza Outbreaks in Long-Term Care Facilities, 2017-2018 Influenza Season, Dallas, Texas

Abstract

BACKGROUND: Record numbers of influenza-related hospitalizations and deaths were estimated to have occurred in the U.S. during the high severity 2017-2018 influenza season. Additionally within Dallas, a record number of influenza outbreaks were reported in long-term care facilities (LTCF). County public health surveillance of influenza-related intensive care unit (ICU) admissions and deaths in acute care hospitals significantly augmented identification of outbreaks in LTCFs.

METHODS: A confirmed LTCF influenza outbreak was defined as at least one laboratory-confirmed influenza case plus at least one case of influenza-like illness (ILI) among facility residents or staff within 72 hours. Outbreaks were either self-reported by facilities, or identified by the health department from investigations of ICU hospitalizations and deaths. Standard CDC guidance for influenza outbreak management was provided to facilities, and daily active surveillance was continued for at least one week after the last case. Data collected from each facility included: numbers of total and ill residents and staff, vaccination rates, dates of illness onset and chemoprophylaxis initiation, hospitalizations and deaths. Characteristics and outcomes were compared using Fisher's exact tests and Chi-square. Data analysis was performed using SAS 9.4.

RESULTS: During this season, 32 confirmed influenza outbreaks were identified in Dallas LTCFs: 17 skilled nursing facilities (SNF); 13 assisted-living facilities (ALF); and 2 mixed SNF/ALF. The outbreaks were predominantly from influenza A (91%) and the average attack rate in residents was 9.8% (range: 1-35%). Average vaccination rates for residents and staff were 82% (n=26) and 64% (n=23), respectively. Influenza hospitalization rates were higher in ALF compared to SNF outbreaks (OR: 2.2; CI=1.3-3.5). Additionally, influenza-associated mortality rates were higher in ALF compared to SNF settings (OR: 3.1; CI=1.1-8.5). Of the 32 outbreaks, 20 (63%) were self-reported by facilities to public health and 12 (38%) were identified through health department review of acute-care hospital reports of influenza-associated ICU hospitalizations. Facilities where outbreak cases were first identified through public health surveillance of ICU admissions had significantly lower overall attack rates (5.9% vs 12.1%, $p = 0.01$) and shorter time to initiation of facility-wide chemoprophylaxis (0.4 vs 2.4 days, $p = 0.05$).

CONCLUSIONS: Under-reporting and delays in recognition of influenza outbreaks in LTCF settings have been a longstanding public health challenge, despite efforts to improve awareness of the importance of prevention and rapid control of such outbreaks. Active surveillance of influenza-associated ICU admissions in acute-care hospitals enabled intentional identification of patients transferred from LTCFs, and earlier interrogation for possible outbreaks in LTCFs.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Healthcare Associated Infections (HAI); Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10968
Abstract Type	Lightning
Abstract Title	Outbreak of Severe Respiratory Illness Associated with Human Metapneumovirus in a Nursing Home -- New Mexico, 2018

Abstract

BACKGROUND: Human metapneumovirus (HMPV) can cause upper and lower respiratory illness. Reinfection with HMPV can occur throughout life, especially among older adults and immunocompromised persons. On February 22, 2018, nursing home A (NH-A) contacted New Mexico Department of Health to report an outbreak of respiratory illness. An investigation was initiated to determine the cause of the illness, characterize the clinical presentation, and limit transmission.

METHODS: A case of respiratory illness was defined as a NH-A resident with at least one of the following signs or symptoms: cough, fever, shortness of breath, or hypoxia (oxygen saturation <90%) with onset between February 15 and March 31, 2018. Nasopharyngeal (NP) swabs were collected from available cases for PCR testing. Chart reviews were conducted on all NH residents to determine case status, symptoms, and underlying conditions.

RESULTS: Forty-nine of 79 (62%) residents were identified as cases. Seventeen (35%) cases were male and the median age was 81 years (range: 55-99). Frequent signs and symptoms included cough (73%), temperature $\geq 99.1^{\circ}\text{F}$ (72%), hypoxia (33%), and shortness of breath (27%). Common underlying medical conditions were heart disease (69%), dementia (63%), other neurological disease (25%), diabetes (18%), chronic lung disease (14%), and cancer (10%). Nine (18%) cases had radiographically-confirmed pneumonia. Nine cases (18%) were hospitalized (median length of stay: 7.3 days). A BioFire Respiratory PCR Panel (20 targets, BioFire Diagnostics, USA) was performed on NP swabs from the initial 7 patients and HMPV was detected in 5 (71%); no other pathogens were detected. CDC tested NP swabs from 31 additional patients using an HMPV singleplex PCR assay and 10 (32%) were positive. In total, laboratory confirmation of HMPV was obtained in 15 out of 38 (39%) cases tested. Four (8%, 2 HMPV-positive) cases died. Enhanced infection control interventions were implemented, including contact and droplet precautions, cohorting cases, suspending admissions, restricting visitation, canceling group activities, intensifying hand hygiene and environmental cleaning, and education for facility staff. The last reported case was on March 16, 2018.

CONCLUSIONS: HMPV should be considered as an etiologic pathogen in a respiratory outbreak, especially during HMPV season. Prompt recognition of respiratory outbreaks and institution of outbreak control measures are key to preventing disease spread, hospitalizations, and deaths. Challenges identified during the outbreak response include maintaining adequate staffing, maintaining supplies necessary for implementation of infection control precautions, the psychological hardship of restricting residents to their rooms, and difficulties controlling the movement of residents with dementia.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Outbreaks; Respiratory Diseases; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11816
Abstract Type	Poster
Abstract Title	Cruise Ship-Associated Legionnaires' Disease, 2005–2017

Abstract

BACKGROUND: Legionnaires' disease (LD) is a severe pneumonia that often requires hospitalization. LD is most commonly acquired by inhaling aerosolized water containing *Legionella* from devices, such as showers and faucets, hot tubs, and decorative fountains, which are often present on cruise ships. Risk factors for LD include age ≥ 50 years, current or former smoking, a weakened immune system, and certain chronic diseases. The CDC *Legionella* travel surveillance program is uniquely positioned to detect clusters of LD associated with cruise ships with interstate as well as international itineraries. However, identification of clusters is challenging because travelers disperse to different jurisdictions, domestically and internationally. Risk of LD can be reduced through effective management of water systems and aerosolizing devices.

METHODS: Cases of LD reported to the Supplemental Legionnaires' Disease Surveillance System (SLDSS) during 2005–2017 and classified as confirmed according to the Council of State and Territorial Epidemiologists case definition were included in this analysis. A cruise-associated case was defined as one in which the patient spent ≥ 1 night on board a cruise ship in the 10 days before symptom onset. A cruise cluster was defined as ≥ 2 cruise-associated cases with travel on the same ship within 12 months.

RESULTS: During 2005–2017, 194 cruise-associated cases were reported to SLDSS. Reported cases fluctuated yearly, with the lowest number of reported cases (8) in 2007 and 2012, and the highest number (27) in 2017. Of patients with reported age (96.9%), 81% were ≥ 50 years. Ninety percent of patients were hospitalized during treatment for LD, and 5% died. During the 10 days prior to symptom onset, patients spent an average of 5 days on board a ship; 51% also reported overnight stays at other accommodations outside their homes during the 10-day exposure period. Twenty-one percent of patients reported hot tub exposure on board the ship. During 2005–2017, the number of cruise clusters identified by CDC varied yearly, with the lowest number of identified clusters (1) in 2005 and 2011, and the highest number of clusters (6) in 2015.

CONCLUSIONS: Most cruise-associated LD cases occur in people who are older, and thus at inherently increased risk for LD. As with cases of LD associated with other settings, cruise-associated LD can be severe. Reporting cruise-associated cases promptly to CDC improves cluster detection and timely public health response to minimize *Legionella* growth and transmission on board ships.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Environmental Exposures; Respiratory Diseases; Waterborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11340
Abstract Type	Poster
Abstract Title	Epidemiologic Modeling of Care-Seeking Behaviors during the 2009 H1N1 Pandemic Influenza A (pH1N1): Return Visits to Clinic

Abstract

BACKGROUND: During the 2009 H1N1 influenza pandemic (pH1N1), the proportion of outpatient visits to clinics and hospitals became elevated especially during the early months of the pandemic due to surges in sick and worried-sick individuals or returning patients seeking care. We determined the prevalence of return visits to clinic and modeled the risk factors associated with it during the 2009 H1N1 influenza pandemic period in Houston, Texas.

METHODS: A retrospective study of patients who participated in the Houston Health Department Influenza Sentinel Surveillance Project was conducted using a subset of data for ILI-related medical care visits to multispecialty clinics in Houston, Texas during the 2009 H1N1 pandemic influenza (April 2009 – April 2010). The data comprised of 2680 individuals who made a total of 2960 clinic visits. Return visit was defined as any visit following the index visit after the wash-out phase prior to the study period. We applied nominal logistic regression and recursive partitioning model analyses to determine the independent predictors and the response probabilities of return visits for individual level covariates (clusters).

RESULTS: The overall mean age of the cohort was 22.9 years. Majority of the cohort were females (56.1%), of age 5-24 years (40.6%) with approximately 61% of them having no documented vaccination history. About 4.56% (n=135) of the cohort had return visits with significant variations observed attributed mainly to age group (67.8%, $p < 0.0001$) and type of vaccine received by patients (17.8%, $p < 0.05$). Patients in age group 0-4 years were 9 times (OR: 8.768, 95%CI: 3.388-29.945, $p < 0.0001$) more likely to have return visits than those who were 50+ years. Similarly, patients who received either seasonal flu (OR: 1.586, 95% CI 1.007-2.500, $p = 0.047$) or pH1N1 (OR: 1.741, 95%CI: 1.085-2.750, $p = 0.022$) vaccines were more likely to encounter return visits compared to those who had no vaccination history. Recursive partition analysis indicated that return visits were more prevalent among patients who were males, of age 0-4 years, had negative test results for pH1N1, and received seasonal flu vaccine (Prob.=0.0913).

CONCLUSIONS: Return visits in our cohort was more prevalent among children and young adults and those that received either seasonal flu or pH1N1 vaccines. Understanding the dynamics in care-seeking behavior during the pandemic and the associated risk factors may be useful in the design of future initiatives aimed at reducing recurrent utilization of the healthcare system and could also assist policymakers with appropriate resource allocation for clusters that are likely to encounter return visits.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Epidemiology; Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11141
Abstract Title	Poster
	Exposure History Mystery: Evaluating Potential Exposure Sources for Georgia Legionellosis Cases, 2017

Abstract

BACKGROUND: Most legionellosis cases are associated with travel, healthcare, whirlpool spa, and respiratory equipment exposures, which are routinely captured on the Centers for Disease Control and Prevention (CDC) Case Report Form (CRF). However, many Georgia legionellosis cases deny these exposures. Enhanced surveillance activities were implemented in 2017 to better characterize potential *Legionella* exposures for Georgia cases. Case-case comparisons were performed to determine if exposures reported among outbreak-associated cases differed from those of sporadic cases.

METHODS: GA Department of Public Health district and state epidemiologists attempted to interview all Georgia legionellosis cases or their surrogates with an expanded Georgia CRF in 2017. Interviewers obtained detailed 14-day exposure histories compared to the CDC 10-day routine history. Routine exposures were defined as those exposures collected on the CDC CRF, including travel, healthcare facilities, respiratory equipment, and whirlpool spas. Sporadic cases were those not associated with a known outbreak. Sporadic and outbreak-associated cases were compared using EpiInfo. Descriptive statistics were calculated in Excel.

RESULTS: 172 legionellosis cases were reported, and 154 were successfully interviewed. 22 interviewed cases were outbreak-associated, and 132 cases were sporadic. Sporadic cases reported routine exposures, such as travel (n=41, 32%) and healthcare facility (n=37, 29%); and other exposures, such as showering away from home (n=33, 26%), grocery stores (n=31, 26%), public gatherings (n=28, 22%), home improvement stores (n=28, 22%), or spending several hours at a location other than home or work (n=25, 20%). Several other potential exposures were evaluated and were reported less frequently. 51 cases (33%) denied all routine exposures on the CDC CRF, and one was associated with an outbreak. Outbreak-associated cases were significantly more likely than sporadic cases to have reported visiting healthcare facilities (OR 8.3, p<0.001), hotels without overnight stay (OR 10.03, p<0.05), and being near whirlpool spas (OR 10.03, p<0.05) than sporadic cases.

CONCLUSIONS: Sporadic cases reported potential exposure sources not routinely collected on the CDC CRF, with one third of 2017 Georgia legionellosis cases denying all routine exposures. Case-case comparisons were significant only for reported exposures associated with outbreaks in Georgia. Enhanced surveillance activities implemented in 2017 enabled identification of potential *Legionella* exposures for sporadic cases by gathering a more detailed exposure history over a longer time than the routine sources captured by the CDC CRF. As Georgia continues to collect detailed exposure histories, increased statistical power may enable implication of likely sources for sporadic legionellosis cases.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Influenza & Other Respiratory Diseases
Consider for Different Presentation?	Waterborne Disease; Infectious Diseases; Respiratory Diseases
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10984
Abstract Type	Poster
Abstract Title	Implementing a Sampling Strategy in the Influenza Hospitalization Surveillance Network, 2017-18 Season and Beyond

Abstract

BACKGROUND: The Influenza Hospitalization Surveillance Network (FluSurv-NET) reports laboratory-confirmed influenza cases from hospitals in designated catchment area of 13 states for hospitalization rate estimation during the influenza season. Historically, clinical and epidemiologic information is collected from each case. During 2017-18, however, nearly twice as many cases (>29,000) were detected compared to previous seasons, with the largest burden in older adults. Therefore, a sampling strategy was implemented for the first time during 2017-18 to reduce the burden of case report abstractions for state surveillance systems and allow timely data collection. We describe a revised sampling strategy developed for future seasons and validated during 2017-18.

METHODS: Minimum data elements were required for all cases to produce age-stratified hospitalization rates. A sampling strategy was implemented for medical chart abstraction of detailed clinical data (e.g., ICU admission, mechanical ventilation). Random samples of cases aged ≥ 50 years were selected from previous seasons to determine the impact of sampling on key variables. Random numbers were prospectively assigned to cases, and thresholds for implementing sampling were set based on historic peak and end-of-season rates. Sites selected one of four sampling strategies (no sampling, 50% of ≥ 65 year olds, 25% of ≥ 65 year olds, 25% of ≥ 65 year olds plus a 50% of 50-64 year olds). Sampling methods were modified for 2018-19; while the four sampling strategies remained the same, minimum sample sizes were determined using sample size calculations for desired confidence intervals around the proportion of cases vaccinated (the variable yielding the most conservative approach). Linear regression was used with previous seasons' data to determine a site threshold (number of cases by a specific week during the season) when sampling could begin in order to achieve the desired sample size.

RESULTS: During 2017-18, half of sites sampled 25% or 50% of cases ≥ 50 years, while the other half elected no sampling. Confidence intervals for key variables were comparable with previous seasons at all sites. For future seasons, at least 5,000 cases in both the 50-64 and ≥ 65 age groups would yield desired precision. A threshold of 1,000 cases in each age group by MMWR Week 1 will be used as the sampling threshold in a given season.

CONCLUSIONS: We assessed sampling schemes at FluSurv-NET sites during 2017-18 for key variables. Use of sampling improves efficiency at FluSurv-NET sites, and allows flexibility based on total case counts.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Epidemiologic Methods; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11675
Abstract Type	Poster
Abstract Title	Novel Human-Bovine Transmission of M. Tuberculosis in the US: A Texas Investigation

Abstract

BACKGROUND: The first documented human-bovine transmission of tuberculosis in the U.S. was reported to the Texas Department of State Health Services (DSHS) in August 2018. The four-month old dairy calf was euthanized after failing routine tuberculosis tests, later identified by the United States Department of Agriculture (USDA) as M. tuberculosis (TB), on a Texas dairy farm. Transmission of M. Bovis has been well documented in cattle since USDA began collecting information in 1975, but, human transmission of TB to cattle is primarily seen in other countries, such as Nigeria and India, where the cattle handler's relationship to cattle is much closer.

METHODS: DSHS approached this incident as a source case investigation, viewing the calf infection as a sentinel event. Staff at the Texas dairy farm were consulted regarding any potential TB suspects. Spoligotype results from the calf isolate were compared against Texas isolates in the Tuberculosis Genotyping Information Management System (TB GIMS) for potentially related human cases. DSHS communicated with USDA and Texas Animal Health Commission (TAHC) to explore the likelihood of human to bovine transmission. DSHS Public Health Region (PHR) 1 staff conducted source case investigation activities to determine whether an infectious TB suspect was still infectious, reported to public health, and potentially exposing others.

RESULTS: Cattle at the dairy farm were tested, and none were positive with TB. Conversations with management at the dairy farm identified a dairy worker who exhibited signs and symptoms of TB but was no longer employed at the farm. Spoligotype results from the calf isolate matched a GENType strain with TB cases in the local region. Given this information, PHR 1 staff re-interviewed cases for potential links. A site visit determined that the dairy farm staff population is transient and difficult to screen, however, symptom screening and education was provided. No source case was identified.

CONCLUSIONS: The possibility of a potentially infectious TB case who worked closely with the dairy calf cannot be ruled out. Current resources do not justify further exploration of this novel transmission. In the future, exploring more targeted investigation and epidemiological data is recommended.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11153
Abstract Type	Poster
Abstract Title	RSV-Associated Deaths in the US According to Death Certificate Data, 2005-16

Abstract

BACKGROUND: In the United States, respiratory infections due to respiratory syncytial virus (RSV) cause an estimated 57,000 hospitalizations and 100-500 deaths annually among children <5 years of age and 177,000 hospitalizations and 14,000 deaths among adults ≥65 years of age. With new vaccines, immunoprophylaxis products, and anti-viral therapies in development, understanding trends in RSV mortality is important. We assess 12 years of US death certificates for RSV-associated deaths.

METHODS: US RSV-associated deaths among all ages from 2005 through 2016 were compiled through the National Center for Health Statistics. Deaths with International Classification of Diseases codes of J12.1 (RSV-pneumonia), J20.5 (RSV-bronchitis), or J21.0 (RSV-bronchiolitis) assigned as either the underlying (i.e., primary) cause of death or a contributing cause of death were considered to be “RSV-associated” for this analysis. To compare the timing of deaths to RSV circulation, RSV laboratory detections were obtained from the National Respiratory and Enteric Virus Surveillance System.

RESULTS: From 2005 to 2016, among 30.5 million US deaths, 1001 (.003%) were assigned an underlying or contributing RSV-associated cause of death. The specific causes were as follows: 697 (70%) RSV-pneumonia, 17 (2%) RSV-bronchitis, 277 (28%) RSV-bronchiolitis, and 10 (1%) with multiple RSV-associated causes. Almost half (48%) were male, 62% were non-Hispanic white, 18% were Hispanic (any race), and 15% were non-Hispanic black. Most deaths were among children <5 (48%) and adults ≥50 (40%) years of age. Almost half of the 1001 deaths (47%) had an RSV-associated cause as the primary underlying cause of death. The number (annual mean) of RSV-associated deaths reported increased from 399 (67) in 2005-2010 to 602 (100) in 2011-2016 (Chi-Square p-value <.0001), mostly due to a 294% increase in RSV-pneumonia coded deaths among adults ≥50 years of age. For comparison, all-cause mortality increased 7% during these time-periods. The trends for deaths by month corresponded closely with those of RSV laboratory positive tests over these years.

CONCLUSIONS: From 2005 to 2016, the number of death certificates with an RSV-associated cause increased, mostly due to increases in RSV-associated pneumonia deaths among older adults. The reasons for this increase are not clear, but likely reflect increased testing using multiplex respiratory panels that include RSV. In the future, surveillance systems that take into account testing practices may help to explain this trend and improve our understanding of RSV-associated mortality before the introduction of new RSV vaccines.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Epidemiology; Infectious Diseases; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11624
Abstract Type	Poster
Abstract Title	Use of Hospital Discharge Data to Evaluate Usefulness of Surveillance for Laboratory-Confirmed Influenza-Associated Hospitalizations

Abstract

BACKGROUND: Nationally, influenza results in an estimated 140,000-710,000 hospitalizations annually. Hospitalizations are an important indicator of the severity of an influenza season. In Pennsylvania, laboratory-confirmed influenza is a reportable condition, and hospitalization status and outcome (survived vs. died) is requested if known. To assess the validity of using hospitalization status as reported to Pennsylvania's electronic disease surveillance system (PA-NEDSS) as a measure of influenza severity, PA-NEDSS hospitalization data was compared to influenza-associated hospitalizations identified in the Pennsylvania Health Care Cost Containment Council (PHC4) hospital discharge database. The PHC4 database contains information on all hospital admissions in the state.

METHODS: We obtained PHC4 data for 15 influenza seasons, from 2003-2017. Influenza-associated admissions were identified using International Classification of Diseases, Ninth Revision, Clinical Modification codes (ICD-9-CM and ICD-10-CM) for influenza. Influenza codes could be in either the primary diagnosis or in first eight secondary diagnoses. Hospitalization rates were calculated using intercensal population estimates calculated by the Pennsylvania State Data Center. To determine degree of validity we calculated the ratio of hospitalizations reported to PA-NEDSS to flu-associated hospitalizations in the PHC4 data, by influenza season.

RESULTS: Throughout the study period, 70,916 influenza-associated hospitalizations were identified in the PHC4 database. Hospitalizations per season ranged from 1217 in the 2011-2012 season (9.5 cases per 100,000 population), to 10,210 in the 2014-2015 season (79.7/100,000 population). Over all seasons, the ratio of flu hospitalizations in PA-NEDSS vs. PHC4 was 0.39. Flu hospitalization ratios varied by season, ranging from 0.05 in the 2002-2003 season (the first season in which PA-NEDSS was used) to 0.54 in the 2014-2015 season. The relationship between flu hospitalizations in PA-NEDSS and PHC4 was strongly linear with a correlation coefficient of 0.98 ($p < 0.0001$). The overall ratio for in-hospital death reporting was 0.63 with a correlation coefficient of 0.65 ($p = 0.0092$).

CONCLUSIONS: The number of hospitalizations associated with lab confirmed influenza reported to PA-NEDSS was much lower than influenza-associated hospitalizations in the PHC4 database. This may be because most influenza reporting to PA-NEDSS is done by laboratories which may not know if the patient is hospitalized. Although PHC4 data is apparently more robust, the data are not timely enough to be used for influenza response activities. However, the ratio of hospitalizations in the PA-NEDSS and PHC4 data is linearly correlated from season to season, indicating that PA-NEDSS hospitalization may still be useful as an indicator of relative severity compared to other seasons.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Surveillance; Hospital Data; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11602
Abstract Type	Quick
Abstract Title	Burden of Influenza Mortality Among American Indians and Alaska Natives: 1999 – 2016

Abstract

BACKGROUND: American Indians and Alaska Natives (AIAN) are the only racial group in the United States that is identified as having a higher risk for developing influenza-related complications. As such, influenza-related mortality has consistently been one of the leading causes of death among AIANs. Additionally, existing estimates for this population are likely low, due to significant degrees of racial misclassification and underreporting of both morbidity and mortality data in the AIAN population.

METHODS: Using data available from the Centers for Disease Control and Prevention (CDC), we analyzed influenza mortality to calculate crude mortality rates in order to identify trends and disparities in the distribution and burden of influenza-related mortality. As influenza disproportionately affects elderly populations, crude rates were used to more accurately capture the impact of influenza-related mortality across various age categories. Results were stratified by geography, race, gender, and age group to improve our understanding of the burden of influenza on AIAN communities. These were used

RESULTS: We found that while mortality rates generally declined across the AIAN population, total number of deaths increased. Additionally, there were significant disparities between AIANs and NHWs. The greatest disparities occurred at the earliest stages of life, with mortality rates for AIAN children under age 5 being over 2 times higher than for NHW children. Moreover, the burden of influenza-related mortality among AIAN adults emerged much earlier in life compared to NHWs. There were also significant disparities in the geographic distribution of influenza-related mortality among AIAN. Because these are largely vaccine-preventable deaths, these results identify an area for a targeted intervention to reduce the overall deaths attributable to influenza.

CONCLUSIONS: The steady decline in AIAN mortality rates was most likely influenced by the increase in the overall AIAN population, which increased by 53.9% from 1999 to 2016. The true burden of mortality among AIANs, however, is likely higher. Ultimately, influenza-related deaths represent vaccine-preventable mortality. Vaccinations themselves are just one factor that contributes to the disproportionate number of influenza-related AIAN deaths. Still, reasons for this are both complex and poorly understood, and represent an important need for further study and research. This, along with ongoing, regular surveillance and improved reporting of influenza-related morbidity and mortality, would provide a more comprehensive picture of how influenza affects the AIAN population from year-to-year.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Minority Health; Tribal Epidemiology; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11011
Abstract Type	Quick
Abstract Title	Deaths Occurring after the 2009 H1N1 Pandemic with Evidence of Influenza Virus in Autopsy Tissue Specimens, October 2010—May 2018

Abstract

BACKGROUND: Influenza infection can lead to severe complications and death in children and adults. During the 2009 H1N1 pandemic, diagnosis of influenza by evaluation of autopsy tissue specimens identified cases potentially missed by clinical testing. We analyzed data from influenza-associated deaths with autopsy tissues submitted to CDC's Infectious Diseases Pathology Branch (IDPB) since the 2009 H1N1 pandemic (October 2010—May 2018).

METHODS: IDPB received autopsy tissues from possible infectious disease-related deaths. Testing for influenza viruses was performed by real-time reverse transcription-polymerase chain reaction (rRT-PCR) on RNA extracted from formalin-fixed, paraffin-embedded tissues for deaths with compatible clinical/epidemiologic history or histopathologic findings. Testing for other pathogens was performed based upon case history and pathologic findings. Clinical data were abstracted from submitted medical/autopsy records. Reported differences were statistically significant at $p < 0.05$.

RESULTS: During October 2010--May 2018, influenza virus was identified in autopsy tissues in 172 deaths from 33 US states/territories, including 76 (44%) pediatric (0-17y; median 6y) and 96 (56%) adult deaths (19-81y; median 47y). Influenza viruses identified included A(H3) (58, 34%), A(H1N1)pdm09 (51, 30%), A(unsubtypeable) (20, 11%), and B (43, 25%). Most deaths (118, 69%) occurred outside the hospital or in the emergency department; 138 (80%) had a medical examiner/coroner (ME/C) autopsy. Pediatric deaths were more likely to have A(H3) (45% vs. 25%) or influenza B (33% vs. 19%); and less likely to have A(H1N1)pdm09 (16% vs. 41%) identified than adults. Pediatric deaths were less likely to have ≥ 1 medical condition (18% vs. 51%) but more likely to have prior laboratory evidence of influenza (76% vs. 42%) than adults. Adults were more likely to have bronchopneumonia (59% vs. 37%) or diffuse alveolar damage (36% vs. 7%) than pediatric deaths; whereas pediatric deaths were more likely to have interstitial pneumonia (32% vs. 10%), tracheitis (68% vs. 26%), or bronchitis (57% vs. 25%) than adults. Over half (92, 54%) had a bacterial co-infection identified in tissue specimens, most commonly *Staphylococcus aureus* (26%) or non-pyogenic *Streptococcus* species (including *S. pneumoniae*) (17%).

CONCLUSIONS: IDPB identified influenza virus in autopsy tissues from deaths that occurred after the 2009 H1N1 pandemic. Age differences were identified that warrant further exploration, including that pediatric deaths were less likely to have underlying medical conditions, more likely to have influenza A(H3) or B, and less likely to have evidence of bronchopneumonia compared to adults. Furthermore, the majority of deaths had ME/C autopsies, emphasizing the importance ME/C in understanding the burden of influenza-associated mortality.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10599
Abstract Type	Quick
Abstract Title	Determinants of Influenza Vaccination and Infection, Brazos County, Texas, 2017

Abstract

BACKGROUND: Seasonal epidemics and pandemics of influenza constitute an enormous public health and socioeconomic burden in the United States. The 2017-18 influenza season was the most severe since the 2009 novel Influenza A (H1N1) pandemic. Like the rest of the country, the State of Texas, also experienced unusually high and persistent influenza activity. However, the factors contributing to this unprecedented high flu activity in Brazos County were unknown.

METHODS: Data on all reported cases of influenza and influenza-like illness (ILI) in Brazos County during December 2017 were collected by the Brazos County Health Department (BCHD) from medical records, including outpatient and emergency room visits, and hospitalizations. Records of influenza vaccines administered between January 1, 2017 and December 31, 2017, were obtained from healthcare providers and other vaccination centers, including pharmacies, as well as from the Texas Vaccines for Children Program. Data analysis was done in STATA.

RESULTS: A total of 1,651 cases of laboratory confirmed influenza were reported among Brazos County residents in December 2017, ten times more than in December 2016. 89% of those who had influenza and 80% of those hospitalized were not vaccinated. Individuals 65 years or older and Hispanics were most likely to be hospitalized for influenza infection. A total of 16,027 influenza vaccinations were given to individuals reporting a residential address in Brazos County between January and December 2017. The overall vaccination coverage was 34%. Children aged 5-17, adults aged 18-49, and Hispanics were least likely to be vaccinated.

CONCLUSIONS: Vaccination coverage in Brazos County (34%) was much lower than the Healthy People 2020 target of 70%. Residents aged 5 – 49 years and Hispanics - were less likely to receive influenza vaccine. The elderly and Hispanics were more likely to have complications such as hospitalizations as a result of infection with influenza. The prevalence of influenza and its severity were higher in the groups who had the lowest vaccination coverage. The majority of individuals who had influenza and those hospitalized for the disease were not vaccinated. The development of targeted health education materials and an increased use of social media, local television and radio, and other communication methods that can reach Hispanic residents are needed. Provision of vaccination for the uninsured and those who cannot afford it is needed.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Disease Prevention; Infectious Diseases; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11733
Abstract Type	Quick
Abstract Title	Enhanced Surveillance Among Children Under Five Years of Age Reported to the New York City Department of Health and Mental Hygiene with Latent Tuberculosis Infection, 2018

Abstract

BACKGROUND: Young children with latent tuberculosis infection (LTBI) are at a higher risk of progression to tuberculosis (TB) disease and of severe disease outcomes. They also represent recent TB transmission. In New York City (NYC) laboratories and healthcare providers must report children younger than five years of age with positive tests for TB infection (TTBI) to the Health Department. For these patients, providers must report results of chest imaging completed to rule out TB disease and any LTBI treatment information. In 2018, the Health Department initiated a project to ensure appropriate evaluation and explore transmission in this group.

METHODS: Data were abstracted from the NYC TB surveillance system for patients younger than five years of age with a positive TTBI reported in 2018. Healthcare providers were contacted to acquire missing chest imaging results and treatment information. Patients with complete reports were referred for parent/guardian interview. Telephone interviews were conducted to elicit demographic information, travel history, and TB history among patients and their families.

RESULTS: In 2018, 99 children younger than five (median age: three years) were reported by 27 facilities. Forty-five (45%) patients were reported by laboratories and 54 (55%) by healthcare providers; 84 (85%) reports were submitted electronically. Sixty-eight (69%) patients had complete evaluation and treatment information available. Of these, 58 (85%) had a single positive TTBI result. Fifty-one (75%) patients were prescribed nine months of isoniazid and 10 (15%) were prescribed four months of rifampin. Seven patients did not initiate treatment due to physician decision (4%) or parental refusal (6%). Interviews were conducted for 26 (38%) patients. Parents of 17 patients were unreachable for interview, six parents refused, and 19 interviews are pending. Of those interviewed, 22 (32%) patients were born outside the United States, 17 (65%) had traveled internationally, and 25 (96%) had at least one foreign-born parent. Median number of days from report to interview completion was 34 (range 8-128).

CONCLUSIONS: Only 27 facilities reported a child younger than five with LTBI in 2018, almost half of which were laboratories. Treatment initiation of four and nine month regimens was high, but completion rates are unknown. Among patients with known birthplace and travel history, most had spent time in a high TB prevalence country, but 15% were born in the United States and had never traveled. These data suggest a need for further efforts to assess and improve reporting, track treatment outcomes, and explore TB transmission dynamics in this high-risk group.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Surveillance; Infectious Diseases; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11144
Abstract Type	Quick
Abstract Title	Implementing and Communicating Weekly State-Level Seasonal Influenza Severity Assessments in Utah

Abstract

BACKGROUND: Influenza activity can be highly variable geographically and temporally. The Utah Department of Health (UDOH) conducts influenza surveillance through multiple national and state-specific surveillance systems to understand and quantify these fluctuations. However, synthesizing and communicating these data remains challenging. Localized, timely, and actionable assessments of seasonal severity may inform public health response and messaging for seasonal and pandemic influenza. In February 2018, during an intense influenza season, UDOH and CDC piloted a state-level influenza season severity index and interactive influenza report.

METHODS:: We assessed seasonal severity at the state-level using the Moving Epidemic Method (MEM), which establishes intensity thresholds (ITs) for selected indicators using the geometric mean and standard deviation of historic peak values. Indicators were selected based on ability to detect influenza activity, timeliness, and historical stability. ITs were calculated based on five prior influenza seasons (2012/13 through 2016/17). Seasonal indicator values were compared to their ITs; results from individual indicators were then combined for an overall severity assessment. UDOH developed an interactive influenza report using open source R packages R Markdown and flexdashboard to compile and communicate weekly MEM severity estimates and influenza surveillance data.

RESULTS: Three indicators selected for the mid-season severity assessment were percent of outpatient visits for influenza-like illness (ILI) from one large healthcare system, rate of influenza-associated hospitalizations, and percent of positive influenza tests from clinical laboratories participating in the National Respiratory and Enteric Virus Surveillance System. Using the MEM, ITs were calculated for each indicator and, when assessed across indicators, the 2017/18 season severity estimate was “High”. MEM implementation was re-evaluated for weekly reporting during the 2018/19 season. The ILI indicator was adjusted to include all Utah reporting sites because updated syndromic surveillance definitions improved data quality. Utah’s seasonal MEM severity assessment is now updated weekly (as of January 1, 2019 was “Low”) and reported automatically with additional surveillance data online.

CONCLUSIONS: This is the first publicly reported state-level application of a MEM framework to assess influenza season severity. Using open-source software, UDOH implemented a method of compiling and disseminating state-specific influenza surveillance data including seasonal severity measures. Timely and geographically relevant assessments of influenza severity are important for local and state public health response. Whether interacting with reporters or partners, through the MEM and automated reporting, UDOH now has a quantifiable way to communicate influenza activity in Utah across multiple indicators.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Information Systems; Communication; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11287
Abstract Type	Quick
Abstract Title	Influenza-Associated Hospitalizations: Beyond Hospital Bed Surveys

Abstract

BACKGROUND: The Massachusetts Department of Public Health (MDPH) integrated emergency department (ED) syndromic surveillance (SyS) data into seasonal influenza-like illness surveillance activities in 2016. Our objective was to explore the additional utility of SyS data for tracking influenza season severity to augment or replace a weekly survey of hospital infection control practitioners (ICPs).

METHODS: National Syndromic Surveillance Platform tools and influenza definition were used to identify influenza-associated ED visits. Influenza-associated ED visits with subsequent admission were identified by discharge disposition and patient class. Total weekly rates of influenza-associated ED admissions per 1,000 admissions were calculated and stratified by age group. ICPs reported weekly total laboratory confirmed influenza hospitalizations via SurveyMonkey and a rate per 1,000 licensed beds was calculated. SyS and ICP based measures were compared by MMWR week for 2015-2016 and 2016-2017 retrospectively, and 2017-2018 prospectively to assess the ability of SyS measures to monitor influenza severity. SAS™ software was utilized to calculate Pearson correlation coefficients between SyS and ICP survey based trends and the timing of each seasonal peak was compared.

RESULTS: From week 40, 2015 – week 31, 2018 influenza hospitalization data were available for 99 weeks from the ICP survey and 148 weeks from the SyS data. The three-season correlation coefficient was 0.98739, individual seasonal coefficients were 0.97800 (2015-2016), 0.98686 (2016-2017), and 0.98913 (2017-2018), ($p < .0001$ for all R values). Age specific rates for influenza-associated admissions were calculated with the SyS data, which was not possible using the survey data. Seasonal peaks in SyS and ICP rates were temporally aligned: 2015-2016 (SyS week 10, ICP week 10), 2016-2017 (SyS week 8, ICP week 7), and 2017-2018 (SyS week 6, ICP week 7). For the 2016-2017 season a secondary peak was visible in week 13 for both metrics, for 2017-2018 a secondary peak was clearly identified in the SyS data for week 14 while none presented in the ICP survey metric.

CONCLUSIONS: SyS influenza-associated hospitalization trends are highly correlated with ICP reported laboratory confirmed influenza hospitalization trends. SyS data collection is consistent and comprehensive and is not dependent on hospital staff availability. Using SyS data, we can also calculate an age specific denominator and can assess seasonal variation by age group. Seasonal peak identification via SyS data is consistent with ICP survey data and secondary peaks were clearly identified in two seasons. Acuity measures derived from SyS data are useful for tracking influenza season severity.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza Surveillance; Syndromic Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11495
Abstract Type	Quick
Abstract Title	Invasive <i>Haemophilus Influenzae</i> Type a Disease Outbreak in an Alaska Village, 2018

Abstract

BACKGROUND: During April–June 2018, a total of 4 cases of pediatric invasive *Haemophilus influenzae* type a (Hia) disease were reported in an Alaska village (Village A; population <650 people); all patients were hospitalized. Invasive Hia disease is uncommon and life-threatening; on average, 5 cases of Hia are reported annually in Alaska. We investigated to identify contacts, provide chemoprophylaxis, and ascertain community colonization.

METHODS: We made 3 visits to Village A; 2 in July and 1 in September. Contacts were people of any age who spent ≥ 4 hours with the patient for ≥ 5 of the 7 days preceding that patient's hospitalization. Contacts (visit 1) and children <10 years (visit 2) were offered rifampin chemoprophylaxis and encouraged to submit nasopharyngeal swabs before and ≥ 4 days after initiating chemoprophylaxis. Community members of any age were encouraged to submit swabs during visits 2 and 3. Swabs were tested, and Hia colonization was culture confirmed. Paired *t*-tests and Fisher's exact tests were used to compare proportions of colonized contacts and community members at different visits.

RESULTS: Patients' age range was 6 months–1.7 years; 3 (75%) were male, 1 died. Fifty-two contacts were identified; 42 (81%) received chemoprophylaxis; 15/42 (36%) provided swabs before and after initiating chemoprophylaxis. Among these 15 contacts, Hia colonization decreased by 67% from visit 1 to visit 2 (20% versus 6.7%, respectively; $P = 0.16$). Chemoprophylaxis was provided to 121/195 (62%) children aged <10 years. During visits 2 and 3, a total of 364 and 114 community members provided swabs, respectively. Community Hia colonization decreased, but not significantly between visit 2 and visit 3 (1.3% versus 0.88%, respectively; $P = 0.67$).

CONCLUSIONS: Hia colonization decreased among contacts and community members after chemoprophylaxis was provided. No additional cases of invasive *H. influenzae* disease occurred in Village A after the intervention.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Outbreaks; Community Health; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Laboratory Testing Practices and Demographic and Clinical Characteristics Associated with Respiratory Syncytial Virus (RSV) Testing Among Hospitalized Pediatric and Adult Patients — Multiple States, 2016–2017

Abstract

BACKGROUND: Several RSV vaccines and therapeutics are in development. Post-licensure evaluation requires accurate disease burden estimates. For laboratory-based surveillance systems that rely on clinician-directed testing, burden estimates must take into account availability and use of RSV laboratory tests. We investigated laboratory testing methods used to diagnose RSV and demographic and clinical characteristics associated with RSV testing in a sample of hospitalized patients.

METHODS: During September 2016, surveys on RSV testing methods were distributed to all laboratories serving hospitals in selected counties in California, New York, and Oregon that participate in the Influenza Hospitalization Surveillance Network (FluSurv-NET), a population-based surveillance system for influenza hospitalizations. Among a sample of hospitals served by laboratories that completed surveys, we collected patient-level data on age, race, ethnicity, sex, admission to the intensive care unit (ICU), outcome, and RSV and influenza testing methods from an age-stratified sample of acute respiratory illness (ARI) hospitalizations (i.e. ≥ 1 ICD10 diagnosis code for influenza and pneumonia). Weighted frequencies were calculated, and Rao-Scott chi-square tests were used to determine significant factors for RSV testing.

RESULTS: The survey was completed by 55 laboratories that serve 75 hospitals. Among respondents, 91% (n=50) offered RSV diagnostic testing; 74% (n=37) offered polymerase chain reaction (PCR) testing, and 62% (n=31) offered rapid antigen diagnostic testing (RADT). RADT (n=26, 55%) and multiplex PCR assays (n=14, 30%) were reported as most frequently used. Forty-four hospitals (59%) identified ARI hospitalizations (n=22,275) with 4,821 (22%) sampled for patient-level data. Pediatric patients (<18 years) were tested more frequently for RSV than adults (≥ 18 years) (61% vs. 44%, $p < 0.01$). Patients tested for influenza were more likely to be tested for RSV than those not tested for influenza (pediatric, 92% vs. 5%, $p < 0.01$; adults, 69% vs. 0%, $p = N/A$). Significant factors for RSV testing among children included age <2 years (79% vs. 53% in 2–17 years; $p < 0.01$) and ICU admission (72% vs. 57% non-ICU, $p < 0.01$). In adults, non-white race was a significant factor for RSV testing (52% vs. 43% among whites; $p = 0.02$).

CONCLUSIONS: During the 2016–2017 RSV season, a majority of surveyed laboratories reported offering laboratory tests for RSV. Children were more likely to be tested compared to adults. RSV testing was significantly associated with influenza testing among all ages. Since $> 1/3$ of children and $> 1/2$ of adults with ARI hospitalizations were not tested for RSV, accurate data on testing practices are critical in determining burden estimates.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	The Epidemiology of Legionnaire's Disease in Houston, 2014-2018

Abstract

BACKGROUND: Legionellosis is a respiratory illness that is mostly (80-90%) caused by the bacterium *Legionella pneumophila*. It is associated with a mild febrile illness, Pontiac fever, or Legionnaires' disease, a source of severe, community-acquired pneumonia. Water is the major natural reservoir for *Legionella*, and the pathogen is found in many different natural and artificial aquatic environments. An abrupt increase in the incidence of Legionnaires' has been noted since 2003 throughout the nation. According to CDC, about 6,000 cases of Legionnaires' disease were reported in the United States in 2015. Incidence rates of Legionnaires for the year 2015 were 1.06 and 1.90 for Texas and the United States respectively. This paper is intended to study trends and patterns in legionnaires' disease cases in Houston, Texas, 2014-2018.

METHODS: Data were extracted from Houston's Electronic Disease Surveillance System (HEDSS), 2014-2018. Confirmed cases were analyzed to examine the epidemiologic trends across years. Incidence rates, case fatality and time lapse from date of diagnosis to date of reporting to the health department were also studied. Data were analyzed using SAS statistical software.

RESULTS: There were 218 cases of LD reported to the City of Houston from 2014 to 2018, 116 (53%) were classified as confirmed. The majority of cases were diagnosed by urinary antigen test (95, 82%). There were four deaths due to legionnaires disease during this period giving a case fatality rate of 3.4%. LD incidence rates increased from 0.71 to 1.36 per 100,000, an average annual increase of 17%. LD incidence was higher among men (58%) compared with women (42%). LD incidence was highest among residents 65 years and older (42,4%). African Americans had the highest incidence of LD (40, 35%) followed by Hispanics (29, 25%). Cases were higher in warmer months specifically in July and August.

CONCLUSIONS: The number of LD cases observed were increasing with each passing year. Cases were higher in the warmer months and the highest among the elderly, men, and those of African American race. The ratio of confirmed cases to those reported were only 53% thus raising awareness and appropriate education to the investigators and providers are highly advised. It is critical to the control of LD that enhanced surveillance is maintained at a high level. Consequently, more consideration should be given for the more widespread use of Legionnaires confirming test when a patient presents with pneumonia.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Surveillance; Epidemiology; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Trends in Reported Legionnaires' Disease in North Carolina, 2010–2017: Increasing Disease or Increasing Detection?

Abstract

BACKGROUND: During 2000–2016 in North Carolina (NC), reported incidence of Legionnaires' disease (LD) increased ~4-fold, similar to national trends. To determine if increasing disease burden in NC is attributable to increased testing, we evaluated the number of LD diagnostic tests performed and positivity rate over time.

METHODS: We requested reports for the number of LD diagnostic tests performed and number positive during 2010–2017, by year and test type (urinary antigen test [UAT], serology, culture, or other) from MicroNet members, representing all ~120 NC hospitals. We calculated percent of positive tests by year and test type and used Poisson regression to estimate changes in positivity rate over time.

RESULTS: Twenty hospitals provided data; 544 tests were positive, representing 47% of reported LD cases during the same period. Analyses included data from eight hospitals with complete data for all years and test types, including five of NC's largest hospital systems. The total number of tests performed increased from 5,138 in 2010 to 9,729 in 2017. UATs were the most frequently reported test across all years (4,524 [88%] in 2010 to 7,487 [77%] in 2017); percent of positive UATs increased from 0.46% to 1.32%. Compared with 2010, rate of positive UATs was significantly higher in each year during 2014–2017; the highest rate occurred in 2017 (rate ratio [RR]: 2.85; 95% CI: 1.78–4.56). Results did not differ substantially when all test types or all hospitals were analyzed.

CONCLUSIONS: Diagnostic testing for LD and number of positive tests increased during 2010–2017; therefore, increased testing contributed to increases in reported LD. However, the positivity rate increased approximately 3-fold, suggesting that increased detection as well as increases in true incidence contributed to increasing disease burden. Identification of factors that contribute to increasing LD is necessary toward implementing effective prevention and control strategies.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Waterborne Disease; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10896
Abstract Type	Quick
Abstract Title	Tuberculosis Transmission Among U.S.-Born Persons — Arkansas, 2010–2018

Abstract

BACKGROUND: During 2010–2018, the Arkansas Department of Health (ADH) investigated 18 genotype-matched cases of tuberculosis (TB) among residents and nearby residents of Desha County, Arkansas, a low TB-incidence rural area that reported 1 case during 2005–2009. ADH and CDC investigated to determine extent of transmission and provide control recommendations as transmission continued during 2018.

METHODS: We reviewed medical records, dates in congregate settings, and interviewed patients to determine patient characteristics and infectious periods. We conducted social media searches to identify epidemiologic linkages and locate potential transmission sites. CDC performed whole-genome sequencing (WGS) on all culture-positive specimens and identified single-nucleotide polymorphisms (SNPs).

RESULTS: We identified 21 cases; 11 during 2010–2013, none during 2014–2015, and 10 during 2016–2018. All were in U.S.-born African American persons. Eighteen had matching genotypes, and 3 clinical cases had epidemiologic links to culture-confirmed cases. Nineteen (91%) cases were in Jefferson, Lincoln, and Desha counties; of those, 10 (53%) were clustered in 2 neighborhoods. Social media searches revealed social links among 12 patients not previously disclosed during interviews. Twelve patients (57%) had ≥ 1 healthcare visit during infectious periods, indicating missed opportunities for diagnosis; 6 patients had infectious periods of >12 months; and 11 of 14 adult patients with pulmonary TB (79%), considered the most infectious, were hospitalized ≥ 1 time during their infectious period. Two adult patients died from TB. WGS analysis indicated 17 available TB isolates were ≤ 2 SNPs of another isolate, consistent with transmission among cases.

CONCLUSIONS: Delayed TB diagnoses and prolonged infectiousness led to TB transmission in this rural community. Response efforts are ongoing; we recommended prioritizing education of community members to present to healthcare with symptoms, disclosure of contacts among patients, and encouraging healthcare providers to conduct appropriate TB diagnostic evaluations to reduce outbreak-associated morbidity and mortality in this region of continued transmission.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Rural Health; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Use of Community Assessment for Public Health Emergency Response (CASPER) Method to Assess Influenza Vaccination and Activity in Brazos County, Texas in 2017-18

Abstract

BACKGROUND: There was a ten-fold increase in influenza activity in Brazos County in the early 2017/18 season compared to the same period in the previous year. Presently, there are no publications on seasonal influenza or vaccination in Brazos County. The recommended flu vaccination coverage in the U.S is 70%. However, vaccination coverage in the US and the state of Texas, in 2016/17 flu season were 46.8% and 43.5% respectively. Vaccination coverage in Brazos County was not known for any year. The objectives of this study were: 1) Identify the determinants of the severe flu activity in the season. 2) Assess vaccination problems and the knowledge, attitude and practices of the population and 3) Evaluate influenza vaccination coverage in the county.

METHODS: Thirty census blocks were selected using the CDC CASPER toolkit. Seven households were selected from each census block for interviews. The questionnaire covered source of health information, cause, transmission/prevention of influenza, flu illness/vaccinations in past 5 years, and perceptions, problems and objections about flu vaccination. Data analysis was in EpiInfo™ 7.2.

RESULTS: Two-hundred and seven households completed the survey on March 2-3, 2018. 20.4% of respondents had ILI/Flu in December 2017. 50% took the flu vaccination in 2017 and 54% of parents vaccinated their children less than 18 years. Majority (76%) of respondents had good knowledge of the transmission/prevention of influenza. More than 70% had no objections to the vaccine nor difficulties in accessing it. Vaccination difficulties included lack of insurance, costs, and absence of vaccination centers. 18% of respondents said they had no time for the vaccination, and 9% said the vaccine was not effective. 52% of the unvaccinated said they would take the vaccine if it were free.

CONCLUSIONS: The self reported vaccination uptake was far lower than the CDC objective. Affordability, accessibility, motivation, and misconceptions about the flu vaccine were major contributing factors for the low vaccination coverage and the severity of ILI/Flu in Brazos County in the 2017/18 season.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Disease Prevention; Infection Control
Consider for Different Presentation?	Yes
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Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Influenza Surveillance Enhancements: Improving Influenza Surveillance to Answer Questions about Disease Impact.

Abstract

Key Objectives:

- Discuss results, challenges and successes from implementation of surveillance enhancements during the 2018 – 2019 influenza season.
- Describe plans for continuing the efforts during the 2019-2020 season.
- Provide a forum for discussion among current participants and jurisdictions that might be interested in participating during the 2019-2020 season.

Brief Summary:

The Influenza Division, Centers for Disease Control and Prevention (CDC) continuously works to improve each component of the U.S. Influenza Surveillance System and expand surveillance capacity to fill gaps. During the 2018-2019 influenza season, CDC, in collaboration with the Council of State and Territorial Epidemiologists (CSTE), supported the enhancement of influenza surveillance at 17 state and local health departments, targeting three priority surveillance gaps at the national level:

- Inability to determine the proportion of outpatient visits for influenza-like illness (ILI) that is due to influenza virus infection;

- Lack of information about the severity of illness associated with influenza viruses tested at public health laboratories;
- Inability to calculate rates of outpatient ILI.

Efforts to address these gaps focused on obtaining systematically collected respiratory specimens from patients presenting with ILI to an ILINet provider, determining whether specimens tested at the public health laboratory were obtained from patients in an inpatient or outpatient setting as a proxy for severity of illness, and estimating the population served by ILINet providers. Additional work was performed to modify existing data reporting and analysis mechanisms to handle these enhancements. During this roundtable session, CDC epidemiologists will share data from the 2018-2019 season and describe how those data were used to address priority surveillance gaps. CDC and other public health partners who participated during the 2018-2019 season will highlight successes and challenges faced during project implementation and discuss plans for continuing these efforts during the upcoming influenza season. Sites considering participation during the 2019-2020 season will have an opportunity learn from those sites already participating and to ask questions of CDC and previous participants.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	No
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Submission Type ID	Roundtable
Abstract Type	10874
Abstract Title	Roundtable
	Leveraging Alternative Data Sources for Surveillance of Influenza-Associated and Respiratory Syncytial Virus-Associated Pediatric Deaths.

Abstract

Key Objectives:

- Describe the different methods state and local health departments are using to conduct surveillance influenza-associated and RSV-associated pediatric deaths
- Discuss and identify standardized surveillance approaches to use across jurisdictions

Brief Summary:

Influenza-associated pediatric deaths are nationally notifiable, however, under reporting and inadequate case investigations highlight the lack of knowledge about reporting influenza-associated pediatric deaths among the healthcare community. Educating and providing reporting reminders in healthcare community can be helpful but under reporting continues to be a major problem. As access to and demand for alternative surveillance tools across notifiable diseases grow (ex: syndromic surveillance, access to timely death records via vital statistics, laboratory testing data, and hospital discharge data), so does surveillance capacity for many notifiable diseases, including influenza-associated pediatric deaths. Recent interest in and a standardized case definition for respiratory syncytial virus (RSV) pediatric mortality can also benefit from the use of these systems and the development of alternative surveillance tools for pediatric mortality should likely be explored together. During this roundtable session, epidemiologists from multiple jurisdictions will share their experiences with and methods for using alternative data sources for influenza-associated pediatric and RSV death case ascertainment. Ideas and methods shared during this roundtable will inform the CSTE Influenza and Viral Respiratory Diseases Subcommittee on how to best develop and provide useful guidance and resources to support the use of alternative data sources for pediatric mortality reporting.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Influenza & Other Respiratory Diseases
Consider for Different Presentation?	Influenza Surveillance; Surveillance; Respiratory Diseases
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Submission Type	Roundtable
ID	11472
Abstract Type	Roundtable
Abstract Title	Public Health Response to Non-Influenza Respiratory Viral Illness Outbreaks in Healthcare Settings

Abstract

Key Objectives:

- Describe health department response and challenges to recent non-influenza viral respiratory disease outbreaks in healthcare settings with an emphasis on adenovirus outbreaks
- Describe guidance for transmission-based precautions, cohorting, hand hygiene, and environmental infection control
- Describe special considerations for types of healthcare facilities where outbreaks of non-influenza respiratory virus outbreaks may occur
- Describe how health departments work with CDC's Division of Viral Diseases and Division of Healthcare Quality Promotion to address non-influenza respiratory virus outbreaks in healthcare settings

Brief Summary:

Outbreaks of non-influenza respiratory viral illnesses such as adenovirus and parainfluenza virus can affect a wide range of U.S. healthcare facilities, including but not limited to hospitals, nursing homes, long-term care facilities, and outpatient clinics. When these outbreaks occur, health departments are often required to provide guidance and oversight with regards to infection control considerations including symptom-based and pathogen-based isolation precautions, cohorting of patients and healthcare personnel, hand hygiene, and environmental cleaning. This session will use recent examples from New Jersey pediatric long-term care facilities to highlight common infection control challenges that are encountered during healthcare facility and public health responses to non-influenza respiratory virus outbreaks. In the fall of 2018, the New Jersey Department of Health (NJDOH) received reports of outbreaks associated with adenovirus and parainfluenza virus occurring in multiple specialized pediatric long-term care facilities. Residents of these facilities had significant underlying medical conditions and required a high level of specialized care. Specific medical countermeasures, such as vaccines and antivirals, are not available for these non-influenza respiratory illnesses and therefore cannot be used to assist in outbreak control. The specialized nature of the medical care being provided at these facilities also presented challenges in outbreak response. Establishing, maintaining and monitoring infection control practices was paramount in the control of these healthcare outbreaks. NJDOH sought guidance from CDC's Division of Viral Diseases and Division of Healthcare Quality Promotion who served as valuable partners by providing resources and engaging in thoughtful discussion on infection control considerations associated with these outbreak responses. This session will also include a description of pertinent CDC healthcare infection control guidelines about non-influenza respiratory viruses and discussion of the challenges in implementing these guidelines in healthcare outbreak settings.

Submission Complete?	Yes
Committee Topic	Infectious Disease Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Collaboration; Outbreaks
Consider for Different Presentation?	No
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